Diabetes risk factors

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June 2, 2023

1 Setup

I am interested in medical research, so I have chosen the Diabetes prediction dataset from Kaggle as the topic of my homework project. The goal of this dataset is to predict whether someone will develop diabetes, based on key indicators of the disease.

1.1 Input data

The dataset is anonymised and contains the following data about 100,000 individuals:

- **Age**: Ranges from 0-80, diabetes is more common amongst older adults.
- **Gender**: Can also have an impact on a person's susceptibility.
- **Body Mass Index (BMI)**: Higher BMI values are linked to higher diabetes risk.
- **Hypertension**: Presistently elevated blood pressure in the arteries, linked to heart disease.
- **Heart disease**: Associated with a risk of developing diabetes.
- **Smoking history**: Considered as a risk factor, can worsen the complications of diabetes.
- **HbA1c level**: Hemoglobin A1c, measures blood sugar level over the past 2-3 months. Over 6.5% indicates diabetes.
- **Blood glucose level**: Key indicator of diabetes.
- **Diabetes**: Target value.

These are some of the key indicators of diabetes, along with demographic data, which could be used to determine risk factors for developing diabetes.

While it is not explicitly stated, I believe the data is on Type 2 diabetes, since Type 1 is a genetic condition.

1.2 Tools

I used Python, the `numpy` and `pandas` libraries for manipulation of the dataset, `matplotlib` and `seaborn` for plotting and visualising and `scipy` and `scikit-learn` for the various statistical analysis and evaluation tools they offer.

[1]:
```python
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import matplotlib.cm as cm
import seaborn as sns
from sklearn.linear_model import LinearRegression
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_squared_error
from scipy.stats import chi2_contingency
```

1.3 Data cleaning and sanity checks

The first step in working with data is making sure it is not flawed. There is no single method that we can follow and guarantee no issues persist, but essentially we need to be careful and thourough and make sure nothing weird is happening in the dataset.

First, I read in the dataset from the csv file.

[2]:
```
df = pd.read_csv('../data/diabetes_prediction_dataset.csv')
df.head(10)
```

[2]:
```
   gender   age  hypertension  heart_disease smoking_history    bmi  \
0  Female  80.0             0              1           never  25.19
1  Female  54.0             0              0         No Info  27.32
2    Male  28.0             0              0           never  27.32
3  Female  36.0             0              0         current  23.45
4    Male  76.0             1              1         current  20.14
5  Female  20.0             0              0           never  27.32
6  Female  44.0             0              0           never  19.31
7  Female  79.0             0              0         No Info  23.86
8    Male  42.0             0              0           never  33.64
9  Female  32.0             0              0           never  27.32

   HbA1c_level  blood_glucose_level  diabetes
0          6.6                  140         0
1          6.6                   80         0
2          5.7                  158         0
3          5.0                  155         0
4          4.8                  155         0
5          6.6                   85         0
6          6.5                  200         1
7          5.7                   85         0
8          4.8                  145         0
9          5.0                  100         0
```

I like check the value ranges for the data and make sure, that the columns are correctly typed:

[3]:
```
df.dtypes
```

[3]:
```
gender                  object
age                    float64
hypertension             int64
heart_disease            int64
smoking_history         object
bmi                    float64
HbA1c_level            float64
```

```
blood_glucose_level      int64
diabetes                 int64
dtype: object
```

We can use the describe method to check the value ranges of the columns:

[4]:
```
df.describe(include='all')
```

[4]:
```
        gender             age  hypertension  heart_disease smoking_history  \
count   100000   100000.000000  100000.00000  100000.000000          100000
unique       3             NaN           NaN            NaN               6
top     Female             NaN           NaN            NaN         No Info
freq     58552             NaN           NaN            NaN           35816
mean       NaN       41.885856       0.07485       0.039420             NaN
std        NaN       22.516840       0.26315       0.194593             NaN
min        NaN        0.080000       0.00000       0.000000             NaN
25%        NaN       24.000000       0.00000       0.000000             NaN
50%        NaN       43.000000       0.00000       0.000000             NaN
75%        NaN       60.000000       0.00000       0.000000             NaN
max        NaN       80.000000       1.00000       1.000000             NaN

                  bmi    HbA1c_level  blood_glucose_level       diabetes
count   100000.000000  100000.000000        100000.000000  100000.000000
unique            NaN            NaN                  NaN            NaN
top               NaN            NaN                  NaN            NaN
freq              NaN            NaN                  NaN            NaN
mean        27.320767       5.527507           138.058060       0.085000
std          6.636783       1.070672            40.708136       0.278883
min         10.010000       3.500000            80.000000       0.000000
25%         23.630000       4.800000           100.000000       0.000000
50%         27.320000       5.800000           140.000000       0.000000
75%         29.580000       6.200000           159.000000       0.000000
max         95.690000       9.000000           300.000000       1.000000
```

This shows, that `gender` and `smoking_history` are actually categorical columns (they have a few unique values), while `hypertension`, `heart_disease`, and `diabetes` are meant to be boolean, and finally `age` should be an integer.

[5]:
```
df['age'] = df['age'].astype(int)
df['gender'] = df['gender'].astype('category')
df['smoking_history'] = df['smoking_history'].astype('category')
df['hypertension'] = df['hypertension'].astype(bool)
df['heart_disease'] = df['heart_disease'].astype(bool)
df['diabetes'] = df['diabetes'].astype(bool)

df.dtypes
```

```
[5]: gender                     category
     age                           int32
     hypertension                   bool
     heart_disease                  bool
     smoking_history            category
     bmi                         float64
     HbA1c_level                 float64
     blood_glucose_level           int64
     diabetes                       bool
     dtype: object
```

Let's check our categorical values:

```
[6]: columns = df.select_dtypes(include='category').columns.tolist()

     for column in columns:
         values = sorted(list(df[column].unique()))
         print(column)
         print(values)
         print()
```

```
gender
['Female', 'Male', 'Other']

smoking_history
['No Info', 'current', 'ever', 'former', 'never', 'not current']
```

I would like to fix the inconsistent values in smoking_history:

```
[7]: df['smoking_history'] = df['smoking_history'].replace({'No Info': 'no_info',␣
       ↪'not current': 'not_current'})

     columns = df.select_dtypes(include='category').columns.tolist()

     for column in columns:
         values = sorted(list(df[column].unique()))
         print(column)
         print(values)
         print()
```

```
gender
['Female', 'Male', 'Other']

smoking_history
['current', 'ever', 'former', 'never', 'no_info', 'not_current']
```

1.3.1 Analising the column values and their distribution

When our data comes from a third party, and we have not collected it ourselves, it is a good idea to check for any inconsistencies in the values.

First, I checked that no values were missing.

[8]:
```
df.isna().sum()
```

[8]:
```
gender                 0
age                    0
hypertension           0
heart_disease          0
smoking_history        0
bmi                    0
HbA1c_level            0
blood_glucose_level    0
diabetes               0
dtype: int64
```

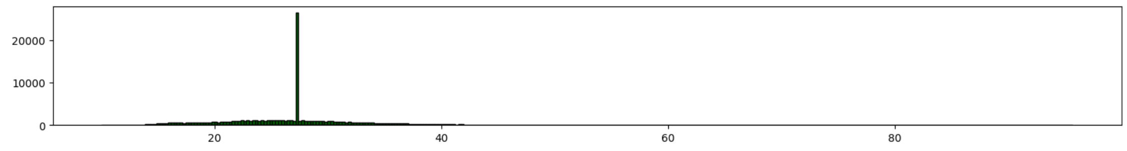
If there were missing values, we could drop them with `df.dropna(inplace=True)`, but it is not needed.

BMI The first weirdness I noticed was with BMI.

Let us plot the values of BMI in a histogram:

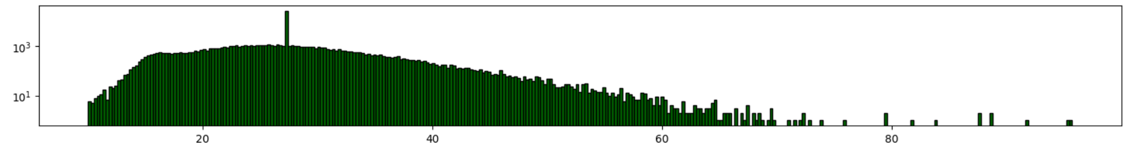
[9]:
```
values = df['bmi']
counts, bins, _ = plt.hist(values, bins='auto', color='darkgreen',␣
  ↪edgecolor='black')

plt.gcf().set_size_inches(18, 2)
plt.show()
```



That doesn't look good. I kept increasing the bins, before leaving them auto, but that singular peak will not disappear. Let's try logarithmic scale, so we can at least see something:

[10]:
```
values = df['bmi']
counts, bins, _ = plt.hist(values, bins='auto', color='darkgreen',␣
  ↪edgecolor='black')
plt.yscale('log')
plt.gcf().set_size_inches(18, 2)
plt.show()
```



Is that a single value of BMI? Let's count the most common values:

[11]:
```
max_count_bin = np.argmax(counts)
max_count = counts[max_count_bin]
max_bin_range = (bins[max_count_bin], bins[max_count_bin + 1])

max_bin_range

unique_values, counts = np.unique(values, return_counts=True)
sorted_indices = np.argsort(counts)[::-1]
sorted_values = unique_values[sorted_indices]
sorted_counts = counts[sorted_indices]

top_10_values = sorted_values[:10]
top_10_counts = sorted_counts[:10]

print(top_10_values)
print(top_10_counts)
```

```
[27.32 23.   27.12 27.8  24.96 22.4  25.   25.6  26.7  24.5 ]
[25495   103   101   100   100    99    99    98    94    94]
```

Yes, for some reason, we have over $\frac{1}{4}$ entries of the dataset with the exact BMI of 27.32. Let's look at these:

[12]:
```
weird_entries = df[df['bmi'] == 27.32]

weird_entries.head(10)
```

[12]:
```
    gender  age  hypertension  heart_disease smoking_history    bmi
1   Female   54         False          False         no_info  27.32  \
2     Male   28         False          False           never  27.32
5   Female   20         False          False           never  27.32
9   Female   32         False          False           never  27.32
10  Female   53         False          False           never  27.32
14  Female   76         False          False         no_info  27.32
15    Male   78         False          False         no_info  27.32
18  Female   42         False          False         no_info  27.32
26    Male   67         False           True     not_current  27.32
```

```
38    Male   50           True          False         current  27.32

    HbA1c_level  blood_glucose_level  diabetes
1           6.6                   80     False
2           5.7                  158     False
5           6.6                   85     False
9           5.0                  100     False
10          6.1                   85     False
14          5.0                  160     False
15          6.6                  126     False
18          5.7                   80     False
26          6.5                  200      True
38          5.7                  260      True
```

These all seem like real entries, not duplicates of the same entry. My best guess for what happened, is that when the BMI was missing, they put down the mean of the rest of the dataset, which is exactly `27.32`.

[13]:
```
df[df['bmi'] != 27.32]['bmi'].mean()
```

[13]:
```
27.321029595329176
```

In a real life scenario, I would clearify this with the person who gave me the data, however for this homework project, I will assume that when a person looks average weight, they may not bother measuring their BMI, so the average is probably a good approximation, so I will accept this.

Another concern I had was with extreme cases of BMI, such as the values 80 and above. I choose to keep these, because they are not overrepresented and diabetes is linked to extreme obesity, so these are important entry points for prediction.

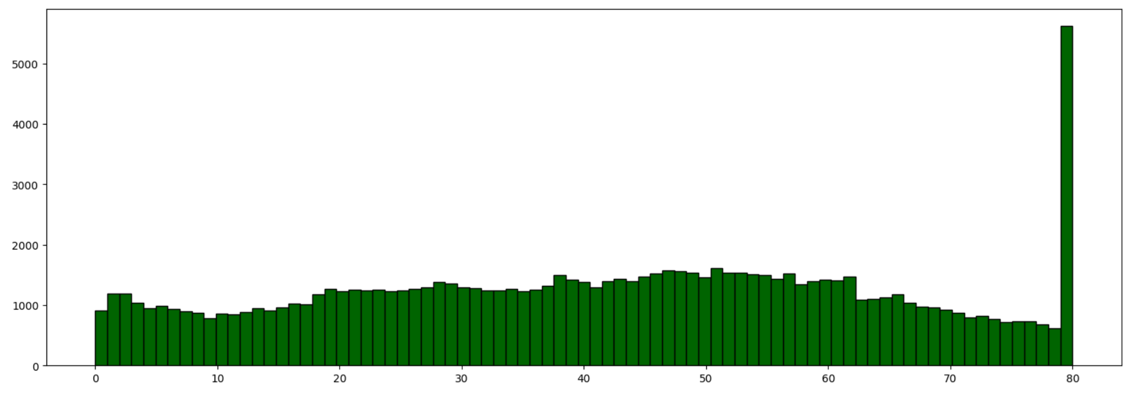
1.3.2 Age

Next issue is with the age.

Let's plot the values:

[14]:
```
values = df['age']
num_bins = values.nunique()
counts, bins, _ = plt.hist(values, bins=num_bins, color='darkgreen',␣
  ↪edgecolor='black')

plt.gcf().set_size_inches(18, 6)
plt.show()
```



We have a lot of people aged 80. It looks like older people are overrepresented in this data and probably not all of them are exactly 80, they just cut off the age to fit into a [0,80] interval.

[15]:
```
df[df['age']==80]['age'].count()
```

[15]:
```
5621
```

In this case, I choose to remove these values, because I feel like this could cause some skewing.

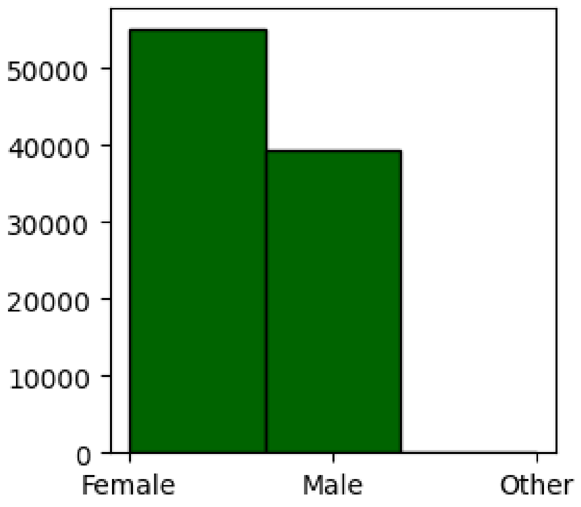
[16]:
```
df = df[df['age'] < 80]
```

1.3.3 Gender

Let's plot the values:

[17]:
```
values = df['gender']
num_bins = values.nunique()
counts, bins, _ = plt.hist(values, bins=num_bins, color='darkgreen',␣
 ↪edgecolor='black')

plt.gcf().set_size_inches(3, 3)
plt.show()
```



The category Other can mean many things. For medical research, we are concerned about the biological sex of the participants, so I will remove these entries too.

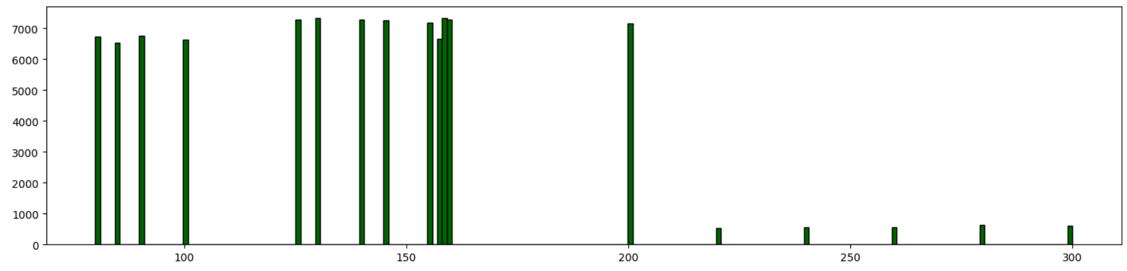
[18]:
```
df = df[df['gender'] != 'Other']
df['gender'] = df['gender'].cat.remove_categories('Other')
df['gender'].unique()
```

[18]:
```
['Female', 'Male']
Categories (2, object): ['Female', 'Male']
```

1.3.4 Blood glucose level

[19]:
```
values = df['blood_glucose_level']
counts, bins, _ = plt.hist(values, bins=200, color='darkgreen',␣
 ↪edgecolor='black')

plt.gcf().set_size_inches(18, 4)
plt.show()
```

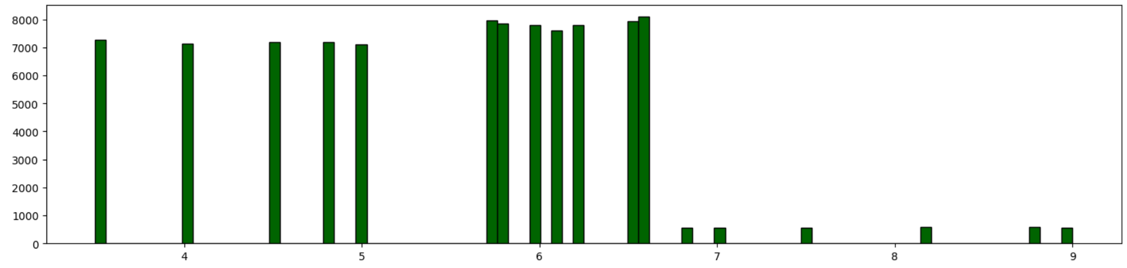


It seems like this is not a continuous spectrum. There is also a concentration of values around 155-160. I'm not sure how to interpret this. The values are probably in mg/dl. For fasting levels, 80-100 is normal, 101-125 is elevated and above 126 is high. Other than that, I would need to ask someone with medical knowledge on why this is happening. For now, I have to accept these, as there is no clear way on how to fix them or if they need to be fixed at all.

1.3.5 Blood sugar level

[20]:
```
values = df['HbA1c_level']
counts, bins, _ = plt.hist(values, bins='auto', color='darkgreen',␣
  ↪edgecolor='black')

plt.gcf().set_size_inches(18, 4)
plt.show()
```



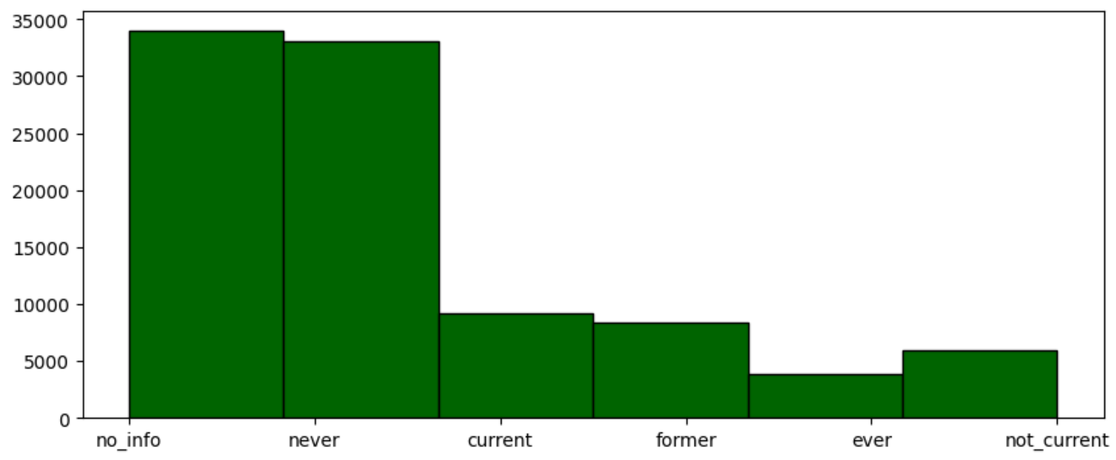
For HbA1c, less than 5.6% is normal, between 5.7% - 6.4% is elevated (prediabetes) and above 6.5% is high (diabetes).

Although increasing the granuality does reveal that not every value is represented, but the precision is only one digit after the integer, so I think this looks okay.

1.3.6 Smoking history

[21]:
```
values = df['smoking_history']
num_bins = values.nunique()
counts, bins, _ = plt.hist(values, bins=num_bins, color='darkgreen',␣
  ↪edgecolor='black')

plt.gcf().set_size_inches(10, 4)
plt.show()
```



We have a large amount of entries with `no_info` as a value. It might be worth removing these later, but I will keep them in for now, because they represent a large chunk of our data.

I was also questioning what `ever` means, given the other possibilities present, but I think it means they have tried smoking in the past, but weren't addicted.

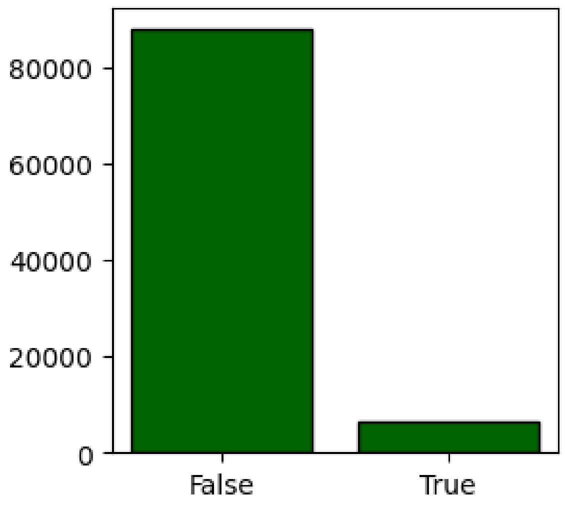
1.3.7 Hypertension

It seems like a reasonable distribution.

[22]:
```
df['hypertension'].value_counts()

value_counts = df['hypertension'].value_counts()

# Plot
plt.figure(figsize=(3,3))
plt.bar(value_counts.index, value_counts.values, color='darkgreen',␣
  ↪edgecolor='black')
plt.xticks(ticks=[0,1], labels=['False', 'True'])
plt.show()
```



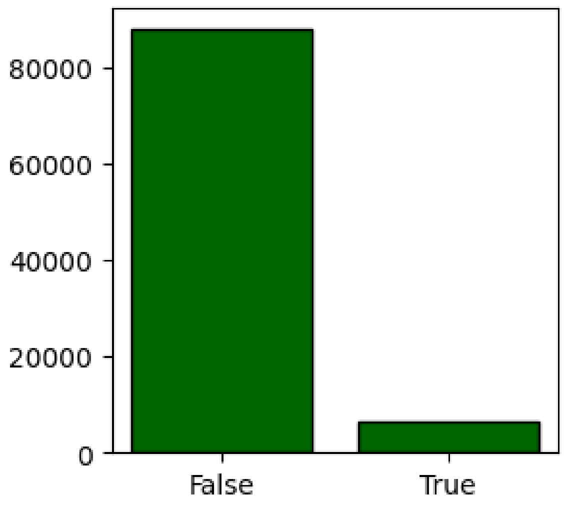
1.3.8 Heart disease

Similarly, this looks okay.

```
[23]: df['heart_disease'].value_counts()

      value_counts = df['hypertension'].value_counts()

      # Plot
      plt.figure(figsize=(3,3))
      plt.bar(value_counts.index, value_counts.values, color='darkgreen',␣
       ↪edgecolor='black')
      plt.xticks(ticks=[0,1], labels=['False', 'True'])
      plt.show()
```



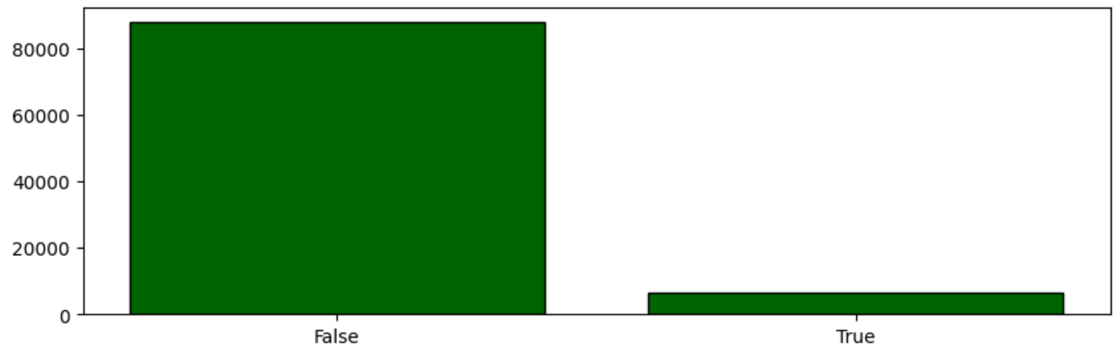
1.3.9 Diabetes

And our target value. This seems like a good ratio, similar to the generic population.

```
[24]: df['diabetes'].value_counts()

      value_counts = df['hypertension'].value_counts()

      # Plot
      plt.figure(figsize=(10,3))
      plt.bar(value_counts.index, value_counts.values, color='darkgreen',␣
        ↪edgecolor='black')
      plt.xticks(ticks=[0,1], labels=['False', 'True'])
      plt.show()
```



2 Analysis

2.1 Multivariate linear regression

The first thing I will try is create a multivariate linear regression model, using all of the available variables.

In order to do this, we must convert the categorical variables into 0/1 variables. This can be done with the `get_dummies` function, as seen below.

```
[25]: df_encoded = pd.get_dummies(df)
      df_encoded.head()
```

```
[25]:    age  hypertension  heart_disease    bmi  HbA1c_level  blood_glucose_level
      1   54         False          False  27.32          6.6                   80  \
      2   28         False          False  27.32          5.7                  158
      3   36         False          False  23.45          5.0                  155
```

```
4   76          True            True  20.14          4.8                 155
5   20         False           False  27.32          6.6                  85

   diabetes  gender_Female  gender_Male  smoking_history_no_info
1     False           True        False                     True  \
2     False          False         True                    False
3     False           True        False                    False
4     False          False         True                    False
5     False           True        False                    False

   smoking_history_current  smoking_history_ever  smoking_history_former
1                    False                 False                   False  \
2                    False                 False                   False
3                     True                 False                   False
4                     True                 False                   False
5                    False                 False                   False

   smoking_history_never  smoking_history_not_current
1                  False                        False
2                   True                        False
3                  False                        False
4                  False                        False
5                   True                        False
```

Then, we separate our target variable.

[26]:
```python
X = df_encoded.drop('diabetes', axis=1)
y = df_encoded['diabetes']
```

And split the data into training and testing datasets, with the ratio of 80% and 20%. It is good practice to seed the pseudorandom generator, so it will always result in the same split, across multiple runs of our notebook.

[27]:
```python
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,␣
 ↪random_state=42)
```

Then we create our multivariate linear regression model, using `scikit-learn`.

[28]:
```python
model = LinearRegression()
model.fit(X_train, y_train)
```

[28]:
```
LinearRegression()
```

The model's coefficients are as follows:

[29]:
```python
coefficients = pd.DataFrame({'Variable': X.columns, 'Coefficient': model.
 ↪coef_}).sort_values(by='Coefficient', ascending=False)
intercept = pd.DataFrame({'Variable': ['Intercept'], 'Coefficient': model.
 ↪intercept_})
```

```
print("Coefficients:")
print(coefficients)
print("\nIntercept:")
print(intercept)
```

```
Coefficients:
                      Variable  Coefficient
2                heart_disease     0.133472
1                 hypertension     0.103687
4                  HbA1c_level     0.076937
11      smoking_history_former     0.015804
7                  gender_Male     0.006450
3                          bmi     0.004050
5          blood_glucose_level     0.002163
13  smoking_history_not_current     0.001371
0                          age     0.001358
10        smoking_history_ever    -0.001578
9      smoking_history_current    -0.001865
12       smoking_history_never    -0.003399
6                gender_Female    -0.006450
8      smoking_history_no_info    -0.010332

Intercept:
    Variable  Coefficient
0  Intercept    -0.814089
```

It is important to note here immediately, that the scale of these coefficients depends on their value sets. For example, gender_Male is between 0 and 1, while BMI is between 10 and 100. For this reason, we cannot compare the relative values of the coefficients, without taking into account the possible values of the variables behind them.

However, the signs (positive or negative) can be looked at and compared, which we will do shortly.

But first, the precision of this model on the test dataset is as follows:

[30]:
```
y_pred = model.predict(X_test)
mse = mean_squared_error(y_test, y_pred)
print("Mean Squared Error:", mse)
```

```
Mean Squared Error: 0.04693052558568325
```

And on the train dataset:

[31]:
```
y_pred = model.predict(X_train)
mse = mean_squared_error(y_train, y_pred)
print("Mean Squared Error:", mse)
```

```
Mean Squared Error: 0.048474640595590854
```

We can conclude, that the model was not overfit and the error is relatively low.

2.2 Independence testing

2.2.1 Gender

Examining the coefficients, the first thing I noticed is the `gender` variables. It seems that, with all other variables present, being male slightly increases, while being female slightly reduces the risk of diabetes.

I wonder if without the other variables, what could we say about the influence of gender on diabetes? I will test the independence of the `gender` and `diabetes` variables in the original dataset using Chi-square test of independence.

At first, I will create the frequency table of their values:

[32]:
```python
crosstab = pd.crosstab(df['gender'], df['diabetes'])
crosstab
```

[32]:
```
diabetes  False  True
gender
Female    51188  3856
Male      35697  3620
```

Then, I will use `scipy`, to compute a Pearson's chi-squared statistic.

The null hypothesis is that the variables are independent.

[33]:
```python
chi2, p, dof, expected = chi2_contingency(crosstab)
print(f"Chi-square value: {chi2}")
print(f"P-value: {p}")
print(f"Degrees of freedom: {dof}")
print("Expected:")
print(expected)
```

```
Chi-square value: 152.1271942474673
P-value: 5.94328803769177e-35
Degrees of freedom: 1
Expected:
[[50682.9933977  4361.0066023]
 [36202.0066023  3114.9933977]]
```

With a p-value of $p = 5,94 \cdot 10^{-35}$ we can say, that we have very strong evidence against our null hypothesis, therefore we can conclude that gender and diabetes are indeed correlated with each other.

The gender of a person influences the likelihood of developing diabetes.

As we can see in the Expected matrix, that is the expected frequencies for the same population size, were these variables independent of each other. We can see that we got less than expected females with diabetes and more than expected males with diabetes.

2.2.2 Smoking history

The other interesting thing I noticed about the multivariate linear regression coefficients is that `smoking_history_current` has a negative coefficient, while `smoking_history_former` and `smoking_history_not_current` have positive coefficients. At least `smoking_history_never` has a negative coefficient too, which makes perfect sense.

I do have tales from friends and family saying that when someone chooses to stop smoking is when the problems start. A more likely explanation is that when people stop smoking, the damage has already been done. When someone is still smoking, maybe they have less years behind them and quitting smoking **earlier** should help lower the risk of diabetes and heart disease (amongst many diseases).

[34]:
```
crosstab = pd.crosstab(df['smoking_history'], df['diabetes'])
crosstab
```

[34]:
```
diabetes          False  True
smoking_history
no_info           32751  1260
current            8227   924
ever               3376   436
former             7004  1372
never             30181  2878
not_current        5346   606
```

[35]:
```
chi2, p, dof, expected = chi2_contingency(crosstab)
print(f"Chi-square value: {chi2}")
print(f"P-value: {p}")
print(f"Degrees of freedom: {dof}")
print("Expected:")
print(expected)
```

```
Chi-square value: 1844.0298560488386
P-value: 0.0
Degrees of freedom: 5
Expected:
[[31316.38849737  2694.61150263]
 [ 8425.98780216   725.01219784]
 [ 3509.98420958   302.01579042]
 [ 7712.3892286    663.6107714 ]
 [30439.81321732  2619.18678268]
 [ 5480.43704497   471.56295503]]
```

[36]:
```
crosstab = pd.crosstab(df['smoking_history'], df['diabetes'])
crosstab
```

[36]:
```
diabetes          False  True
smoking_history
no_info           32751  1260
```

```
current          8227    924
ever             3376    436
former           7004   1372
never           30181   2878
not_current      5346    606
```

[37]:
```
chi2, p, dof, expected = chi2_contingency(crosstab)
print(f"Chi-square value: {chi2}")
print(f"P-value: {p}")
print(f"Degrees of freedom: {dof}")
print("Expected:")
print(expected)
```

```
Chi-square value: 1844.0298560488386
P-value: 0.0
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Expected:
[[31316.38849737  2694.61150263]
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 [30439.81321732  2619.18678268]
 [ 5480.43704497   471.56295503]]
```

The p-value is so small, the numerical representation cannot display it. This means smoking history has indeed a strong influence on whether or not someone develops diabetes.

I would like to further investigate this relationship. Since diabetes is a binary variable, it is hard to see exactly the effects of smoking on it. However, we have a few numerical variables in the dataset, which are strong indicators of diabetes, such as various measurements of blood levels and BMI.

So I will continue exploring the effects of smoking on these variables further.

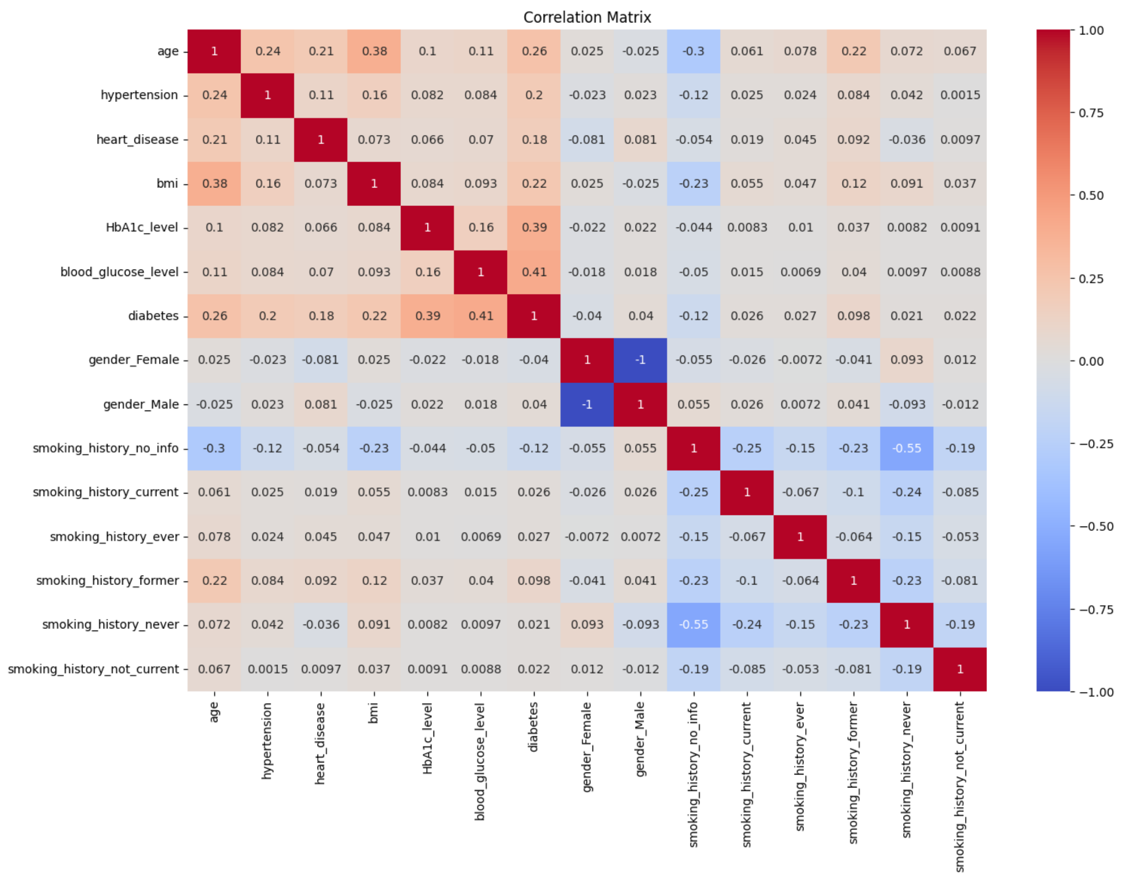
2.3 Correlation matrix

In order to establish which numerical variables have a strong relationship with diabetes, I will be using a correlation matrix heatmap to visualise these 1-1 relationships.

[38]:
```
correlation_matrix = df_encoded.corr()

plt.figure(figsize=(15, 10))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm', center=0)

plt.title('Correlation Matrix')
plt.show()
```



We can see on the heatmap, that `blood_glucose_level` and `HbA1c_level` have the strongest correlation to diabetes, so I will be exploring the effects of smoking on these variables.

2.4 Testing the mean of categories

Smoking history is a categorical variable, which means it defines different groups of people. For these groups, I can calculate the mean of `blood_glucose_level` and `HbA1c_level`, then, I can investigate whether or not the differences in the results are statistically significant.

[39]:
```
df.groupby('smoking_history')[['blood_glucose_level']].mean().
↪sort_values('blood_glucose_level')
```

[39]:
```
                 blood_glucose_level
smoking_history
no_info                   135.019729
never                     138.245107
ever                      139.076600
not_current               139.088878
current                   139.614905
former                    142.896968
```

Here, we can see that the average blood glucose level slightly increases, as someone has more history with smoking. Interestingly again, current smokers rank below former smokers. This can again be due to the fact that former smokers may have a longer smoking history than current smokers.

```
[40]: df.groupby('smoking_history')[['HbA1c_level']].mean().sort_values('HbA1c_level')
```

```
[40]:                  HbA1c_level
      smoking_history
      no_info             5.457690
      never               5.531640
      current             5.546694
      not_current         5.557023
      ever                5.571800
      former              5.646036
```

However, for `HbA1c_level`, the level of `ever`, which I assume means "smoked a bit a long time ago" seems really high on the ranking.

```
[41]: import scipy.stats as stats

      # Get the unique categories of smoking history
      smoking_categories = ['ever', 'former'] # df['smoking_history'].unique()

      # Create a list comprehension to create list of 'HbA1c_level' for each smoking␣
       ↪history category
      data = [df.loc[df['smoking_history'] == category, 'HbA1c_level'] for category␣
       ↪in smoking_categories]

      # Perform the ANOVA
      f_stat, p_val = stats.f_oneway(*data)

      print('F statistic:', f_stat)
      print('p-value:', p_val)
```

```
F statistic: 11.402418239496091
p-value: 0.0007357788133329733
```