In [320…

```
pip install pandas numpy scikit-learn matplotlib seaborn imblearn shap
```

```
Requirement already satisfied: pandas in c:\users\lzyda\appdata\local\packages\pytho
nsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python310\si
te-packages (1.5.3)
Requirement already satisfied: numpy in c:\users\lzyda\appdata\local\packages\python
softwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python310\sit
e-packages (1.23.5)
Requirement already satisfied: scikit-learn in c:\users\lzyda\appdata\local\packages
\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python
310\site-packages (1.3.2)
Requirement already satisfied: matplotlib in c:\users\lzyda\appdata\local\packages\p
ythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python31
0\site-packages (3.6.3)
Requirement already satisfied: seaborn in c:\users\lzyda\appdata\local\packages\pyth
onsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python310\s
ite-packages (0.13.1)
Requirement already satisfied: imblearn in c:\users\lzyda\appdata\local\packages\pyt
honsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python310
\site-packages (0.0)
Collecting shap
  Obtaining dependency information for shap from https://files.pythonhosted.org/pack
ages/61/8d/d0790fbbde36aeed7e87516f15d163daddb07ca34c6f736e29e02bddf4c7/shap-0.44.0-
cp310-cp310-win_amd64.whl.metadata
  Downloading shap-0.44.0-cp310-cp310-win_amd64.whl.metadata (24 kB)
Requirement already satisfied: python-dateutil>=2.8.1 in c:\users\lzyda\appdata\loca
l\packages\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packa
ges\python310\site-packages (from pandas) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in c:\users\lzyda\appdata\local\packages
\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python
310\site-packages (from pandas) (2023.3)
Requirement already satisfied: scipy>=1.5.0 in c:\users\lzyda\appdata\local\packages
\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python
310\site-packages (from scikit-learn) (1.11.4)
Requirement already satisfied: joblib>=1.1.1 in c:\users\lzyda\appdata\local\package
s\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\pytho
n310\site-packages (from scikit-learn) (1.3.1)
Requirement already satisfied: threadpoolctl>=2.0.0 in c:\users\lzyda\appdata\local
\packages\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packag
es\python310\site-packages (from scikit-learn) (3.2.0)
Requirement already satisfied: contourpy>=1.0.1 in c:\users\lzyda\appdata\local\pack
ages\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\py
thon310\site-packages (from matplotlib) (1.0.7)
Requirement already satisfied: cycler>=0.10 in c:\users\lzyda\appdata\local\packages
\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python
310\site-packages (from matplotlib) (0.11.0)
Requirement already satisfied: fonttools>=4.22.0 in c:\users\lzyda\appdata\local\pac
kages\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\p
ython310\site-packages (from matplotlib) (4.38.0)
Requirement already satisfied: kiwisolver>=1.0.1 in c:\users\lzyda\appdata\local\pac
kages\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\p
ython310\site-packages (from matplotlib) (1.4.4)
Requirement already satisfied: packaging>=20.0 in c:\users\lzyda\appdata\local\packa
ges\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\pyt
hon310\site-packages (from matplotlib) (23.1)
Requirement already satisfied: pillow>=6.2.0 in c:\users\lzyda\appdata\local\package
s\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\pytho
n310\site-packages (from matplotlib) (9.5.0)
```

```
Requirement already satisfied: pyparsing>=2.2.1 in c:\users\lzyda\appdata\local\pack
ages\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\py
thon310\site-packages (from matplotlib) (3.0.9)
Requirement already satisfied: imbalanced-learn in c:\users\lzyda\appdata\local\pack
ages\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\py
thon310\site-packages (from imblearn) (0.11.0)
Requirement already satisfied: tqdm>=4.27.0 in c:\users\lzyda\appdata\local\packages
\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python
310\site-packages (from shap) (4.65.0)
Collecting slicer==0.0.7 (from shap)
  Downloading slicer-0.0.7-py3-none-any.whl (14 kB)
Requirement already satisfied: numba in c:\users\lzyda\appdata\local\packages\python
softwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python310\sit
e-packages (from shap) (0.58.1)
Collecting cloudpickle (from shap)
  Obtaining dependency information for cloudpickle from https://files.pythonhosted.o
rg/packages/96/43/dae06432d0c4b1dc9e9149ad37b4ca8384cf6eb7700cd9215b177b914f0a/cloud
pickle-3.0.0-py3-none-any.whl.metadata
  Downloading cloudpickle-3.0.0-py3-none-any.whl.metadata (7.0 kB)
Requirement already satisfied: six>=1.5 in c:\users\lzyda\appdata\local\packages\pyt
honsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python310
\site-packages (from python-dateutil>=2.8.1->pandas) (1.16.0)
Requirement already satisfied: colorama in c:\users\lzyda\appdata\local\packages\pyt
honsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-packages\python310
\site-packages (from tqdm>=4.27.0->shap) (0.4.6)
Requirement already satisfied: llvmlite<0.42,>=0.41.0dev0 in c:\users\lzyda\appdata
\local\packages\pythonsoftwarefoundation.python.3.10_qbz5n2kfra8p0\localcache\local-
packages\python310\site-packages (from numba->shap) (0.41.1)
Downloading shap-0.44.0-cp310-cp310-win_amd64.whl (447 kB)
   ---------------------------------------- 0.0/448.0 kB ? eta -:--:--
   ---------------------------------------  440.3/448.0 kB 13.9 MB/s eta 0:00:01
   ---------------------------------------- 448.0/448.0 kB 9.3 MB/s eta 0:00:00
Downloading cloudpickle-3.0.0-py3-none-any.whl (20 kB)
Installing collected packages: slicer, cloudpickle, shap
Successfully installed cloudpickle-3.0.0 shap-0.44.0 slicer-0.0.7
Note: you may need to restart the kernel to use updated packages.
[notice] A new release of pip is available: 23.2.1 -> 23.3.2
[notice] To update, run: C:\Users\lzyda\AppData\Local\Microsoft\WindowsApps\PythonSo
ftwareFoundation.Python.3.10_qbz5n2kfra8p0\python.exe -m pip install --upgrade pip
```

In [234…

```
## Data Acquisition and Processing
```

In [262…

```
import pandas as pd

nhgh_file_path = "./nhgh.tsv"
data = pd.read_csv(nhgh_file_path, sep='\t')

data.head()
```

Out[262…

	seqn	sex	age	re	income	tx	dx	wt	ht	bmi	leg	arr
0	51624	male	34.166667	Non-Hispanic White	[25000,35000)	0	0	87.4	164.7	32.22	41.5	40
1	51626	male	16.833333	Non-Hispanic Black	[45000,55000)	0	0	72.3	181.3	22.00	42.0	39
2	51628	female	60.166667	Non-Hispanic Black	[10000,15000)	1	1	116.8	166.0	42.39	35.3	39
3	51629	male	26.083333	Mexican American	[25000,35000)	0	0	97.6	173.0	32.61	41.7	38
4	51630	female	49.666667	Non-Hispanic White	[35000,45000)	0	0	86.7	168.4	30.57	37.5	36

In [263…

```
# Convert to tidy format and ensure data types are correct and consistent

# Check for missing values
missing_values = data.isnull().sum()

# Normalize strings to lowercase
data.columns = [col.lower() for col in data.columns]

print("Missing Values:\n", missing_values)
print("\nData Types:\n", data.dtypes)
```

```
Missing Values:
 seqn         0
sex           0
age           0
re            0
income      320
tx            0
dx            0
wt            0
ht            0
bmi           0
leg         231
arml        179
armc        188
waist       239
tri         481
sub         971
gh            0
albumin      89
bun          89
SCr          89
dtype: int64

Data Types:
 seqn          int64
sex           object
age          float64
re            object
income        object
tx             int64
dx             int64
wt           float64
ht           float64
bmi          float64
leg          float64
arml         float64
armc         float64
waist        float64
tri          float64
sub          float64
gh           float64
albumin      float64
bun          float64
scr          float64
dtype: object
```

In [264…

```python
from sklearn.impute import SimpleImputer

# Normalize data within the 're' column to lowercase
data['re'] = data['re'].str.lower()

# Convert to correct type based on data repo
# Convert 'bun' to numeric, coerce errors, and then to int
data['bun'] = pd.to_numeric(data['bun'], errors='coerce').astype('Int64')

# Create an imputer object with a median filling strategy
```

```
numeric_imputer = SimpleImputer(strategy='median')

# List of columns to impute
columns_to_impute = ['leg', 'arml', 'armc', 'waist', 'tri', 'sub',
                     'albumin', 'bun', 'scr']

# Apply imputation to the specified columns
data[columns_to_impute] = numeric_imputer.fit_transform(data[columns_to_impute])

# For categorical variable 'income', impute with the mode
income_imputer = SimpleImputer(strategy='most_frequent')
data['income'] = income_imputer.fit_transform(data[['income']])

# Check for missing values again to confirm the imputation
missing_values_after_imputation = data.isnull().sum()
print("Missing Values After Imputation:\n", missing_values_after_imputation)
```

```
Missing Values After Imputation:
 seqn       0
sex         0
age         0
re          0
income      0
tx          0
dx          0
wt          0
ht          0
bmi         0
leg         0
arml        0
armc        0
waist       0
tri         0
sub         0
gh          0
albumin     0
bun         0
scr         0
dtype: int64
```

In [265…

```
# Double check if string type enums follows the legend
sex_types = ["male", "female"]

re_types = ["mexican american", "other hispanic", "non-hispanic white",
            "non-hispanic black", "other race including multi-racial"]

income_types = ["[0,5000)", "[5000,10000)", "[10000,15000)", "[15000,20000)",
                "[20000,25000)", "[25000,35000)", "[35000,45000)",
                "[45000,55000)", "[55000,65000)", "[65000,75000)",
                "> 20000", "< 20000", "[75000,100000)", ">= 100000"]

# Check for inconsistencies in 'sex'
sex_check = data['sex'].str.lower().isin(sex_types)

# Check for inconsistencies in 're'
re_check = data['re'].str.lower().isin(re_types)
```

```
# Check for inconsistencies in 'income'
income_check = data['income'].str.lower().isin(income_types)

# Count of rows not matching the types
non_matching_sex = data[~sex_check].shape[0]
non_matching_re = data[~re_check].shape[0]
non_matching_income = data[data['income'].notna()  & ~income_check].shape[0] # ther



(non_matching_sex, non_matching_re, non_matching_income)
# Ideally, we want (0,0,0), which indicates all values follow the the enum values
```

Out[265… (0, 0, 0)

In [266…
```
# Create a binary variable for diabetes status as it is useful for us
# Assuming 'gh' is the glycohemoglobin level and 6.5% or higher indicates diabetes
data['diabetes_status'] = data['gh'] >= 6.5
```

In [267…
```
# SQLite3 Integration and export
import sqlite3

with sqlite3.connect("./diabetes_data.db") as conn:
    data.to_sql("diabetes_data", conn, if_exists="replace", index=False)
```

In [268…
```
# Testing some SQL Queries:

# get number of people with diabetes based by gender
with sqlite3.connect('./diabetes_data.db') as conn:
    query = """
    SELECT COUNT(*) as Num, sex
    FROM diabetes_data
    WHERE gh >= 6.5
    GROUP BY sex
    """
    diabetes_patients = pd.read_sql_query(query, conn)

# Display the first few rows of the retrieved data
diabetes_patients.head()
```

Out[268…

	Num	sex
0	291	female
1	337	male

In [269…
```
with sqlite3.connect('./diabetes_data.db') as conn:
    male_query = """
    SELECT COUNT(*) as Num, re, sex
    FROM diabetes_data
    WHERE gh >= 6.5 AND sex = 'male'
    GROUP BY re
    """
```

```
    male_diabetes_patients_by_re = pd.read_sql_query(male_query, conn)

# Display the first few rows of the retrieved data
male_diabetes_patients_by_re.head()
```

Out[269…

	Num	re	sex
0	79	mexican american	male
1	69	non-hispanic black	male
2	137	non-hispanic white	male
3	32	other hispanic	male
4	20	other race including multi-racial	male

In [270…

```
with sqlite3.connect('./diabetes_data.db') as conn:
    female_query = """
    SELECT COUNT(*) as Num, re, sex
    FROM diabetes_data
    WHERE gh >= 6.5 AND sex = 'female'
    GROUP BY re
    """
    female_diabetes_patients_by_re = pd.read_sql_query(female_query, conn)

# Display the first few rows of the retrieved data
female_diabetes_patients_by_re.head()
```

Out[270…

	Num	re	sex
0	77	mexican american	female
1	66	non-hispanic black	female
2	88	non-hispanic white	female
3	35	other hispanic	female
4	25	other race including multi-racial	female

In [271…

```
# Exploratory Data Analysis

# explore and plot some distributions
```

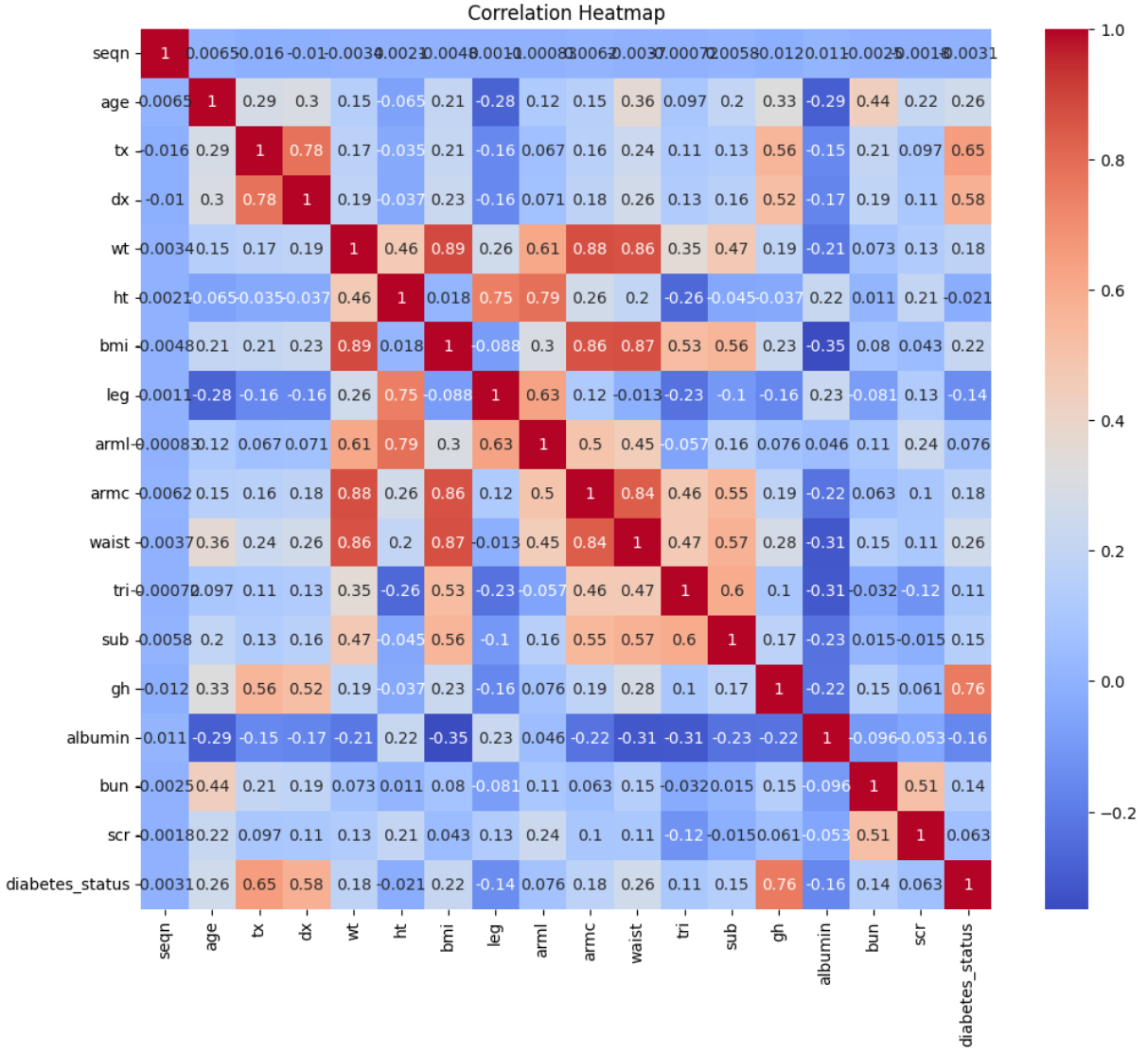
In [272…

```
import matplotlib.pyplot as plt
import seaborn as sns
```

In [273…

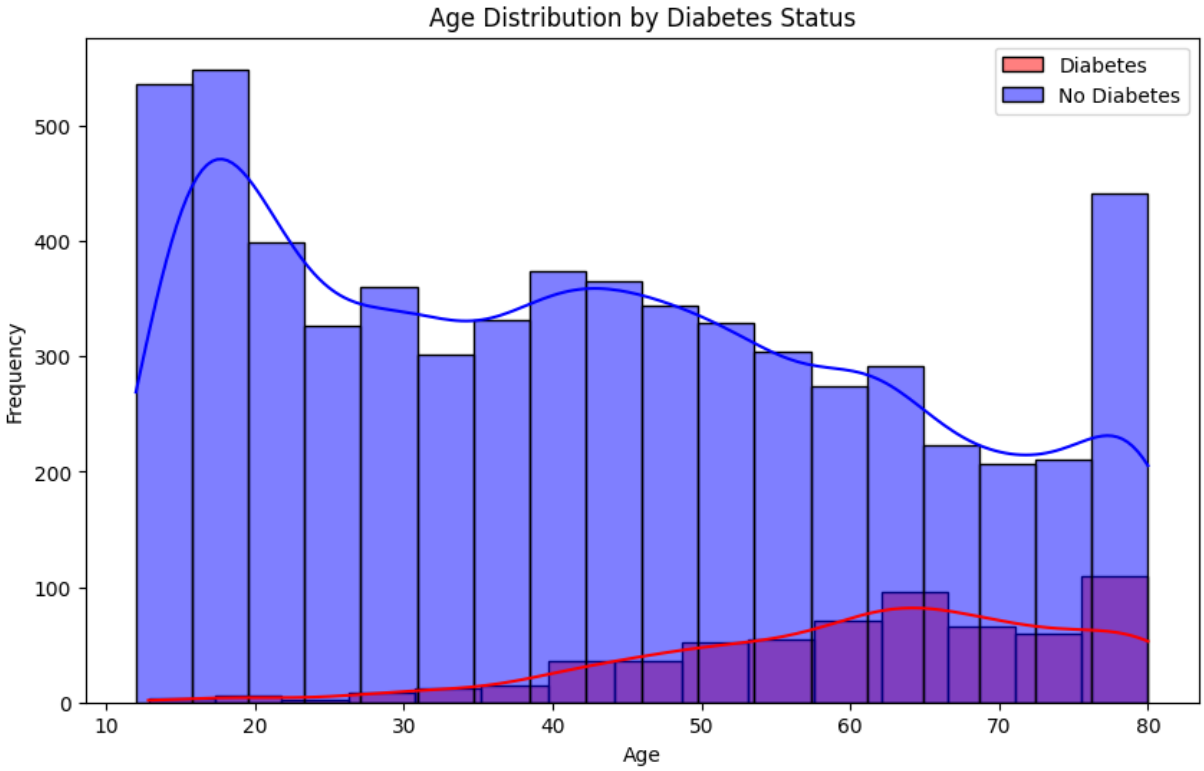
```
# Correlation Heatmap
plt.figure(figsize=(12, 10))
sns.heatmap(data.corr(), annot=True, cmap='coolwarm')
plt.title('Correlation Heatmap')
plt.show()
```

```
C:\Users\lzyda\AppData\Local\Temp\ipykernel_40768\1044403631.py:3: FutureWarning: Th
e default value of numeric_only in DataFrame.corr is deprecated. In a future versio
n, it will default to False. Select only valid columns or specify the value of numer
ic_only to silence this warning.
  sns.heatmap(data.corr(), annot=True, cmap='coolwarm')
```



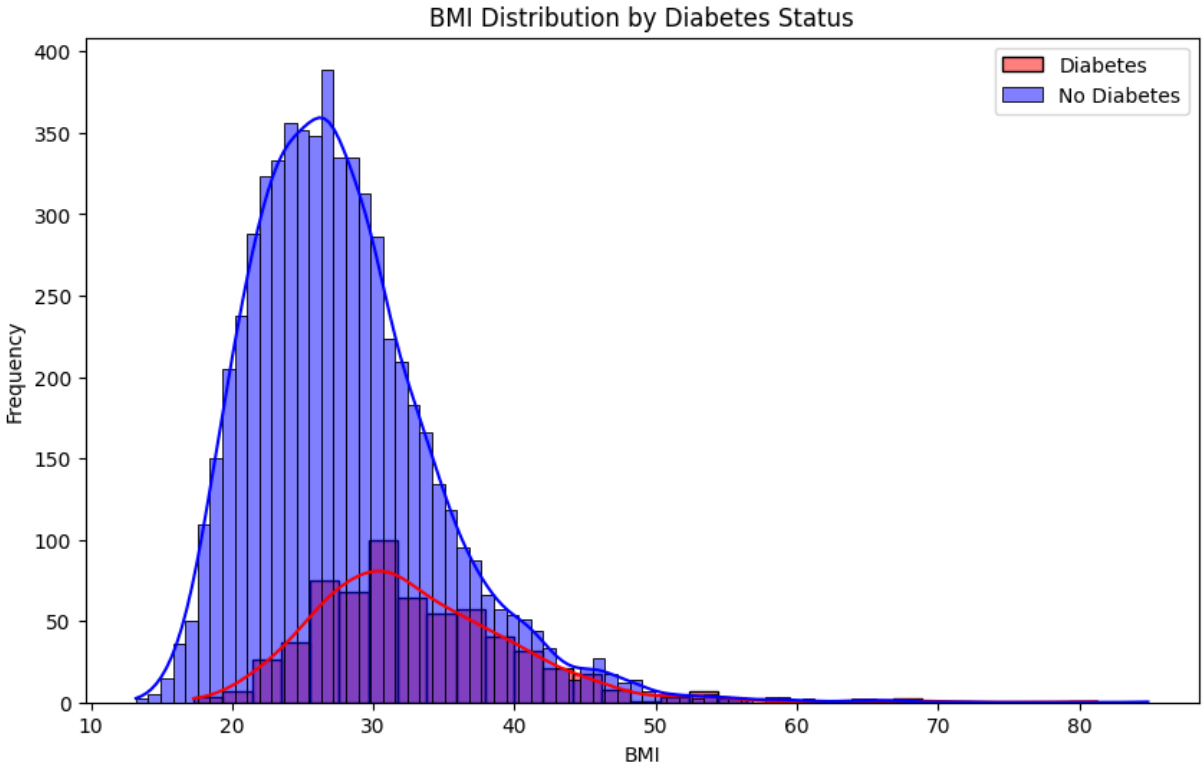
In [274…

```
# Age Distribution by Diabetes Status
plt.figure(figsize=(10, 6))
sns.histplot(data[data['gh'] >= 6.5]['age'], color='red', label='Diabetes', kde=Tru
sns.histplot(data[data['gh'] < 6.5]['age'], color='blue', label='No Diabetes', kde=
plt.title('Age Distribution by Diabetes Status')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.legend()
plt.show()

## Finding: Diabetes patients tend to be older
```



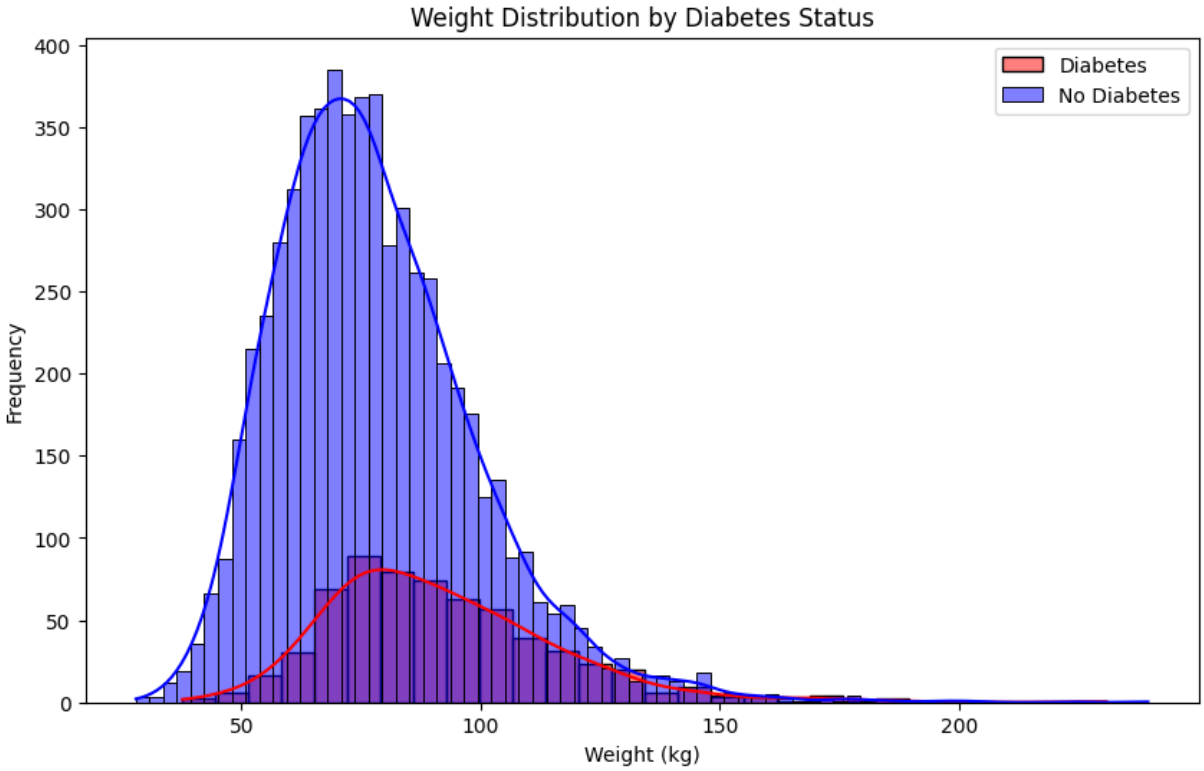
In [275…

```
# BMI Distribution by Diabetes Status
plt.figure(figsize=(10, 6))
sns.histplot(data[data['gh'] >= 6.5]['bmi'], color='red', label='Diabetes', kde=Tru
sns.histplot(data[data['gh'] < 6.5]['bmi'], color='blue', label='No Diabetes', kde=
plt.title('BMI Distribution by Diabetes Status')
plt.xlabel('BMI')
plt.ylabel('Frequency')
plt.legend()
plt.show()

## Finding: Diabetes patients tend have a higher median BMI
```



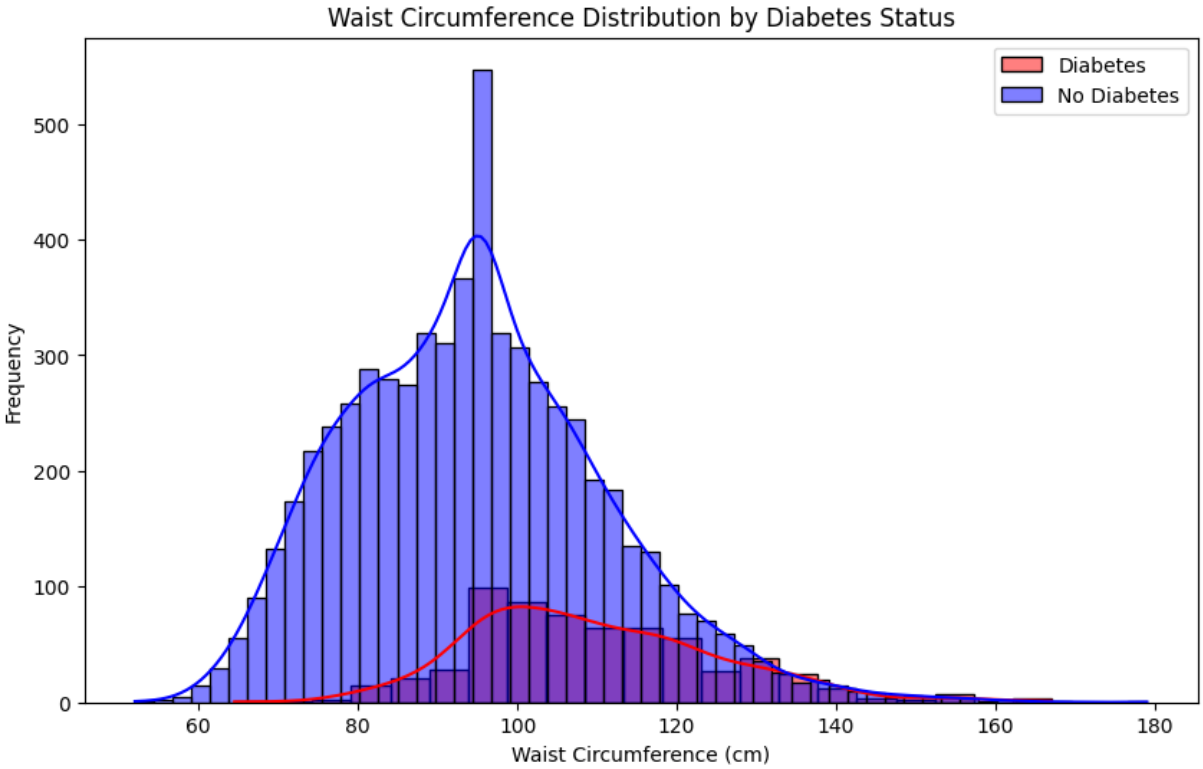
In [276…

```
# Weight Distribution by Diabetes Status
plt.figure(figsize=(10, 6))
sns.histplot(data[data['gh'] >= 6.5]['wt'], color='red', label='Diabetes', kde=True
sns.histplot(data[data['gh'] < 6.5]['wt'], color='blue', label='No Diabetes', kde=T
plt.title('Weight Distribution by Diabetes Status')
plt.xlabel('Weight (kg)')
plt.ylabel('Frequency')
plt.legend()
plt.show()

# Finding:
# Weight, which is closely linked to BMI.
# Also has a slightly higher median weight for diabetes
```



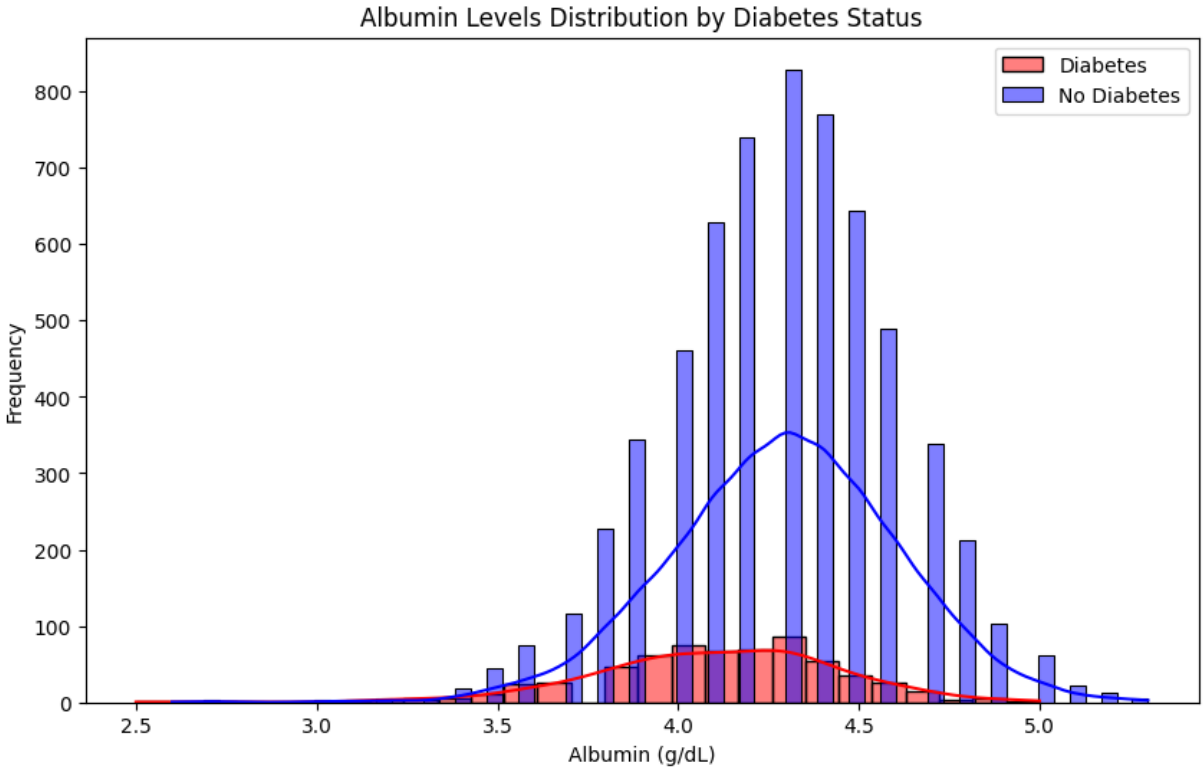
In [277…

```
# Waist Circumference Distribution by Diabetes Status
plt.figure(figsize=(10, 6))
sns.histplot(data[data['gh'] >= 6.5]['waist'], color='red', label='Diabetes', kde=T
sns.histplot(data[data['gh'] < 6.5]['waist'], color='blue', label='No Diabetes', kd
plt.title('Waist Circumference Distribution by Diabetes Status')
plt.xlabel('Waist Circumference (cm)')
plt.ylabel('Frequency')
plt.legend()
plt.show()

# Finding:
# Waist size, which is closely linked to BMI.
# Also has a slightly higher median weight for diabetes
```



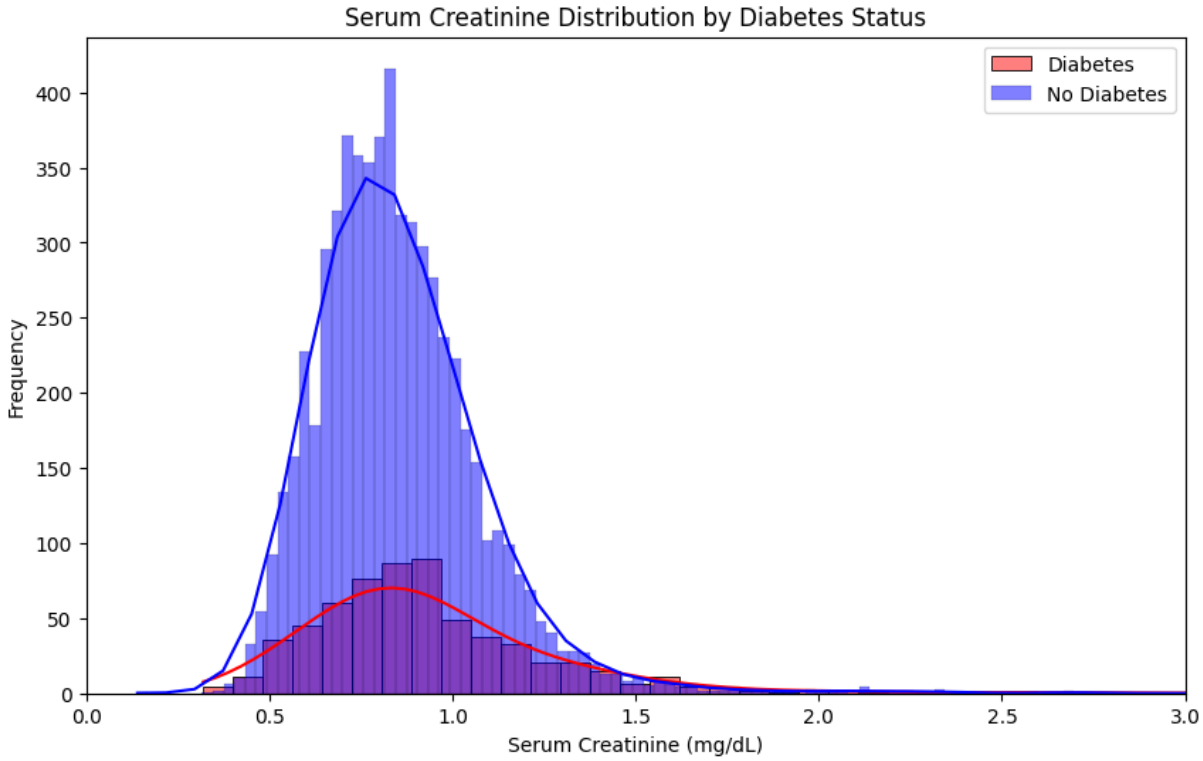
In [278…

```
# Albumin Levels Distribution by Diabetes Status
plt.figure(figsize=(10, 6))
sns.histplot(data[data['gh'] >= 6.5]['albumin'], color='red', label='Diabetes', kde
sns.histplot(data[data['gh'] < 6.5]['albumin'], color='blue', label='No Diabetes',
plt.title('Albumin Levels Distribution by Diabetes Status')
plt.xlabel('Albumin (g/dL)')
plt.ylabel('Frequency')
plt.legend()
plt.show()


# Finding:
# Albumin in diabetes patients are very slightly lower on average than a normal per
```



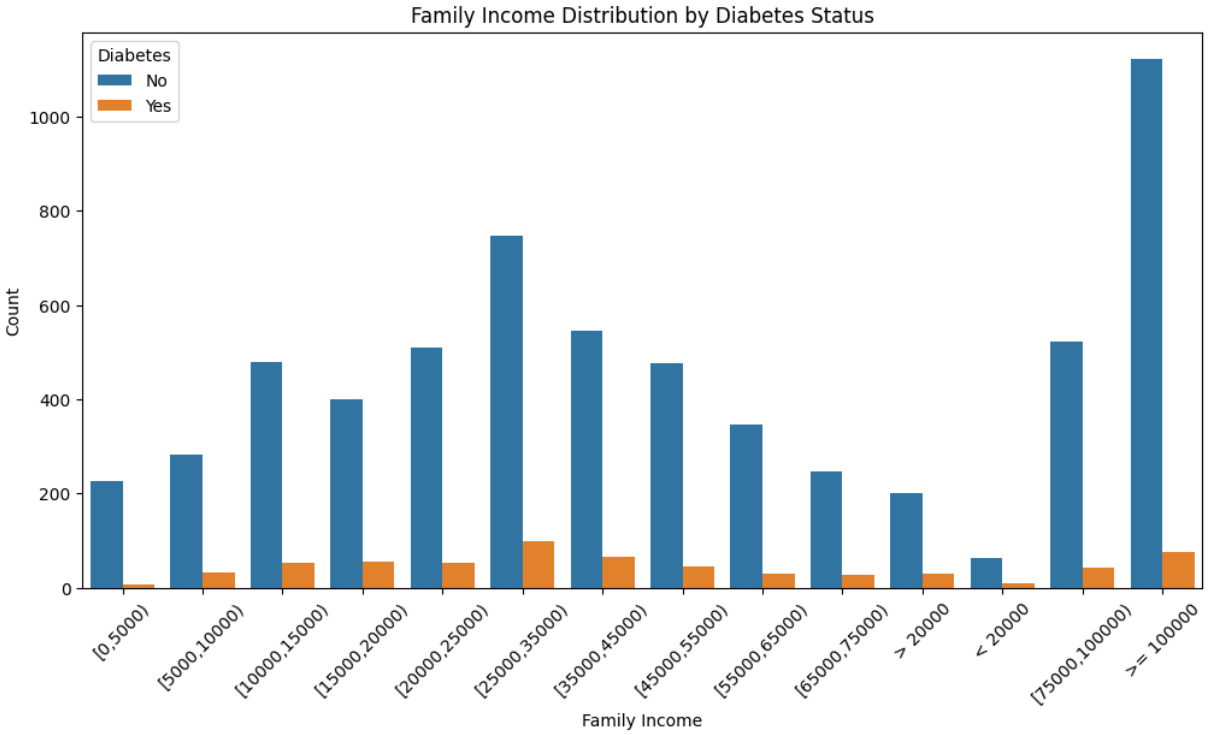
In [279…

```
# SCr Distribution by Diabetes Status
plt.figure(figsize=(10, 6))
sns.histplot(data[data['gh'] >= 6.5]['scr'], color='red', label='Diabetes', kde=Tru
sns.histplot(data[data['gh'] < 6.5]['scr'], color='blue', label='No Diabetes', kde=
plt.title('Serum Creatinine Distribution by Diabetes Status')
plt.xlabel('Serum Creatinine (mg/dL)')
plt.ylabel('Frequency')
plt.legend()
plt.xlim(0, 3)
plt.show()

# Finding:
# Serum Creatinine doesn't seem to have an effect on diabetes patients
```



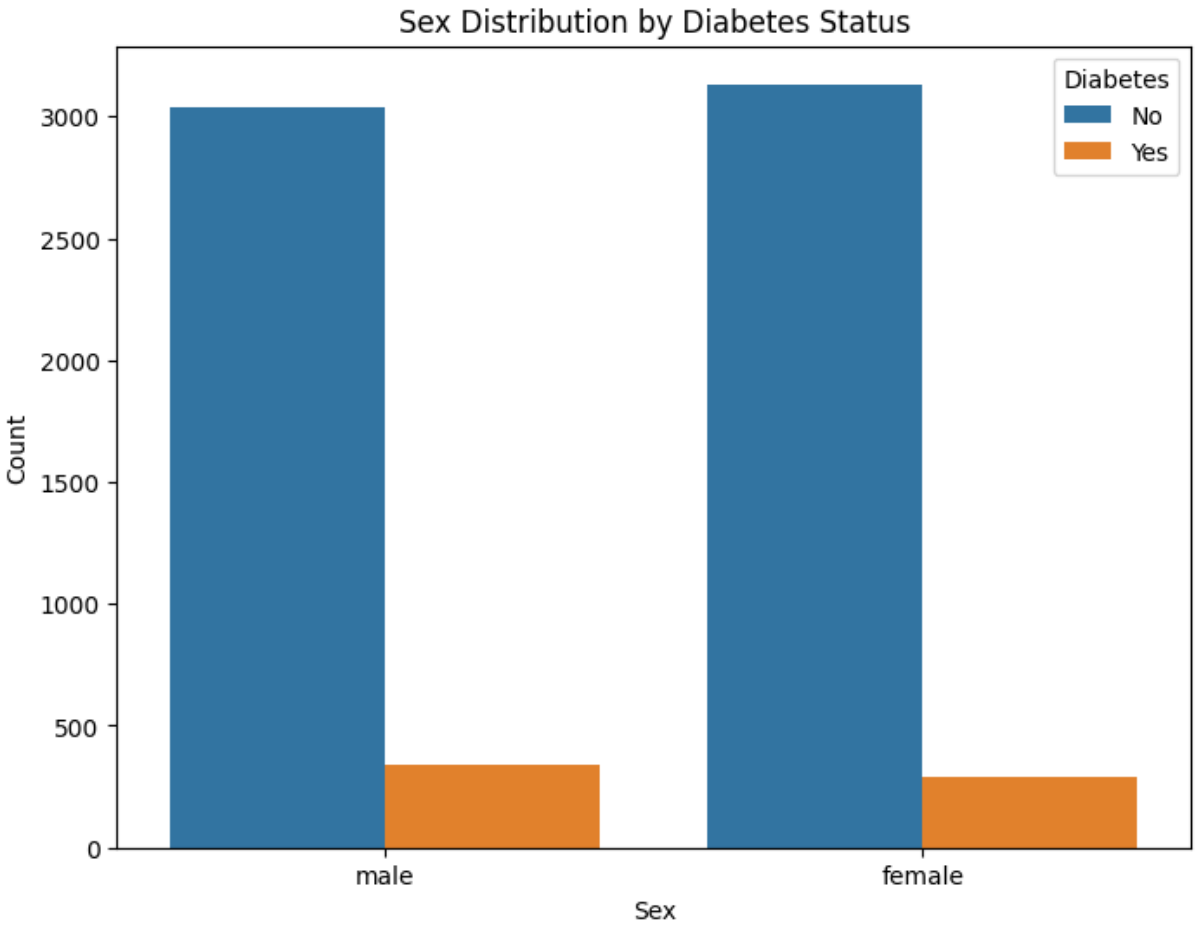
In [280…

```
# Family Income Distribution by Diabetes Status
plt.figure(figsize=(12, 6))
sns.countplot(x='income', hue=(data['gh'] >= 6.5), data=data, order=income_types)
plt.title('Family Income Distribution by Diabetes Status')
plt.xlabel('Family Income')
plt.ylabel('Count')
plt.legend(title='Diabetes', labels=['No', 'Yes'])
plt.xticks(rotation=45)
plt.show()
```



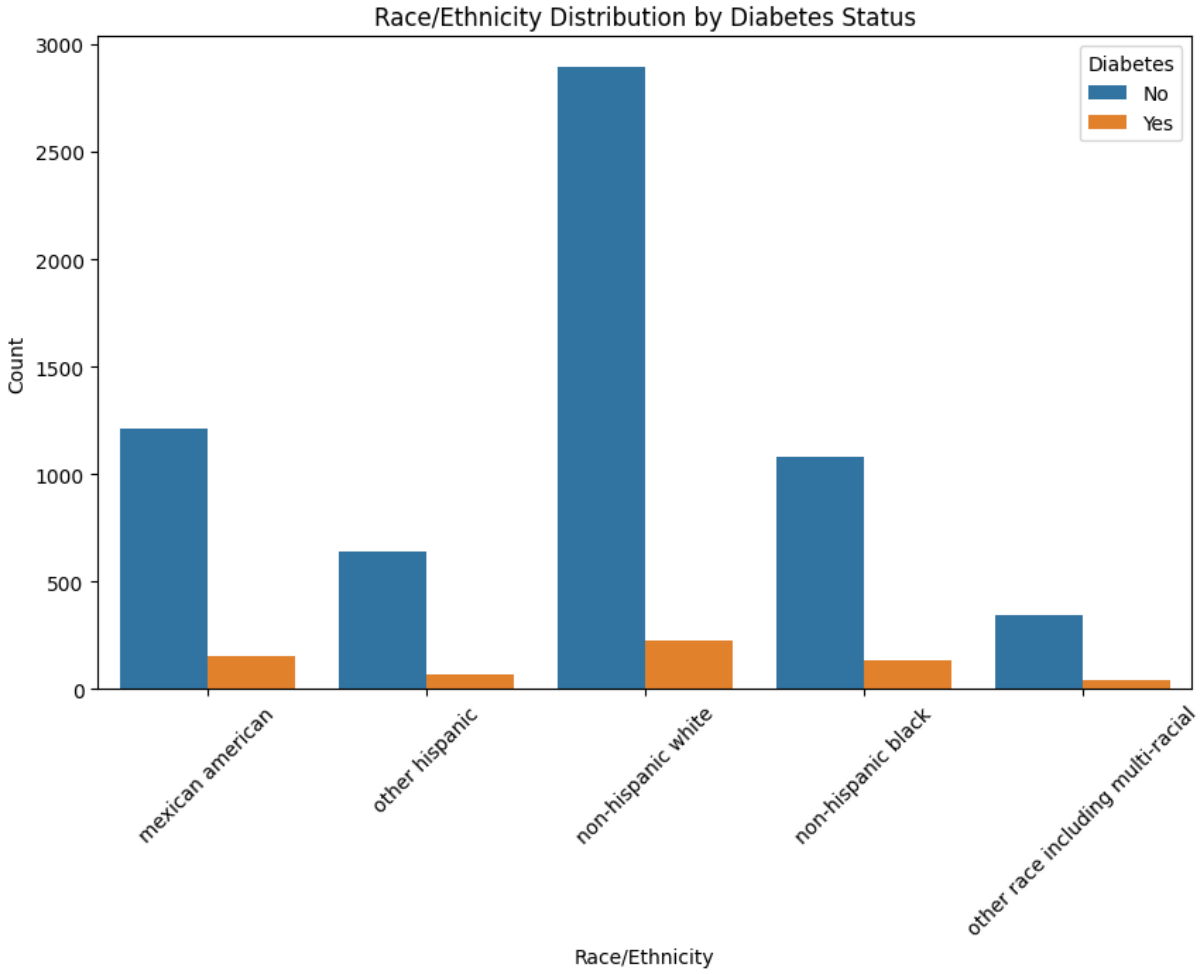
In [281…

```
plt.figure(figsize=(8, 6))
sns.countplot(x='sex', hue=(data['gh'] >= 6.5), data=data, order=sex_types)
plt.title('Sex Distribution by Diabetes Status')
plt.xlabel('Sex')
plt.ylabel('Count')
plt.legend(title='Diabetes', labels=['No', 'Yes'])
plt.show()
```



In [282…

```
plt.figure(figsize=(10, 6))
sns.countplot(x='re', hue=(data['gh'] >= 6.5), data=data, order=re_types)
plt.title('Race/Ethnicity Distribution by Diabetes Status')
plt.xlabel('Race/Ethnicity')
plt.ylabel('Count')
plt.legend(title='Diabetes', labels=['No', 'Yes'])
plt.xticks(rotation=45)
plt.show()
```



In [283…

```
## Feature Engineering for our model

# Categorize age into groups
data['age_group'] = pd.cut(data['age'], bins=[0, 18, 35, 50, 65, float('inf')],
                           labels=['<18', '18-35', '36-50', '51-65', '>65'])

# Categorize BMI into groups
data['bmi_category'] = pd.cut(data['bmi'], bins=[0, 18.5, 25, 30, float('inf')],
                              labels=['Underweight', 'Normal', 'Overweight', 'Obese

# Calculate Waist-to-Height Ratio
data['whtr'] = data['waist'] / data['ht']

# Create interaction terms
data['age_bmi_interaction'] = data['age'] * data['bmi']
data['age_whtr_interaction'] = data['age'] * data['whtr']
```

In [284…

```
# Original features
original_features = ['age', 'bmi', 'waist', 'bun', 'scr', 'albumin', 'wt', 'ht']
# tx and dx is somewhat directly associated with predicting diabetes_status,
# let's not use this in this case

# Engineered features
engineered_features = ['age_bmi_interaction', 'whtr', 'age_whtr_interaction']
```

```
# Categorical features that need to be converted to dummy variables
categorical_features = ['sex', 're', 'income', 'bmi_category', 'age_group']

# Combine all features
feature_columns = original_features + engineered_features
```

In [285…
```
data.columns
```

Out[285…
```
Index(['seqn', 'sex', 'age', 're', 'income', 'tx', 'dx', 'wt', 'ht', 'bmi',
       'leg', 'arml', 'armc', 'waist', 'tri', 'sub', 'gh', 'albumin', 'bun',
       'scr', 'diabetes_status', 'age_group', 'bmi_category', 'whtr',
       'age_bmi_interaction', 'age_whtr_interaction'],
      dtype='object')
```

In [286…
```
# Convert categorical variables to dummy/indicator variables
data = pd.get_dummies(data, columns=categorical_features, drop_first=True)

# Now, update feature_columns to include the dummy variables
# Exclude the original categorical columns as they are now represented by the dummy
excluded_features = ['seqn', 'gh', 'diabetes_status', 'tx', 'dx']
feature_columns = [col for col in data.columns if col not in categorical_features a
```

In [287…
```
print(f"feature columns: {feature_columns}\n---\ndata.columns: {data.columns}")
```

```
feature columns: ['age', 'wt', 'ht', 'bmi', 'leg', 'arml', 'armc', 'waist', 'tri',
'sub', 'albumin', 'bun', 'scr', 'whtr', 'age_bmi_interaction', 'age_whtr_interactio
n', 'sex_male', 're_non-hispanic black', 're_non-hispanic white', 're_other hispani
c', 're_other race including multi-racial', 'income_> 20000', 'income_>= 100000', 'i
ncome_[0,5000)', 'income_[10000,15000)', 'income_[15000,20000)', 'income_[20000,2500
0)', 'income_[25000,35000)', 'income_[35000,45000)', 'income_[45000,55000)', 'income
_[5000,10000)', 'income_[55000,65000)', 'income_[65000,75000)', 'income_[75000,10000
0)', 'bmi_category_Normal', 'bmi_category_Overweight', 'bmi_category_Obese', 'age_gr
oup_18-35', 'age_group_36-50', 'age_group_51-65', 'age_group_>65']
---
data.columns: Index(['seqn', 'age', 'tx', 'dx', 'wt', 'ht', 'bmi', 'leg', 'arml', 'a
rmc',
       'waist', 'tri', 'sub', 'gh', 'albumin', 'bun', 'scr', 'diabetes_status',
       'whtr', 'age_bmi_interaction', 'age_whtr_interaction', 'sex_male',
       're_non-hispanic black', 're_non-hispanic white', 're_other hispanic',
       're_other race including multi-racial', 'income_> 20000',
       'income_>= 100000', 'income_[0,5000)', 'income_[10000,15000)',
       'income_[15000,20000)', 'income_[20000,25000)', 'income_[25000,35000)',
       'income_[35000,45000)', 'income_[45000,55000)', 'income_[5000,10000)',
       'income_[55000,65000)', 'income_[65000,75000)', 'income_[75000,100000)',
       'bmi_category_Normal', 'bmi_category_Overweight', 'bmi_category_Obese',
       'age_group_18-35', 'age_group_36-50', 'age_group_51-65',
       'age_group_>65'],
      dtype='object')
```

In [288…
```
from sklearn.model_selection import train_test_split

# Define features (X) and target variable (y)
X = data[feature_columns]
y = data['diabetes_status']

# Split the dataset into a training set and a testing set
```

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_sta

# Output the shapes of the resulting sets
print("Training set shape:", X_train.shape)
print("Testing set shape:", X_test.shape)
```

```
Training set shape: (5436, 41)
Testing set shape: (1359, 41)
```

In [289…

```
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score, precision_score, recall_score, roc_auc_
from sklearn.metrics import classification_report, confusion_matrix
```

In [290…

```
# Function to evaluate model performance
def evaluate_model(model, X_test, y_test):
    y_pred = model.predict(X_test)
    accuracy = accuracy_score(y_test, y_pred)
    precision = precision_score(y_test, y_pred)
    recall = recall_score(y_test, y_pred)
    roc_auc = roc_auc_score(y_test, y_pred)
    print(f"Accuracy: {accuracy:.2f}")
    print(f"Precision: {precision:.2f}")
    print(f"Recall: {recall:.2f}")
    print(f"ROC-AUC: {roc_auc:.2f}")
    print(classification_report(y_test, y_pred))
    print(confusion_matrix(y_test, y_pred))
```

In [294…

```
# Logistic Regression
logreg_model = LogisticRegression(max_iter=1000)
logreg_model.fit(X_train, y_train)

# Evaluate Logistic Regression
print("\nLogistic Regression Performance:")
evaluate_model(logreg_model, X_test, y_test)

# Precision and recall are pretty low. Lets do some feature selection
```

```
Logistic Regression Performance:
Accuracy: 0.90
Precision: 0.43
Recall: 0.07
ROC-AUC: 0.53
              precision    recall  f1-score   support

       False       0.91      0.99      0.95      1224
        True       0.43      0.07      0.13       135

    accuracy                           0.90      1359
   macro avg       0.67      0.53      0.54      1359
weighted avg       0.86      0.90      0.86      1359

[[1211   13]
 [ 125   10]]
```

```
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  n_iter_i = _check_optimize_result(
```

In [291…

```python
## Feature selection using RFECV

from sklearn.feature_selection import RFECV
from sklearn.model_selection import StratifiedKFold

# Initialize Logistic Regression model
logreg_model = LogisticRegression(max_iter=1000)

# Create RFECV (Recursive Feature Elimination with Cross-Validation) object
rfecv = RFECV(estimator=logreg_model, step=1, cv=StratifiedKFold(5), scoring='accur

# Fit RFECV
rfecv.fit(X, y)

# Print the optimal number of features
print("Optimal number of features : %d" % rfecv.n_features_)
```

```
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```

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C:\Users\lzyda\AppData\Local\Packages\PythonSoftwareFoundation.Python.3.10_qbz5n2kfr
a8p0\LocalCache\local-packages\Python310\site-packages\sklearn\linear_model\_logisti
```

```
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STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

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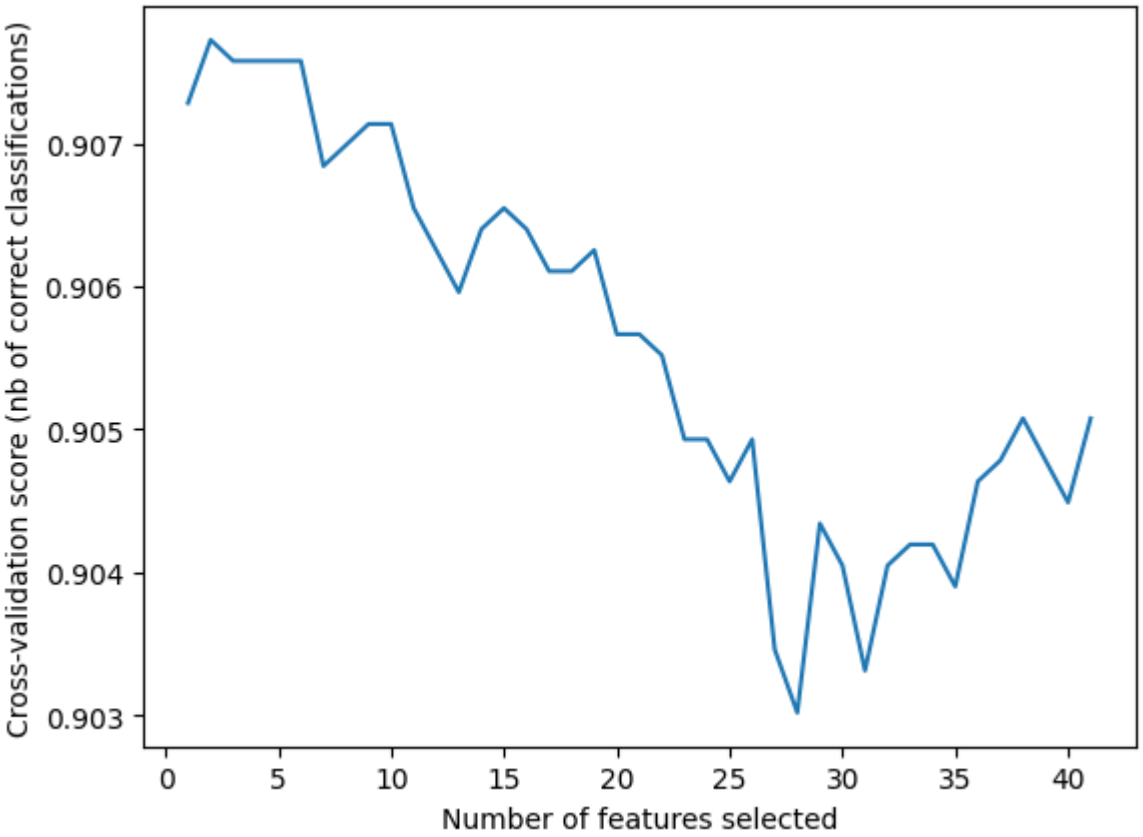
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
Optimal number of features : 2
```

In [292…

```python
grid_scores = rfecv.cv_results_['mean_test_score']

# Plot number of features VS. cross-validation scores
plt.figure()
plt.xlabel("Number of features selected")
plt.ylabel("Cross-validation score (nb of correct classifications)")
plt.plot(range(1, len(grid_scores) + 1), grid_scores)
plt.show()
```



In [295…

```python
### LogReg with RFE feature selection
# Identify which features were selected by RFECV
selected_features = [f for f, s in zip(feature_columns, rfecv.support_) if s]
```

```python
# Print selected features
print("Selected Features:\n", selected_features)

# Rebuild the model using only selected features
X_selected = X[selected_features]

# Split the dataset into a training set and a testing set
X_train_sel, X_test_sel, y_train, y_test = train_test_split(X_selected, y, test_siz

# Fit the model
logreg_model.fit(X_train_sel, y_train)

# Evaluate the model
print("Model Performance with Selected Features:")
evaluate_model(logreg_model, X_test_sel, y_test)

# Precision and Recall are now 0. RFE is probably only predicting the majority clas
# This is especially since my dataset is unbalanced. (Num Diabetes << Num Non Diabe
```

```
Selected Features:
 ['age_group_51-65', 'age_group_>65']
Model Performance with Selected Features:
Accuracy: 0.90
Precision: 0.00
Recall: 0.00
ROC-AUC: 0.50
              precision    recall  f1-score   support

       False       0.90      1.00      0.95      1224
        True       0.00      0.00      0.00       135

    accuracy                           0.90      1359
   macro avg       0.45      0.50      0.47      1359
weighted avg       0.81      0.90      0.85      1359

[[1224    0]
 [ 135    0]]
```

```
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a8p0\LocalCache\local-packages\Python310\site-packages\sklearn\metrics\_classificati
on.py:1471: UndefinedMetricWarning: Precision is ill-defined and being set to 0.0 du
e to no predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
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trol this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```

In [ ]:

```
# Log reg with Over-sampling using SMOTE (Synthetic Minority Over-sampling Techniqu
# This helps to handle imbalanced datasets

from imblearn.over_sampling import SMOTE

smote = SMOTE()
X_resampled, y_resampled = smote.fit_resample(X, y)

# Split the resampled data
X_train_res, X_test_res, y_train_res, y_test_res = train_test_split(X_resampled, y_
```

In [298…

```
# Fit the model on resampled data
logreg_model.fit(X_train_res, y_train_res)

# Evaluate the model
print("Logistic Model Performance with Resampled Data:")
evaluate_model(logreg_model, X_test_res, y_test_res)

# We observe that the precision and accuracy significantly improves
```

```
Model Performance with Resampled Data:
Accuracy: 0.91
Precision: 0.91
Recall: 0.90
ROC-AUC: 0.91
              precision    recall  f1-score   support

       False       0.91      0.91      0.91      1275
        True       0.91      0.90      0.90      1192

    accuracy                           0.91      2467
   macro avg       0.91      0.91      0.91      2467
weighted avg       0.91      0.91      0.91      2467

[[1165  110]
 [ 118 1074]]
C:\Users\lzyda\AppData\Local\Packages\PythonSoftwareFoundation.Python.3.10_qbz5n2kfra8p0\LocalCache\local-packages\Python310\site-packages\sklearn\linear_model\_logistic.py:460: ConvergenceWarning: lbfgs failed to converge (status=1):
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Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
```

In [305…

```python
# Decision Tree Model
dtree_model = DecisionTreeClassifier()

# Fit the model on resampled data
dtree_model.fit(X_train_res, y_train_res)

# Evaluate the model
print("Decision Tree Performance with Resampled Data:")
evaluate_model(dtree_model, X_test_res, y_test_res)
```

```
Decision Tree Performance with Resampled Data:
Accuracy: 0.90
Precision: 0.87
Recall: 0.92
ROC-AUC: 0.90
              precision    recall  f1-score   support

       False       0.92      0.87      0.90      1275
        True       0.87      0.92      0.89      1192

    accuracy                           0.90      2467
   macro avg       0.90      0.90      0.90      2467
weighted avg       0.90      0.90      0.90      2467

[[1115  160]
 [  98 1094]]
```

In [303…

```python
# Hyper parameter tuning
from sklearn.model_selection import GridSearchCV
```

```
# Set the parameters for grid search
param_grid = {
    'max_depth': [10, 20, 30, 40, 50, None],
    'min_samples_split': [2, 5, 10, 20],
    'min_samples_leaf': [1, 2, 4, 8]
}

grid_search = GridSearchCV(estimator=DecisionTreeClassifier(),
                           param_grid=param_grid,
                           cv=5,  # Number of folds
                           n_jobs=-1,  # Use all available cores
                           scoring='accuracy')  # Can use other metrics like 'roc_a
grid_search.fit(X_train_res, y_train_res)

# Best parameter set
print("Best parameters found: ", grid_search.best_params_)
```

```
Best parameters found:  {'max_depth': 30, 'min_samples_leaf': 2, 'min_samples_spli
t': 2}
```

In [306…

```
# Evaluate the best model found by GridSearchCV
best_dtree_model = grid_search.best_estimator_
print("\nDecision Tree Performance with Best Parameters:")
evaluate_model(best_dtree_model, X_test_res, y_test_res)
```

```
Decision Tree Performance with Best Parameters:
Accuracy: 0.90
Precision: 0.90
Recall: 0.90
ROC-AUC: 0.90
              precision    recall  f1-score   support

       False       0.91      0.90      0.91      1275
        True       0.90      0.90      0.90      1192

    accuracy                           0.90      2467
   macro avg       0.90      0.90      0.90      2467
weighted avg       0.90      0.90      0.90      2467

[[1152  123]
 [ 117 1075]]
```

In [309…

```
# Random Forest Model
rf_model = RandomForestClassifier()
rf_model.fit(X_train_res, y_train_res)

# Evaluate Random Forest
print("\nRandom Forest Performance:")
evaluate_model(rf_model, X_test_res, y_test_res)

## Random Forest seems to perform the best. Let's ultimately use and interpret this
```

```
Random Forest Performance:
Accuracy: 0.94
Precision: 0.94
Recall: 0.94
ROC-AUC: 0.94
              precision    recall  f1-score   support

       False       0.94      0.95      0.94      1275
        True       0.94      0.94      0.94      1192

    accuracy                           0.94      2467
   macro avg       0.94      0.94      0.94      2467
weighted avg       0.94      0.94      0.94      2467

[[1206   69]
 [  75 1117]]
```

In [311…

```python
## Hyperparameter tuning to finetune RF model
from sklearn.model_selection import GridSearchCV

# Define the parameter grid
param_grid = {
    'n_estimators': [100, 200, 300],
    'max_depth': [10, 20, 30, None],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4]
}

# Initialize GridSearchCV
grid_search = GridSearchCV(estimator=RandomForestClassifier(),
                           param_grid=param_grid,
                           cv=3,  # 3-fold cross-validation
                           n_jobs=-1,  # Use all available cores
                           verbose=2)

# Fit GridSearchCV
grid_search.fit(X_train_res, y_train_res)

# Best hyperparameters
print("Best hyperparameters:\n", grid_search.best_params_)
```

```
Fitting 3 folds for each of 108 candidates, totalling 324 fits
Best hyperparameters:
 {'max_depth': None, 'min_samples_leaf': 1, 'min_samples_split': 2, 'n_estimators':
200}
```

In [312…

```python
# Best model
best_rf_model = grid_search.best_estimator_

# Evaluate the best model
print("\nRandom Forest Performance with Best Hyperparameters:")
evaluate_model(best_rf_model, X_test_res, y_test_res)
```

```
Random Forest Performance with Best Hyperparameters:
Accuracy: 0.95
Precision: 0.95
Recall: 0.94
ROC-AUC: 0.95
              precision    recall  f1-score   support

       False       0.94      0.95      0.95      1275
        True       0.95      0.94      0.94      1192

    accuracy                           0.95      2467
   macro avg       0.95      0.95      0.95      2467
weighted avg       0.95      0.95      0.95      2467

[[1213   62]
 [  71 1121]]
```

In [313…

```python
## Lets use RF Model as our main model.
## Performing CV to validate stability of performance

from sklearn.model_selection import cross_val_score

# Perform cross-validation
cv_scores = cross_val_score(best_rf_model, X_resampled, y_resampled, cv=5)
print("Cross-validation scores:", cv_scores)
```

```
Cross-validation scores: [0.81678152 0.96595055 0.96149169 0.95865424 0.96553122]
```

In [315…

```python
## The first fold is quite low, so lets investigate further.
## This could hint that the model may be sensitive to the data input.

# Custom k-fold so we can narrow down any specific folds

from sklearn.model_selection import KFold
import numpy as np

# Number of splits
n_splits = 5
kf = KFold(n_splits=n_splits, shuffle=True, random_state=42)

# Store the scores and fold data
fold_scores = []
fold_data = []

for train_index, test_index in kf.split(X_resampled):
    X_train_fold, X_test_fold = X_resampled.iloc[train_index], X_resampled.iloc[tes
    y_train_fold, y_test_fold = y_resampled.iloc[train_index], y_resampled.iloc[tes

    # Fit the model on this fold
    rf_model.fit(X_train_fold, y_train_fold)

    # Evaluate the model
    score = rf_model.score(X_test_fold, y_test_fold)
    fold_scores.append(score)

    # Store test data of this fold
```

```
    fold_data.append((X_test_fold, y_test_fold, score))

# Print scores for each fold
print("Fold scores:", fold_scores)

## Outlier fold doesn't appear anymore. It may have been just an unlucky streak for
```

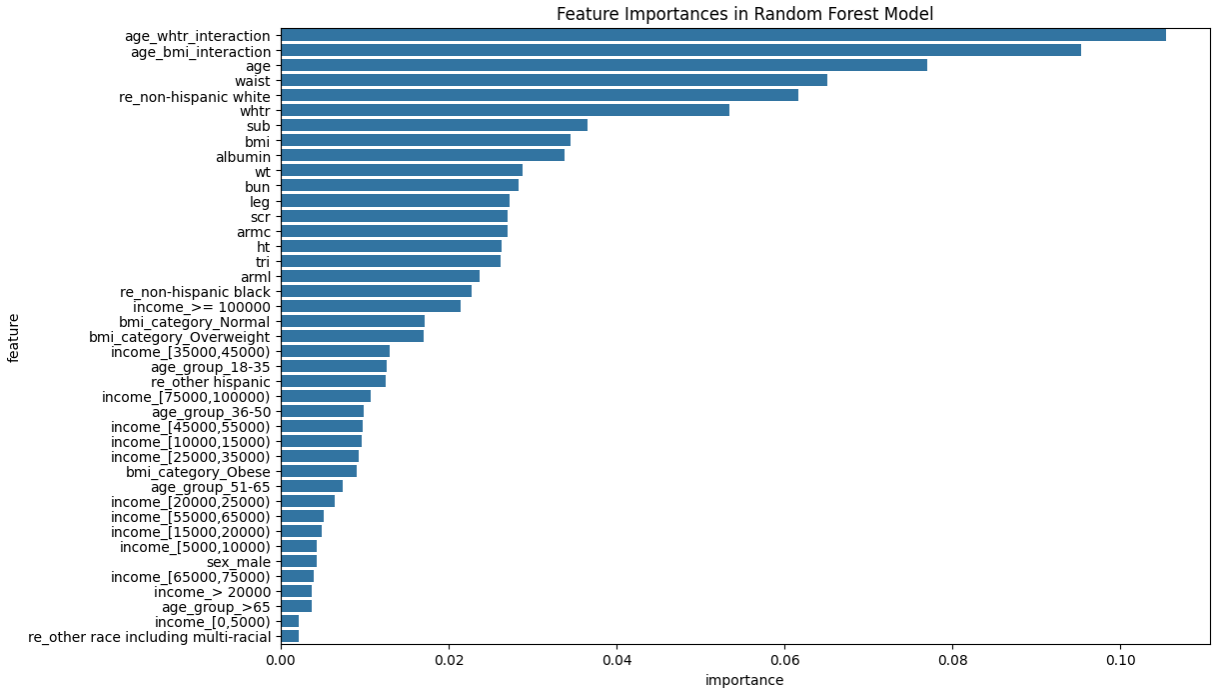
```
Fold scores: [0.9448723145520875, 0.9387920551276855, 0.9448723145520875, 0.94527766
5180381, 0.9456609894566099]
```

In [316…

```
## Further outlier fold analysis (not used)

# # Identify the outlier fold
# outlier_fold_index = np.argmin(fold_scores)
# outlier_data = fold_data[outlier_fold_index]

# # Outlier fold's test data
# X_test_outlier, y_test_outlier, outlier_score = outlier_data

# # Analyze the outlier data
# # You can look at distributions of features, class proportions, etc.
# print("Outlier Fold Score:", outlier_score)
# print("Class Distribution in Outlier Fold:", y_test_outlier.value_counts())
```

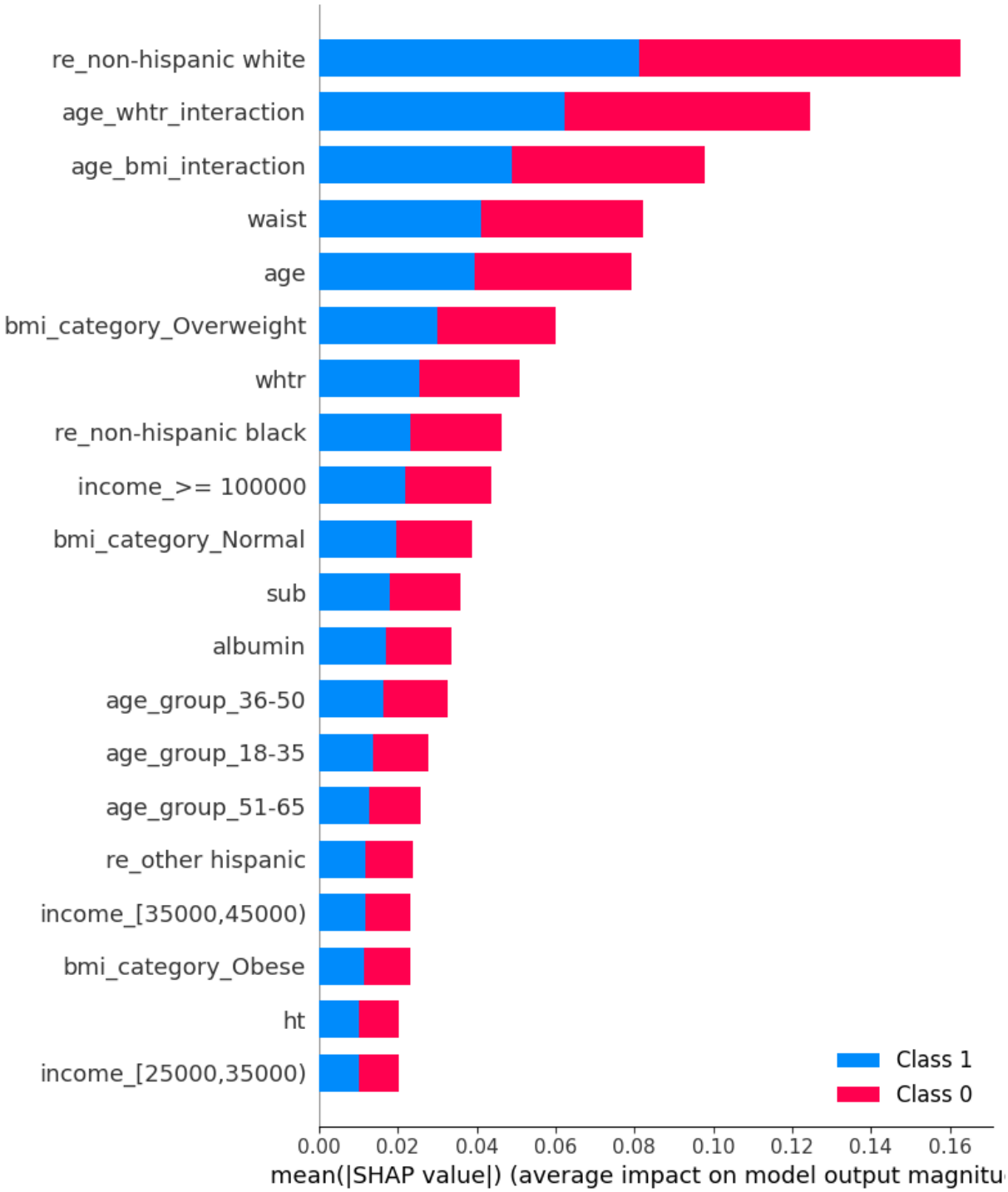
In [318…

```
import matplotlib.pyplot as plt

# Get feature importances of finetuned model
importances = best_rf_model.feature_importances_

# Convert the importances into a DataFrame
feature_importances = pd.DataFrame({'feature': X_train_res.columns, 'importance': i

# Sort the DataFrame by importance
feature_importances = feature_importances.sort_values(by='importance', ascending=Fa

# Plotting
plt.figure(figsize=(12,8))
sns.barplot(x='importance', y='feature', data=feature_importances)
plt.title('Feature Importances in Random Forest Model')
plt.show()

## The graph hints at which features contribute the most to diabetes prediction:
# Top 3: Age & Waist Height ratio interaction, Age & BMI Interaction, Age
```



In [322…

```
## SHAP (SHapley Additive exPlanations) to interpret model
import shap

# Create the SHAP explainer and compute SHAP values
explainer = shap.TreeExplainer(best_rf_model)
shap_values = explainer.shap_values(X_test_res)

# Plot summary plot
shap.summary_plot(shap_values, X_test_res, plot_type="bar")
```



In [323…

```
# Using both importance graphs, we can deduce the following important features:

# Importance of Age and one's "body weight"
# - Age & Waist Height ratio interaction,
# - Age & BMI Interaction,
# - Age
# - Waist Size
# - Waist Height ratio

# Strong correlation to RE
# - RE_non-hispanic-white
```