```
# Importing required packages
from pandas import read_csv
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.compose import ColumnTransformer
from sklearn.preprocessing import OneHotEncoder
from sklearn.preprocessing import StandardScaler
import matplotlib.pyplot as plotPointer
import numpy as np
import seaborn as sns
```

Documentation for Importing Required Packages

1. **Package Imports**:
    - `from pandas import read_csv`: Imports the `read_csv` function from the `pandas` library for reading CSV files.
    - `from sklearn.model_selection import train_test_split`: Imports the `train_test_split` function from `sklearn.model_selection` for splitting data into training and testing sets.
    - `from sklearn.metrics import accuracy_score`: Imports the `accuracy_score` function from `sklearn.metrics` for calculating accuracy.
    - `from sklearn.compose import ColumnTransformer`: Imports the `ColumnTransformer` class from `sklearn.compose` for transforming columns.
    - `from sklearn.preprocessing import OneHotEncoder`: Imports the `OneHotEncoder` class from `sklearn.preprocessing` for one-hot encoding.
    - `from sklearn.preprocessing import StandardScaler`: Imports the `StandardScaler` class from `sklearn.preprocessing` for feature scaling.
    - `import matplotlib.pyplot as plotPointer`: Imports the `matplotlib.pyplot` module for data visualization.
    - `import numpy as np`: Imports the `numpy` library for numerical operations.
    - `import seaborn as sns`: Imports the `seaborn` library for enhanced data visualization.

```
from google.colab import files
uploaded=files.upload()
```

Choose Files No file chosen Upload widget is only available when the cell has been executed in the current browser session. Please rerun this cell to enable.

from google.colab import files: Imports the files module from the Google Colab library. uploaded=files.upload(): Executes the command to upload files.

```
strokesData = read_csv('healthcare-dataset-stroke-data.csv')
# strokesData.head()
strokesData
```

	id	gender	age	hypertension	heart_disease	ever_married	work_type
0	9046	Male	67.0	0	1	Yes	Private
1	51676	Female	61.0	0	0	Yes	Self-employed

```
strokesData = strokesData.dropna()
```

The code strokesData = strokesData.dropna() removes rows with missing (NaN) values from the DataFrame strokesData and updates the DataFrame with the missing values removed.

```
if 'id' in strokesData :
 strokesData = strokesData.drop('id', axis=1)

strokesData
```

	gender	age	hypertension	heart_disease	ever_married	work_type	Reside
0	Male	67.0	0	1	Yes	Private	
2	Male	80.0	0	1	Yes	Private	
3	Female	49.0	0	0	Yes	Private	
4	Female	79.0	1	0	Yes	Self-employed	
5	Male	81.0	0	0	Yes	Private	
...	...	...	...	...	...	...	
5104	Female	13.0	0	0	No	children	
5106	Female	81.0	0	0	Yes	Self-employed	
5107	Female	35.0	0	0	Yes	Self-employed	
5108	Male	51.0	0	0	Yes	Private	

Documentation for Removing Column 'id' from DataFrame

1. **Column Removal**:
   - `if 'id' in strokesData:` : Checks if a column named 'id' exists in the `strokesData` DataFrame.
   - If the column exists, the following line is executed:
     - `strokesData = strokesData.drop('id', axis=1)` : Removes the column 'id' from the DataFrame using the `drop` method with `axis=1`.
2. **DataFrame Display**:
   - `strokesData` : Displays the DataFrame `strokesData` after the column removal.

```
#Checking Unique Values for some columns
# Marital Status
strokesData.ever_married.unique()
```

```
array(['Yes', 'No'], dtype=object)
```

```
# Work Type
strokesData.work_type.unique()
```

```
array(['Private', 'Self-employed', 'Govt_job', 'children', 'Never_worked'],
      dtype=object)
```

```
# Residence Urban/Rural
strokesData.Residence_type.unique()
```

```
array(['Urban', 'Rural'], dtype=object)
```

```
# Smoking Status
strokesData.smoking_status.unique()
```

```
array(['formerly smoked', 'never smoked', 'smokes', 'Unknown'],
      dtype=object)
```

```
# Gender
strokesData.gender.unique()
```

```
array(['Male', 'Female', 'Other'], dtype=object)
```

```
# Spliting the data in training and testing subsets
D = strokesData.values
# iloc to select specefic rows
x = strokesData.iloc[:,:-1]
y = strokesData.iloc[:,-1]
```

Documentation for Data Splitting Using iloc

1. **Data Preparation**:
   - `D = strokesData.values`: Retrieves the values from the `strokesData` DataFrame and assigns them to the variable `D`.
   - `x = strokesData.iloc[:,:-1]`: Selects all rows and all columns except the last one from the `strokesData` DataFrame. This is done to extract features and assign them to the variable `x`.
   - `y = strokesData.iloc[:,-1]`: Selects all rows and only the last column from the `strokesData` DataFrame. This is done to extract target labels and assign them to the variable `y`.
2. **Train-Test Splitting** (Commented Out):
   - The line `# x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.50, random_state=1)` is commented out. It suggests that the split using `train_test_split` is not being used here.

```
transformingColoumn = ColumnTransformer(transformers = [('encoder', OneHotEncoder(), [0,4,5,6,9])], remainder='passthrough')
x = np.array(transformingColoumn.fit_transform(x))
x
x_train, x_test, y_train, y_test = train_test_split(x,y,test_size=0.50, random_state = 1)
```

Documentation for Data Transformation and Train-Test Split

1. **Column Transformation**:
   - `transformingColoumn = ColumnTransformer(transformers=[('encoder', OneHotEncoder(), [0, 4])], remainder='passthrough')`: Initializes a `ColumnTransformer` named `transformingColoumn`.
   - Categorical columns at indices 0 and 4 are encoded using `OneHotEncoder`.
   - `remainder='passthrough'` ensures that non-transformed columns are included as well.
2. **Applying Transformation**:
   - `x = np.array(transformingColoumn.fit_transform(x))`: Applies the transformations defined by `transformingColoumn` to the input features (`x`).
   - Transformed data is stored in the NumPy array `x`.
3. **Train-Test Split**:
   - `x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=0.50, random_state=1)`: Splits the transformed features (`x`) and target labels (`y`) into training and testing subsets.
   - The testing subset size is set to 50% of the dataset.

- The `random_state=1` parameter ensures

```
sc = StandardScaler()
x_train_scaled = sc.fit_transform(x_train)
x_test_scaled = sc.fit_transform(x_test)
```

Documentation for Feature Scaling Using StandardScaler

This documentation outlines the code that performs feature scaling using the `StandardScaler` from scikit-learn.

Code Explanation

1. **StandardScaler Initialization**:
   - `sc = StandardScaler()`: Initializes a `StandardScaler` object named `sc`.
2. **Scaling Training Features**:
   - `x_train_scaled = sc.fit_transform(x_train)`: Scales the training features (`x_train`) using the `fit_transform` method of the `StandardScaler`.
   - The scaling is done to standardize the features and bring them to similar scales.
3. **Scaling Testing Features**:
   - `x_test_scaled = sc.fit_transform(x_test)`: Scales the testing features (`x_test`) using the `fit_transform` method of the same `StandardScaler` instance.
   - It's important to note that the same scaler is used for both training and testing data to ensure consistency.

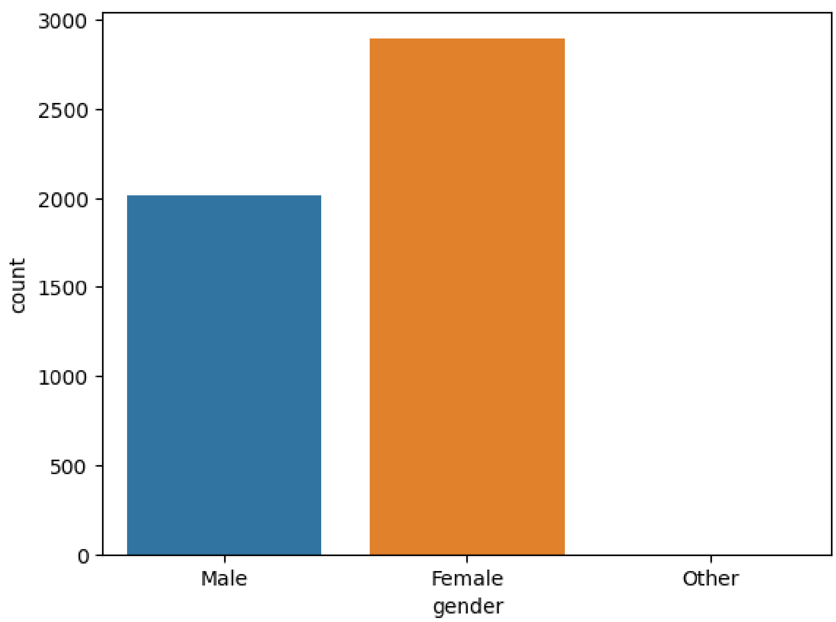
```
# Define a function to calculate the mean and standard deviation of a dataset
def mean_and_stddev(dataset):
    mean = np.mean(dataset, axis=0)
    stddev = np.std(dataset, axis=0)
    return mean, stddev

# Define a function to calculate the Gaussian probability density function
def gaussian_pdf(x, mean, stddev):
    exponent = np.exp(-((x - mean) ** 2) / (2 * (stddev ** 2)))
    return (1 / (np.sqrt(2 * np.pi) * stddev)) * exponent

# Define a function to train a Gaussian Naive Bayes classifier
def train_gaussian_naive_bayes(X, y):
    classes = np.unique(y)
    class_priors = {}
    class_means = {}
    class_stddevs = {}

    for c in classes:
        X_c = X[y == c]
        class_priors[c] = len(X_c) / len(X)
        class_means[c], class_stddevs[c] = mean_and_stddev(X_c)

    return class_priors, class_means, class_stddevs

# Define a function to make predictions using the Gaussian Naive Bayes classifier
def predict_gaussian_naive_bayes(X, class_priors, class_means, class_stddevs):
    predictions = []
    for x in X:
        class_scores = {}
        for c in class_priors:
            prior = class_priors[c]
            likelihood = np.prod(gaussian_pdf(x, class_means[c], class_stddevs[c]))
            class_scores[c] = prior * likelihood
        predicted_class = max(class_scores, key=class_scores.get)
        predictions.append(predicted_class)
    return predictions
```

```
# Train the Gaussian Naive Bayes model
class_priors, class_means, class_stddevs = train_gaussian_naive_bayes(x_train_scaled, y_train)

# Make predictions on the test data
y_prediction_NB = predict_gaussian_naive_bayes(x_test_scaled, class_priors, class_means, class_stddevs)

# Calculate the accuracy
correct_predictions = np.sum(y_prediction_NB == y_test)
accuracy = correct_predictions / len(y_test)
print('The accuracy of the NB for Testing is: {:.4f}'.format(accuracy))
```

```
The accuracy of the NB for Testing is: 0.9605
```

```
sns.countplot(x=strokesData['gender'])
```

```
<Axes: xlabel='gender', ylabel='count'>
```



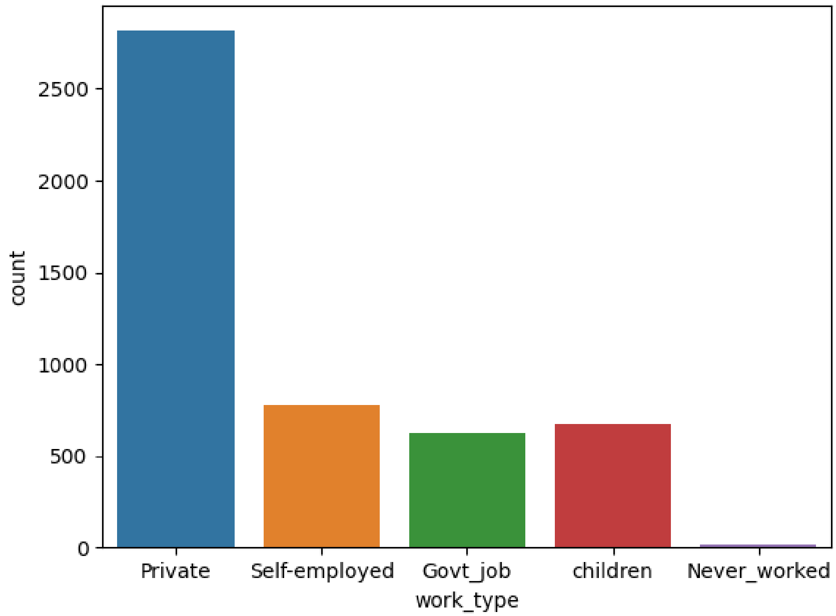
The code uses Seaborn's countplot to create a bar chart. It counts the occurrences of each category in the 'gender' column of the DataFrame strokesData and visualizes the distribution of genders.

```
sns.countplot(x=strokesData['ever_married'])
```

```
<Axes: xlabel='ever_married', ylabel='count'>
```

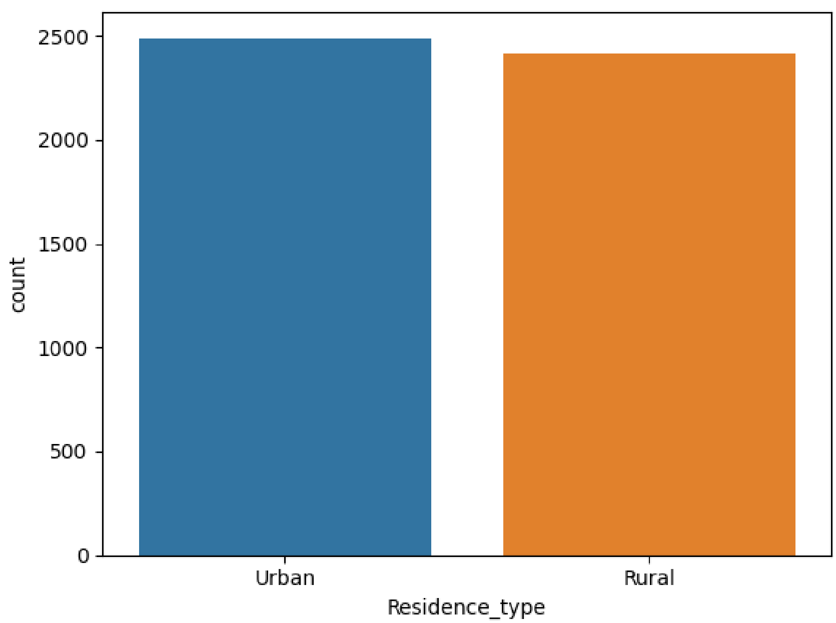
```
sns.countplot(x=strokesData['work_type'])
```

```
<Axes: xlabel='work_type', ylabel='count'>
```



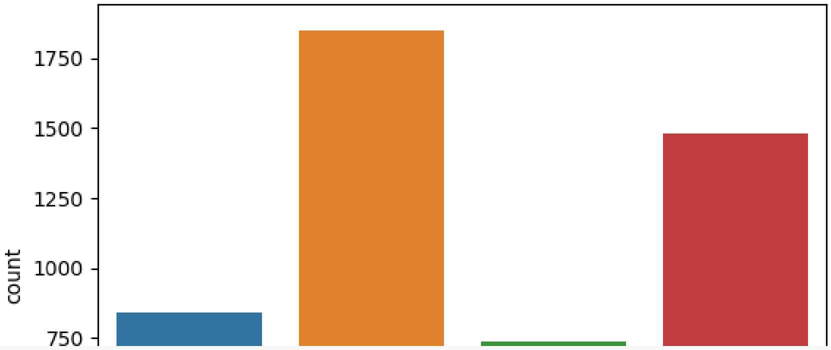

```
sns.countplot(x=strokesData['Residence_type'])
```

```
<Axes: xlabel='Residence_type', ylabel='count'>
```



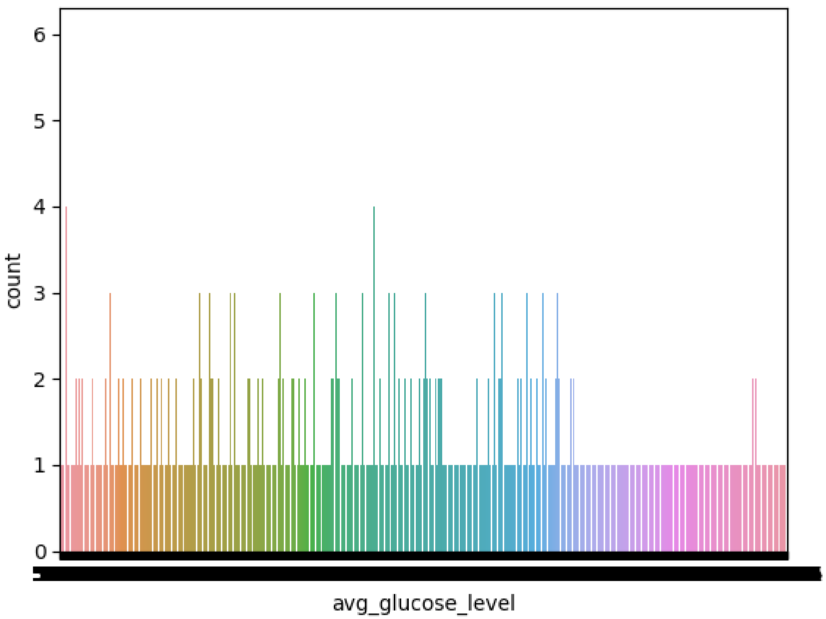

```
sns.countplot(x=strokesData['smoking_status'])
```

```
<Axes: xlabel='smoking_status', ylabel='count'>
```



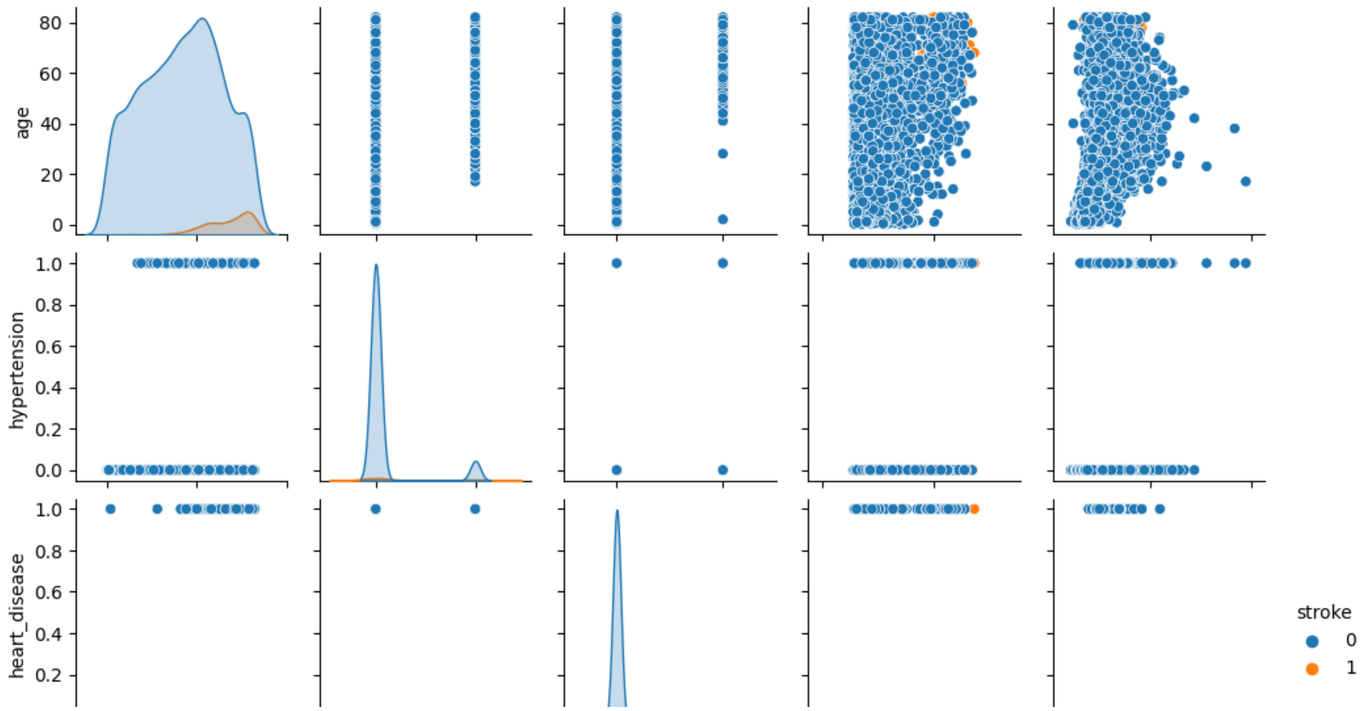

```
sns.countplot(x=strokesData['avg_glucose_level'])
```

```
<Axes: xlabel='avg_glucose_level', ylabel='count'>
```




```
sns.pairplot(strokesData,hue="stroke",height=2)
```

```
<seaborn.axisgrid.PairGrid at 0x7f11fe9ffc40>
```



The code uses Seaborn's pairplot to create a grid of scatterplots and histograms. It visualizes relationships between variables in the DataFrame strokesData, with different colors for each point based on the 'stroke' column, and each subplot has a height of 2 units.