MachineLearningandOptimization_CT7205_4107143_ChanaySubasingha

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1 Machine Learning Assignment Report

This report presents analysis of two datasets. Exploratory analysis has been carriedout to analyse data. Leanear models, machine learning models have been used to train model.

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Module Title: CT7205 - Machine Learning and Optimization

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[ ]:
```
# Import libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.linear_model import LinearRegression
from sklearn.metrics import mean_squared_error, r2_score, confusion_matrix,␣
 ↪classification_report, accuracy_score
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.naive_bayes import GaussianNB
from sklearn import svm
from sklearn.ensemble import RandomForestClassifier
from sklearn.ensemble import AdaBoostClassifier
from sklearn.model_selection import GridSearchCV, RandomizedSearchCV
import tensorflow as tf
from sklearn.preprocessing import LabelEncoder
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import MinMaxScaler
import warnings
warnings.filterwarnings('ignore')
```

1.1 Question 1. Medical Insurance

1.1.1 introduction

The dataset contains data on medical costs and related variables. People around the world use medical insurance to cover their medical costs such as hospital visits, doctor appointments, and surgeries. Insurance companies calculate premiums depending on the analysis of the insured person's health and lifestyle factors related to health. Some conditions are related to certain diseases, such as smoking related to lung cancer. Other factors such as the age of the person number of dependents under the insurance coverage are also important factors to consider to predict medical costs.

Identifying the relationship and approximate medical cost per individual helps insurance companies to manage insurance premiums more productively. The correct prediction helps insurance companies to offer better plans, and people get more value from their insurance plans. This analysis uses the below independent variables to predict the medical cost of an individual.

- age: age of the primary beneficiary
- sex: insurance contractor gender: female or male
- bmi: body mass index calculated by weight in kilograms divided by the square of the height in centimetres
- children: number of children covered by health insurance
- smoker: yes or no
- region: the payees' residential area in the US, northeast, southeast, southwest, northwest
- medicalCost: individual medical costs billed by medical insurance.

1.1.2 Data Understanding

Examining the dataset more closely is a part of the data understanding step. This phase is essential for preventing unforeseen issues during data preparation and model training.

Accessing and exploring the dataset using tables and visualising graphs are necessary for data interpretation. This permits the assessment of the data quality and selection of the most suitable data transformation and prediction models.

[ ]:
```
# Read data from csv
df1 = pd.read_csv('insurance.csv')
df1.head()
```

[ ]:

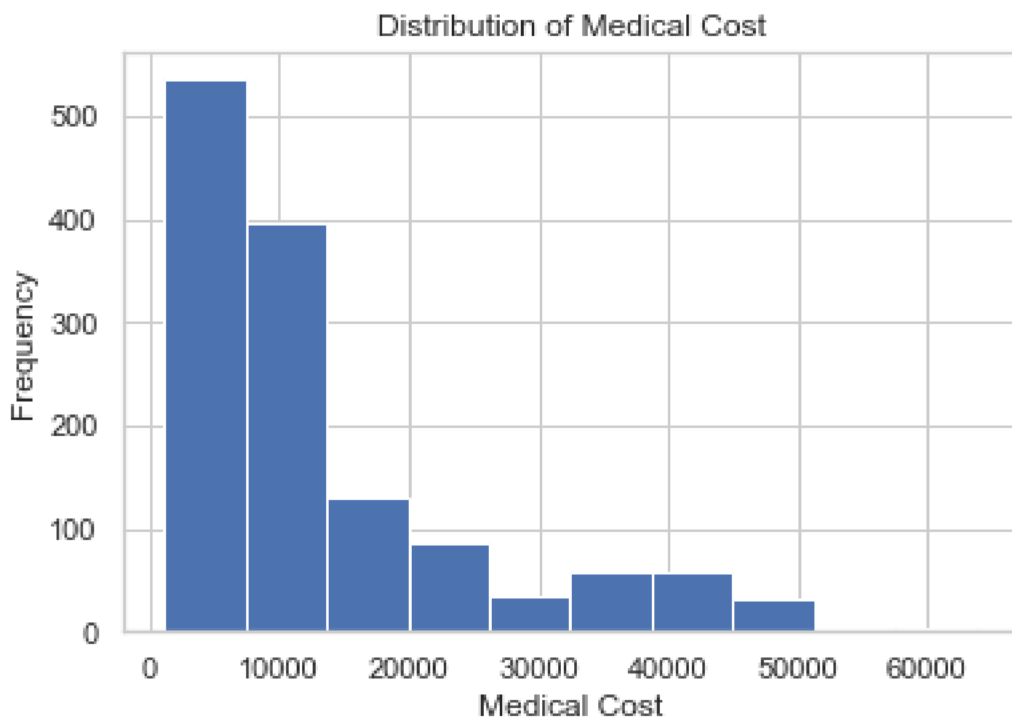
	age	sex	bmi	children	smoker	region	medicalCost
0	19	female	27.900	0	yes	southwest	16884.92400
1	18	male	33.770	1	no	southeast	1725.55230
2	28	male	33.000	3	no	southeast	4449.46200
3	33	male	22.705	0	no	northwest	21984.47061
4	32	male	28.880	0	no	northwest	3866.85520

[ ]:
```
print('Number of rows and columns in the dataset: ', df1.shape)
print('The dataset has 1338 observations and seven variables, including six␣
 ↪dependent variables and the target variable.')
```

```
Number of rows and columns in the dataset:  (1338, 7)
The dataset has 1338 observarions and seven variables, including six dependent
variables and the target variable.
```

The distribution of the target variable is analysed to select a method to predict data. A histogram is used here because the target variable has continous values.

[ ]:
```
# Distribution of the target class
medicalCost = df1[['medicalCost']].to_numpy()

plt.hist(medicalCost)
plt.xlabel('Medical Cost')
plt.ylabel('Frequency')
plt.title('Distribution of Medical Cost')
plt.show()
print('Figure 1: Distribution of the Medical Cost')
```

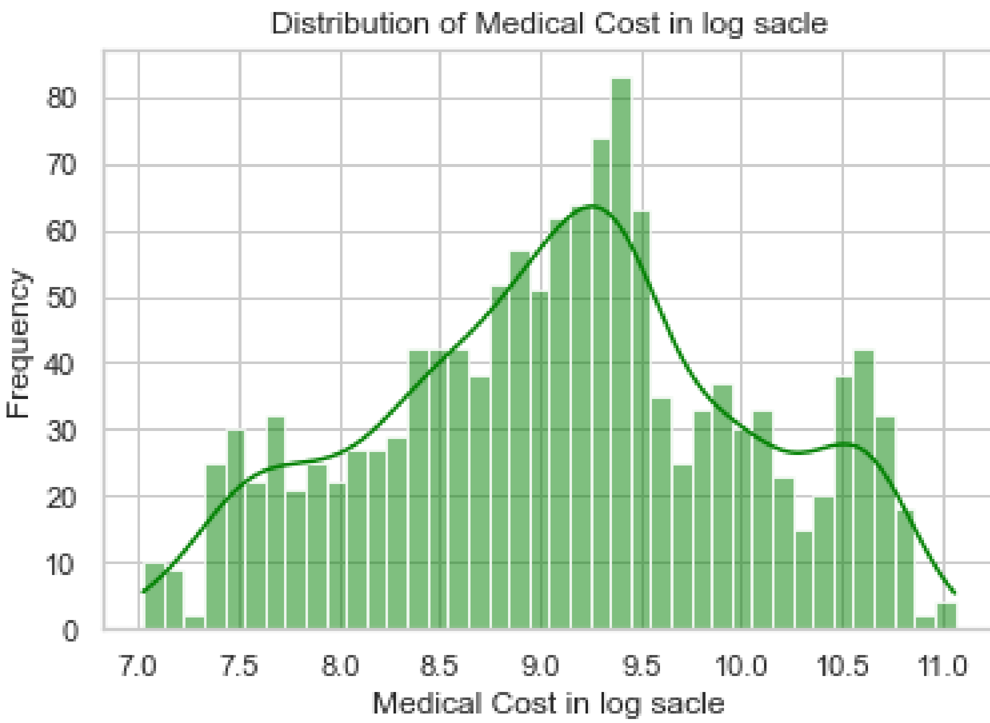



```
Figure 1: Distribution of the Medical Cost
```

The target variable, medical cost values are known and present in the dataset. Therefore, a supervised method is more suitable for predicting medical costs.

Since the target variable has continuous values, as shown in figure 1, regression analysis is better for predicting medical costs than classification or clustering. Additionally, for classification, labelled classes have to introduce to the medical cost variable and clustering is mainly done when the target class is unknown.

[ ]:
```
# Distribution of the log transformation of the target class
sns.histplot(np.log(df1['medicalCost']), bins=40,
             color='green', stat='count', kde=True)
plt.xlabel('Medical Cost in log sacle')
plt.ylabel('Frequency')
plt.title('Distribution of Medical Cost in log sacle')
plt.show()

print('Figure 2: Distribution of Medical Cost in log sacle')
```




```
Figure 2: Distribution of Medical Cost in log sacle
```

Medical cost is highly skewed. According to the figure 1, majority of the values lies below 2000, while maximum value exceeds 60000. Therefore, a log scale is used to visualise data in order to extract features of the dense area of the distribution. Log scale values of the medical cost show a distribution closer to a normal distribution. There are three modes and one of them is prominent.

[ ]:
```
# Percentage of values missing in each column
for column in df1.columns:
    percentage = df1[column].isnull().mean()
    print(f'{column}: {round(percentage*100,4)}%')
```

```
age: 0.0%
sex: 0.0%
bmi: 0.0%
```

```
children: 0.0%
smoker: 0.0%
region: 0.0%
medicalCost: 0.0%
```

Analysis of missing values found that there are no missing values in the dataset.

[ ]:
```
print('Table 1: Basic statistics of the continous variables')
df1.describe()
```

```
Table 1: Basic statistics of the continous variables
```

[ ]:

	age	bmi	children	medicalCost
count	1338.000000	1338.000000	1338.000000	1338.000000
mean	39.207025	30.663397	1.094918	13270.422265
std	14.049960	6.098187	1.205493	12110.011237
min	18.000000	15.960000	0.000000	1121.873900
25%	27.000000	26.296250	0.000000	4740.287150
50%	39.000000	30.400000	1.000000	9382.033000
75%	51.000000	34.693750	2.000000	16639.912515
max	64.000000	53.130000	5.000000	63770.428010

The age variable has values from 18 to 64. A mean of 39.2 for the age variable shows that distribution is approximately balanced, with slightly more observations having lower values. The standard deviation of 14 shows a high spread of values over the range.

BMI shows that half of the values range from 26.2 to 34.6. A small standard deviation shows a low spread.

The children variable has close to 25% of values with zero, and half of the values are less than or equal to one. This shows a highly skewed distribution. The standard deviation of 1.2 shows low spread of the values around mean 1.09

[ ]:
```
# Distribution of the continous variables
fig, ax = plt.subplots(1, 3, figsize=(15, 4))

plt.subplot(1, 3, 1)
plt.hist(df1.iloc[:, 0], rwidth=0.9)
plt.xlabel(df1.columns[0], fontsize=15)

plt.subplot(1, 3, 2)
plt.hist(df1.iloc[:, 2], rwidth=0.9)
plt.xlabel(df1.columns[2], fontsize=15)

plt.subplot(1, 3, 3)
plt.hist(df1.iloc[:, 3], rwidth=0.9)
plt.xlabel(df1.columns[3], fontsize=15)
plt.tight_layout()
plt.show()
```

```python
print('Figure 3: Distribution of the continous variables')
```

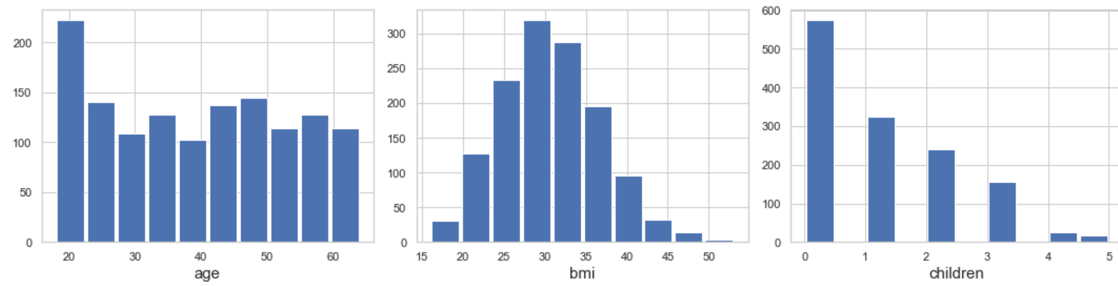


Figure 3: Distribution of the continous variables

Figure 3 shows the distribution of the continuous variables. The age distribution shows a closely uniform distribution with a higher bar at age 20. This shows that there is more observation recorded for ages around 20. Age values have a minimum of 18 and a maximum of 64 when compared to Table 1.

Bmi shows a unimodal normal distribution with a mean of 30.6. Values lie from 15.96 to 53.13 and have a standard deviation of 6.0. This shows most people are in the unhealthy range of Bmi as per the NHS guidelines (2022).

The number of children per individual is declining sharply with the number of children. There are close to 600 individuals with no children and little over 300 individuals with one child, and only 18 individuals with five children. The mean of the distribution is 1.09, with a minimum of 0 and a maximum of 5, suggesting a highly skewed distribution

[ ]:
```python
# Boxplot of the continous variables
fig, ax = plt.subplots(1, 4, figsize=(15, 5))

plt.subplot(1, 4, 1)
plt.boxplot(df1[['age']])
plt.xlabel(df1.columns[0], fontsize=15)

plt.subplot(1, 4, 2)
plt.boxplot(df1[['bmi']])
plt.xlabel(df1.columns[2], fontsize=15)

plt.subplot(1, 4, 3)
plt.boxplot(df1[['children']])
plt.xlabel(df1.columns[3], fontsize=15)

plt.subplot(1, 4, 4)
plt.boxplot(df1[['medicalCost']])
plt.xlabel(df1.columns[6], fontsize=15)

plt.tight_layout()
```

```python
plt.show()
print('Figure 4: Boxplot of the continous variables')
```

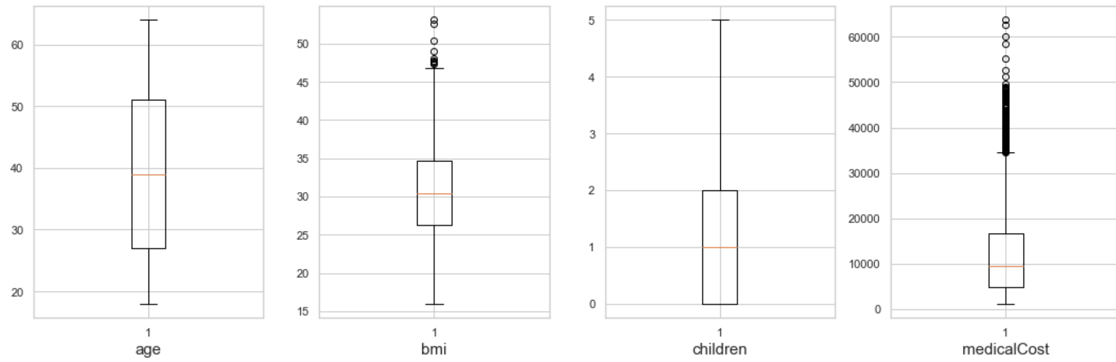


Figure 4: Boxplot of the continous variables

Figure 4 shows that the age variable has a more balanced distribution and no outliers. Bmi is also a balanced distribution. However, it has outliers at the higher end of the distribution, The anaysis is not removing outliers as they can be important to certain health conditions such as obesity. The number of children variable has no outliers, but there are more individuals with a low number of children than a high number of children, as seen in histograms in Figure 3.

The target variable medical cost has more low-cost values than high-cost values. There are a lot of outliers at the higher end, and few outliers exist over 50000. The outliers with highest values are analised further.

[ ]:
```python
# Extreme outliers are analised more closely.
df1[df1['medicalCost'] > 50000]
```

[ ]:

	age	sex	bmi	children	smoker	region	medicalCost
34	28	male	36.400	1	yes	southwest	51194.55914
543	54	female	47.410	0	yes	southeast	63770.42801
577	31	female	38.095	1	yes	northeast	58571.07448
819	33	female	35.530	0	yes	northwest	55135.40209
1146	60	male	32.800	0	yes	southwest	52590.82939
1230	52	male	34.485	3	yes	northwest	60021.39897
1300	45	male	30.360	0	yes	southeast	62592.87309

There are no clear patterns or no prominent features identified except every one is smokers from this outlier of the medical cost variable. It does not seems like errornous data. Therefore, they are not dropped from the analysis. These values can result from an accident or emergency surgeries, so they might add value to the analysis.

[ ]:
```python
# Bar chart of medical cost vs gender
sns.set_theme(style="whitegrid")
sns.barplot(x='sex', y='medicalCost', data=df1, ci=None)
plt.ylabel('Medical Cost')
```

```
plt.ylabel('Sex')
plt.title('Medical Cost vs Gender')
plt.show()
print('Figure 5: Medical cost vs Gender')
```

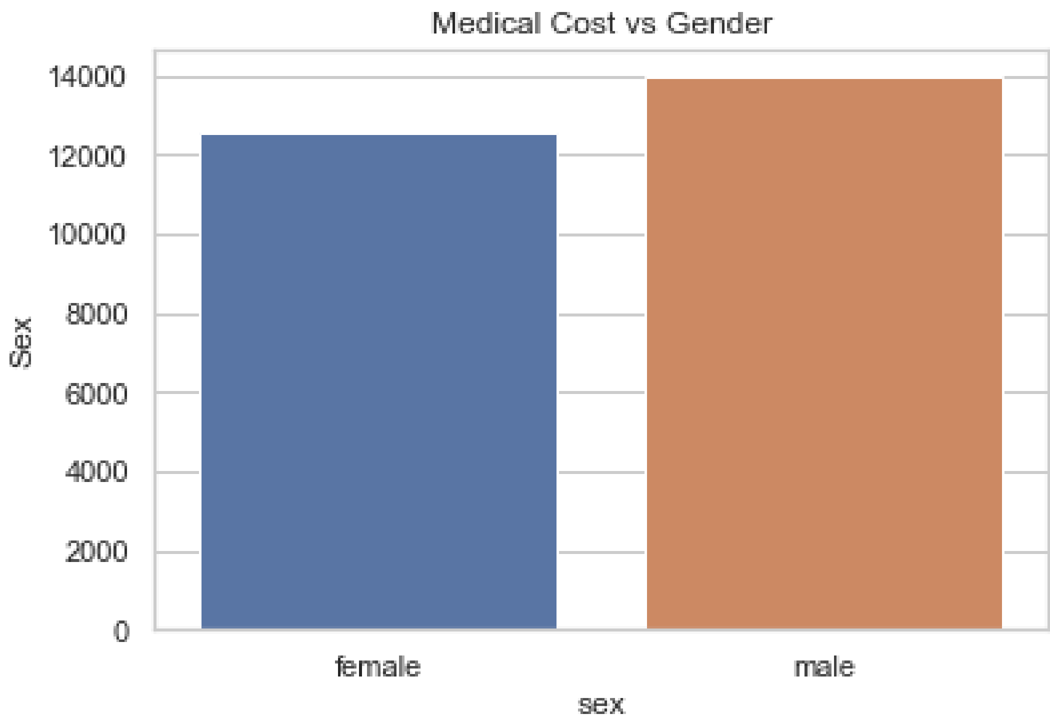


Figure 5: Medical cost vs Gender

According to figure 5, Even though males has higher medical cost recorded at around 14000, there is only slight difference in the medical costs as females have medical expense recorded just below 13000.

[ ]:
```
# Violin plot of medical cost vs gender
f = plt.figure(figsize=(14, 6))

sns.violinplot(x='sex', y='medicalCost', data=df1, palette='Wistia')
plt.title('Violin plot of Medical Cost vs sex')
plt.show()
print('Figure 6: Violin plot of Medical Cost vs Gender')
```

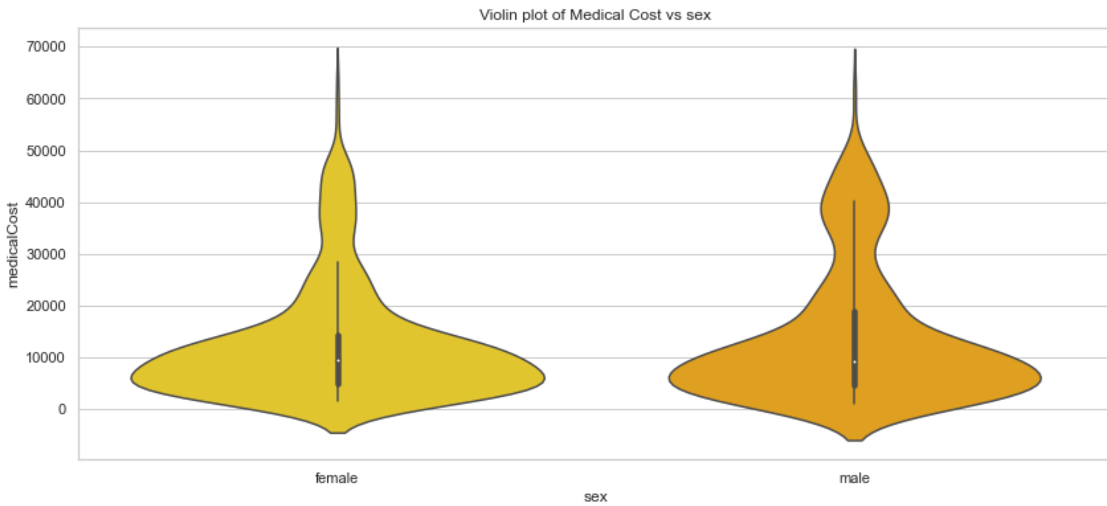
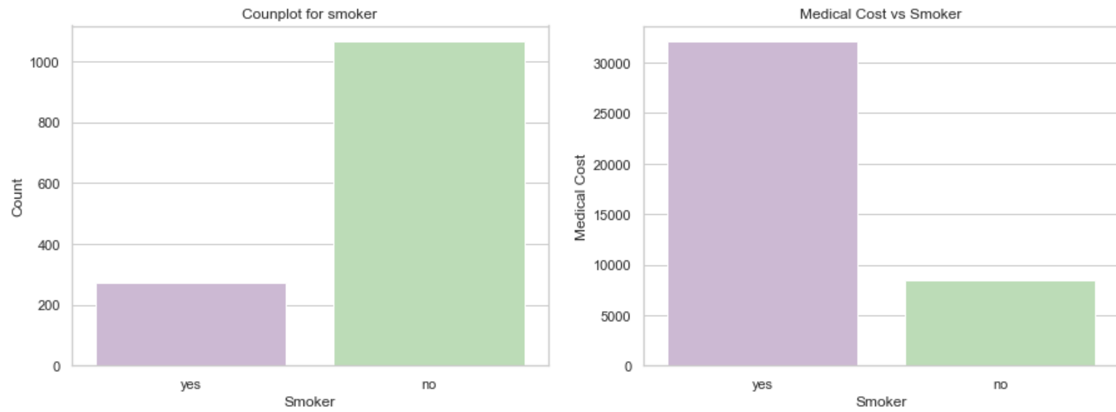


Figure 6: Violin plot of Medical Cost vs Gender

Figure 6 shows that there are more males in the higher range of medical costs than females. For the lower range around zero to 20000, the distribution shows approximately the same number of individuals for males and females. The mean is also same in the two distributions and closer to the population mean of 13270 when refence to the table 1.

```
[ ]: f = plt.figure(figsize=(15, 5))
ax = f.add_subplot(121)
sns.countplot(x='smoker', palette='PRGn', data=df1, ax=ax)
print('Figure 2.1: Number of observations representing each value of the smoker␣
 ↪label')
plt.ylabel('Count')
plt.xlabel('Smoker')
plt.title('Counplot for smoker')

# Bar chart of medical cost vs smoking
sns.set_theme(style="whitegrid")
ax = f.add_subplot(122)
sns.barplot(x='smoker', y='medicalCost',
            palette='PRGn', data=df1, ci=None, ax=ax)
plt.ylabel('Medical Cost')
plt.xlabel('Smoker')
plt.title('Medical Cost vs Smoker')
plt.show()
print('Figure 7: Medical Cost vs Smoker')

plt.show()
```

Figure 2.1: Number of observations representing each value of the smoker label



`Figure 7: Medical Cost vs Smoker`

According to figure 7, it is clear that smoking individuals have spent more on medical costs. This graph shows a drastic difference in medical costs for smoking and non-smoking individuals. The dataset only has around 250 smokers; in contrast, there are over 1000 non-smokers.

[ ]:
```
# Violin plot of medical cost vs smoking
f = plt.figure(figsize=(14, 6))

sns.violinplot(x='smoker', y='medicalCost', data=df1, palette='magma')
plt.title('Violin plot of Medical Cost vs Smoker')
plt.axhline(y=35000, color='g', linestyle='dotted')
plt.axhline(y=7000, color='b', linestyle='dotted')

plt.show()
print('Figure 8: Violin plot of Medical Cost vs Smoker')
```

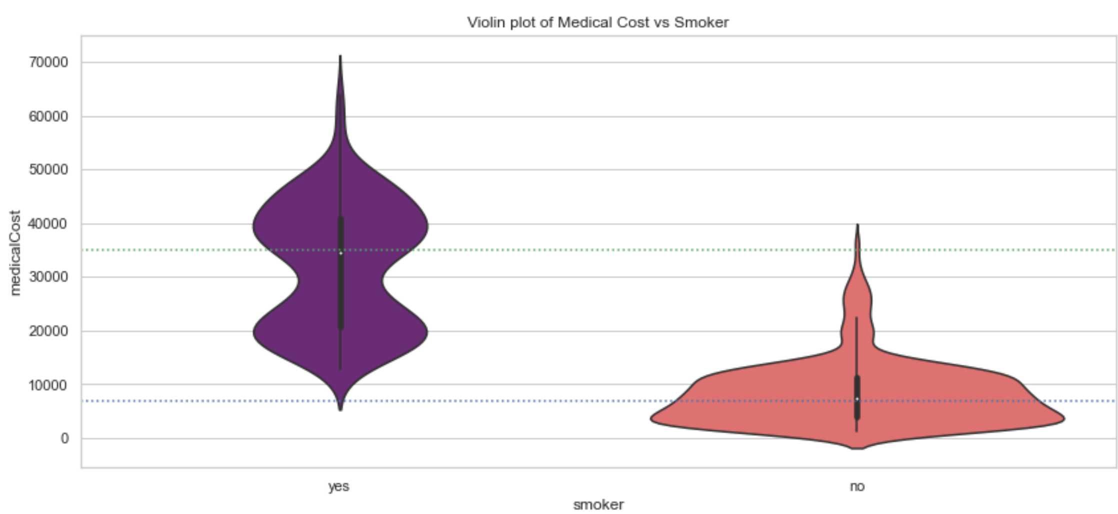


Figure 8: Violin plot of Medical Cost vs Smoker

Figure 8 shows that the medical cost for smokers is a much wide range compared to non-smokers. It is clear also that the highest value of medical cost for a non-smoking person is around 40000, and most values distributed below 20000; while for a smoking person, the medical cost goes over 60000, majority of the records lie between 15000 to 50000. The average Medical cost for a non-smoker is approximately 7000; for a smoker, the minimum medical cost is around 7000. The highest value of medical expenditure for non-smoking individuals and mean value for smoking individuals lie very closely. These observations show that there is a significant difference in medical costs for smoking and non-smoking person.

```
[ ]: sns.set_theme(style="whitegrid")
     sns.barplot(x='region', y='medicalCost', data=df1, palette='PuBuGn', ci=None)
     plt.ylabel('Medical Cost')
     plt.ylabel('Region')
     plt.title('Medical Cost vs Region')
     plt.show()
     print('Figure 9: Medical Cost vs Region')
```

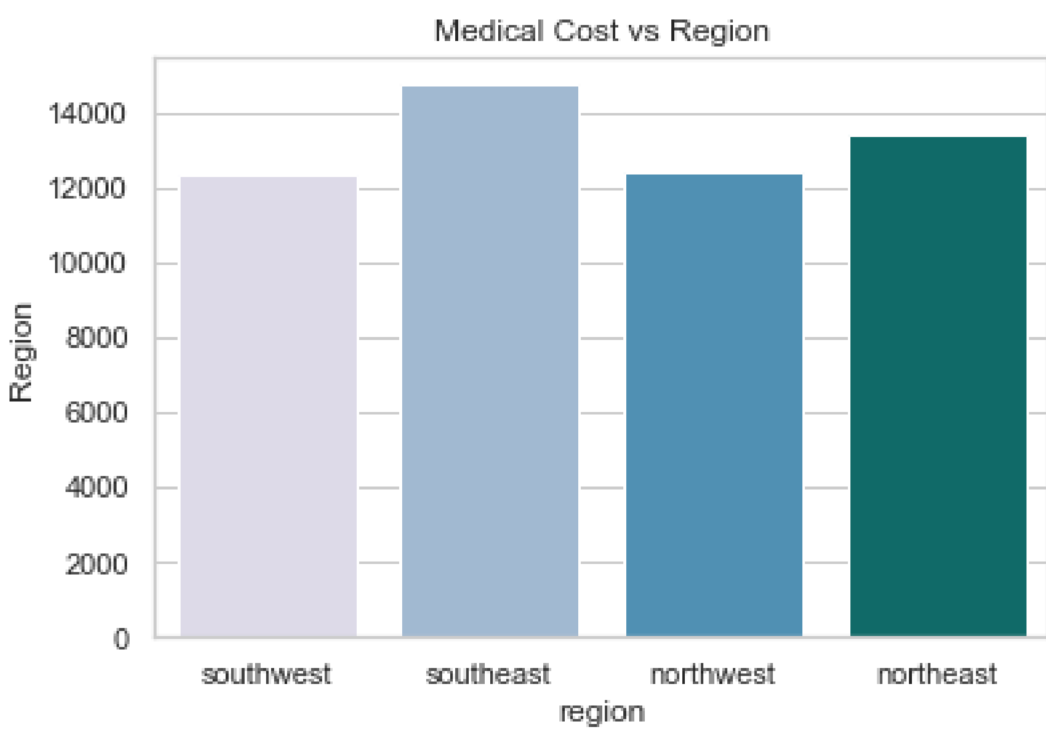
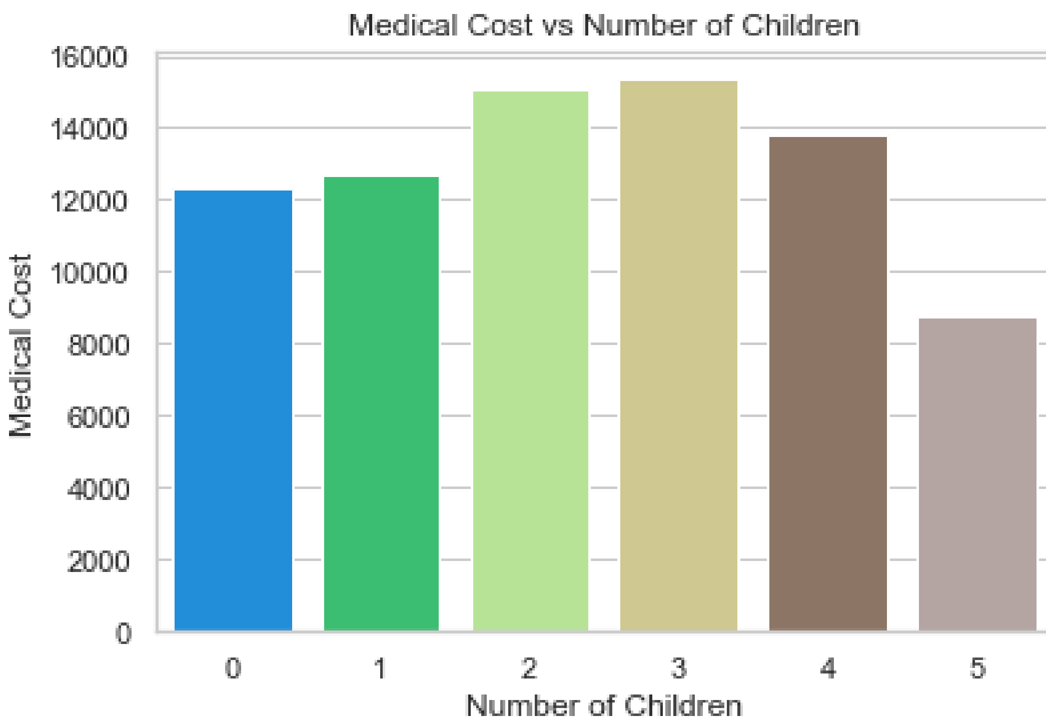


Figure 9: Medical Cost vs Region

Medical cost does not show much difference in the region. Southeast shows a slightly higher value for the medical cost, and the northeast shows the lowest value.

[ ]:
```
sns.set_theme(style="whitegrid")
sns.barplot(x='children', y='medicalCost',
            data=df1, palette='terrain', ci=None)
plt.ylabel('Medical Cost')
plt.xlabel('Number of Children')
plt.title('Medical Cost vs Number of Children')
plt.show()
print('Figure 10: Medical Cost vs Number of Children')
```




```
Figure 10: Medical Cost vs Number of Children
```

Medical cost vs a number of children shows that individuals with two and three children spend more on medical costs than other groups. The lowest value for medical cost resulted from individuals with five children.

[ ]:
```
sns.set_theme(style="whitegrid")
sns.barplot(x='sex', y='medicalCost', hue='region',
            data=df1, palette='PuBuGn', ci=None)
plt.ylabel('Medical Cost')
plt.xlabel('Sex')
plt.title('Medical Cost vs Gender grouped by Region')
plt.show()
print('Figure 11: Medical Cost vs Gender grouped by Region')
```

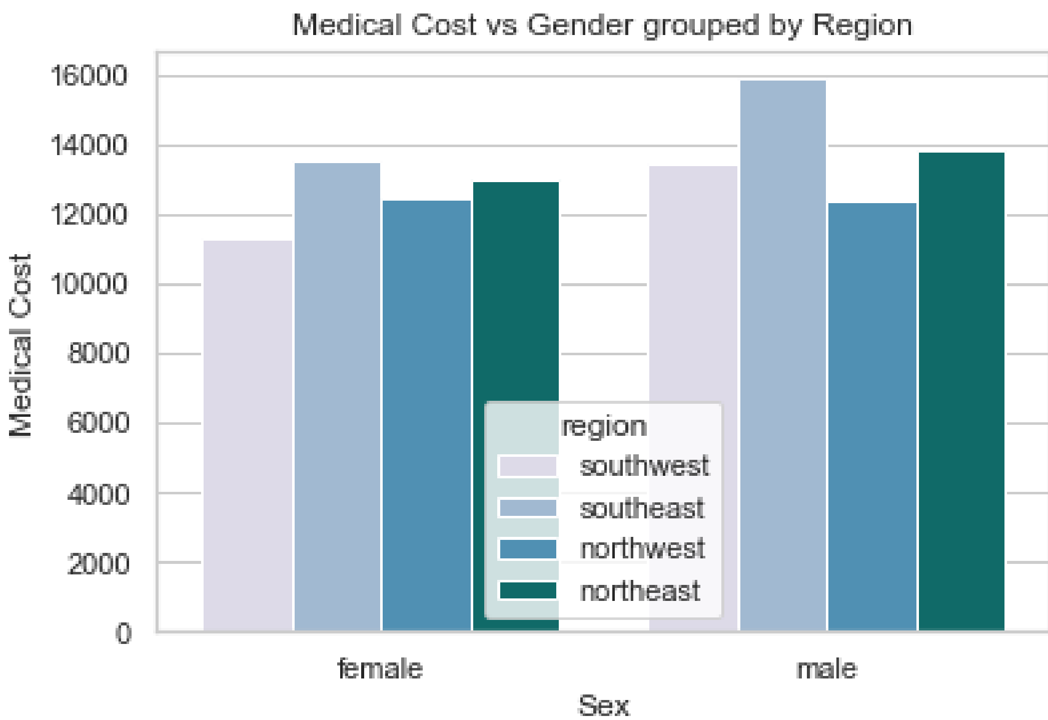


Figure 11: Medical Cost vs Gender grouped by Region

Medical cost for gender, when grouped by region, shows the highest for the southeast, same as the graph for the whole population in figure 9. However, in contrast to figure 9, the lowest for females was recorded from the southwest, while the lowest for males was recorded from the northwest, as same as figure 9.

[ ]:
```
f = plt.figure(figsize=(15, 5))
ax = f.add_subplot(131)
sns.scatterplot(x='age', y='medicalCost', data=df1,
                palette='magma', hue='region', ax=ax)
ax.set_title('Scatter plot of Medical Cost vs Age')

ax = f.add_subplot(132)
sns.scatterplot(x='bmi', y='medicalCost', data=df1,
                palette='viridis', hue='region')
ax.set_title('Scatter plot of Medical Cost vs BMI')

ax = f.add_subplot(133)
sns.scatterplot(x='children', y='medicalCost', data=df1,
                palette='YlOrBr', hue='region')
ax.set_title('Scatter plot of Medical Cost vs Children')
plt.show()
```

```python
print('Figure 12: Medical Cost vs Cotinous variables and Region')
```

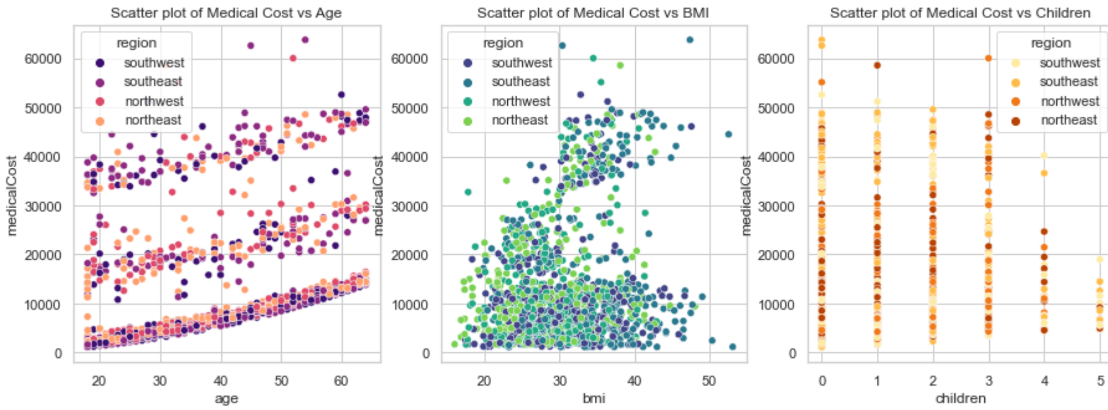


Figure 12: Medical Cost vs Cotinous variables and Region

Medical costs are getting higher with age. According to figure 12, there are three separate regions for medical spending when plotted with age. Further analysis can be done to identify any factors affecting this separation. Bmi values for the highest medical costs lie towards the highest end. There are not many high medical cost records in the lower BMIs. However, no clear patterns are visible with the BMI and medical costs. As discussed when analysing figure 10, individuals with five children show lower values for medical costs. The highest numbers are recorded among individuals with no children.

Scatter plots do not show any identifiable pattern with the region in any of the plots.

[ ]:
```python
f = plt.figure(figsize=(15, 5))
ax = f.add_subplot(131)
sns.scatterplot(x='age', y='medicalCost', data=df1,
                palette='ocean', hue='smoker', ax=ax)
ax.set_title('Scatter plot of Medical Cost vs Age')

ax = f.add_subplot(132)
sns.scatterplot(x='bmi', y='medicalCost', data=df1,
                palette='twilight_shifted', hue='smoker')
ax.set_title('Scatter plot of Medical Cost vs BMI')

ax = f.add_subplot(133)
sns.scatterplot(x='children', y='medicalCost', data=df1,
                palette='gist_earth', hue='smoker')
ax.set_title('Scatter plot of Medical Cost vs Children')
plt.show()

print('Figure 13: Medical Cost vs Cotinous variables and Smoker')
```

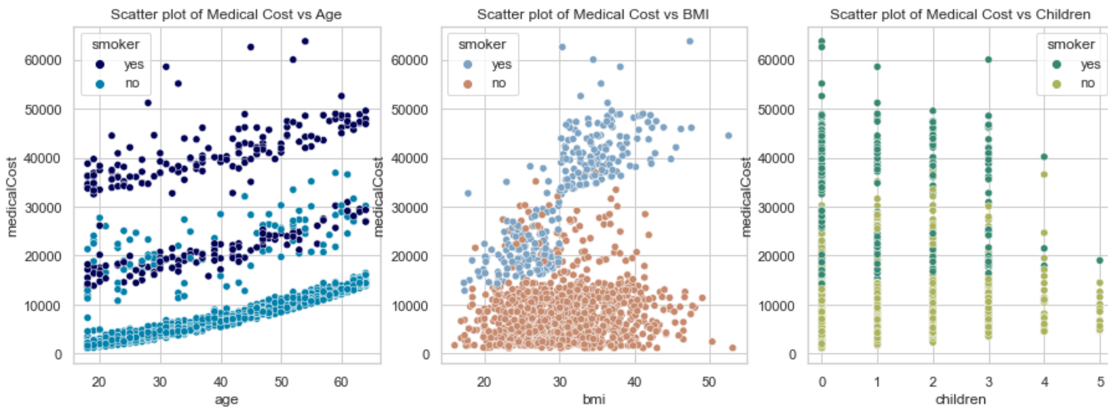


Figure 13: Medical Cost vs Cotinous variables and Smoker

Figure 13 shows the band that appears in medical cost vs age relates to smoking. The lowest band only has non-smoking individuals. The middle band has both smoking and non-smoking individuals, while the upper ban only has smoking individuals. The other two graphs also show more smoking individuals at the higher end of the graph.

1.1.3 Transform categorical varibles to numerical

Lable encoding is used where ever possible to avoid increasing dimensionality. When there are more than two unique values in the column and no specific ordering, Dummy values are used.

[ ]:
```
# The lable encoding is used to transform smoker and sex variables
le = LabelEncoder()

# Sex variable
le.fit(df1.sex.drop_duplicates())
df1.sex = le.transform(df1.sex)

# Smoker variable
le.fit(df1.smoker.drop_duplicates())
df1.smoker = le.transform(df1.smoker)
```

[ ]:
```
# Dummy variable introduced for region variable
df1_encode = pd.get_dummies(data=df1, prefix='RE', prefix_sep='_',
                            columns=['region'],
                            drop_first=False,
                            dtype='int8')

df1_encode.head(2)
```

[ ]:
```
   age  sex    bmi  children  smoker  medicalCost  RE_northeast  RE_northwest  \
0   19    0  27.90         0       1   16884.9240             0             0
1   18    1  33.77         1       0    1725.5523             0             0
```

	RE_southeast	RE_southwest
0	0	1
1	1	0

1.1.4 Correlation

Correlation is used to identify the relationship between variables and to choose the three best predictors for medical cost. Since there are outliers, Spearman correlation was used here as it calculates correlation using the ranking method. Moreover, the Pearson correlation compares numerical relationships and is sensitive to outliers.

[ ]:
```python
plt.figure(figsize=(15, 5))

# plot the heatmap
# Since there are outliers Spearman correlation was used here.
sns.heatmap(df1_encode.corr(method='pearson'),
            cmap='BuPu',
            annot=True,)
plt.show()
print('Figure 14: Correlation plot for all the variables in the dataset')
```

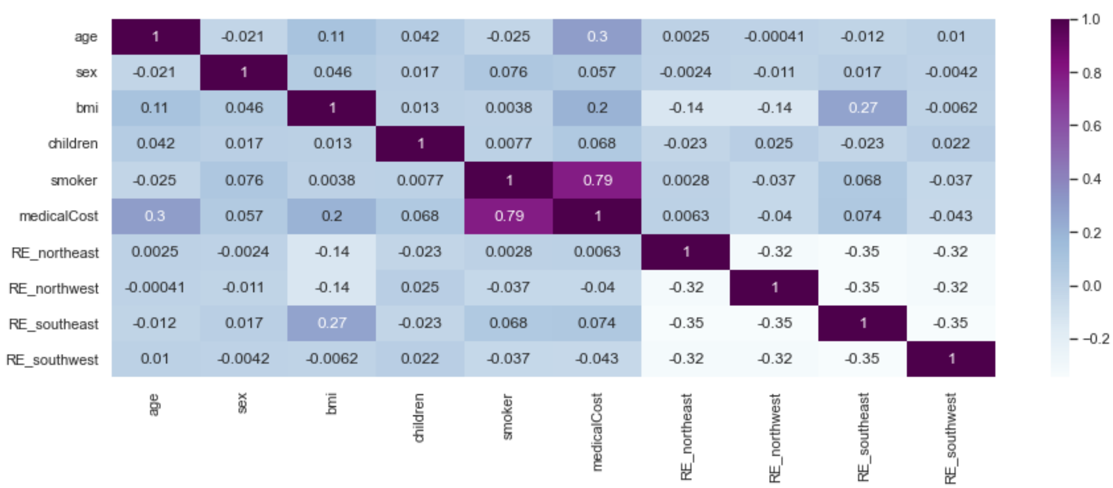


Figure 14: Correlation plot for all the variables in the dataset

Correlation analysis shows the highest correlation with the smoker column and second higher for the age column, and the third for BMI. The smoker variable shows a strong positive correlation with 0.79. Age and BMI show a weak positive correlation with 0.3 and 0.2. All the other variables show almost no correlation, with a correlation coefficient of less than 0.1. Therefore age, smoker and BMI are identified as the best three predictors for medical cost.

1.1.5 Simple linear models to predict medical cost

Simple linear model to predict medical cost with age

[ ]:
```
x1 = df1_encode[['age']]
y = df1_encode[['medicalCost']]
x1_train, x1_test, y_train, y_test = train_test_split(
    x1, y, test_size=0.2, random_state=3)
model = LinearRegression()
model.fit(x1_train, y_train)
r_sq = model.score(x1_train, y_train)
print(f'coefficient of determination: {r_sq}')
print(f'intercept: {model.intercept_}')
print(f'slope: {model.coef_}')
y_pred = model.predict(x1_test)

mse = mean_squared_error(y_test, y_pred)
print(f'Mean squared error: {mse}')

r2 = r2_score(y_test, y_pred)
print(f'R-squared: {r2}')
```

```
coefficient of determination: 0.08919404064482284
intercept: [3089.27775168]
slope: [[258.24833494]]
Mean squared error: 137276316.90775076
R-squared: 0.08984531343011881
```

The model has an R-squared of 0.08, which suggest the dependent variable does not explain the variation of the independent variable properly, as the R-squared is closer to 0 than 1. The slope of 258 shows that for each year increase in age, there is a 258 increase in medical cost. The mean squared error is equal to 137,276,316, a fairly large value. As figure 15 shows, the three bands of medical costs had to predict when using simple regression. Figure 15 also shows the inrease of the medical cost when the age increases.

[ ]:
```
sns.regplot(x=x1_train, y=y_train, color='#66AA88')
plt.show()
print('Figure 15: Regression line for Medical Cost and Age')
```

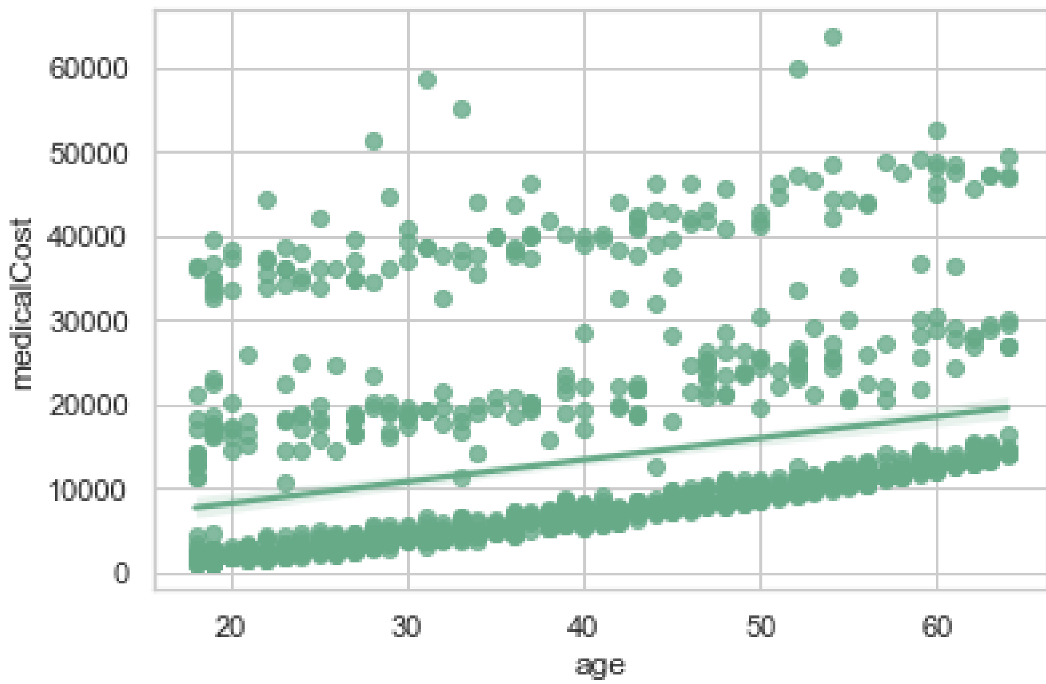


Figure 15: Regression line for Medical Cost and Age

The higher value of residual error can be resulted from the significant variation of medical cost for a certain age value as seen in figure 15.

Simple linear model to predict medical cost with smoker

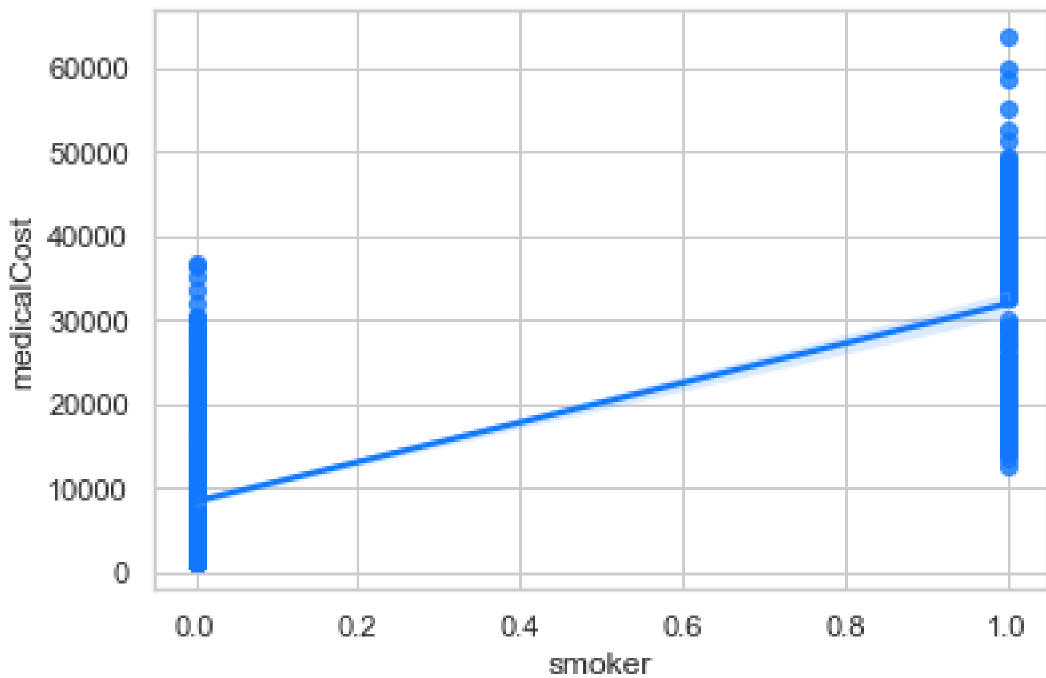
```
[ ]: x1 = df1[['smoker']]
y = df1[['medicalCost']]
x1_train, x1_test, y_train, y_test = train_test_split(
    x1, y, test_size=0.2, random_state=3)
model = LinearRegression()
model.fit(x1_train, y_train)
r_sq = model.score(x1_train, y_train)
print(f'coefficient of determination: {r_sq}')
print(f'intercept: {model.intercept_}')
print(f'slope: {model.coef_}')
y_pred = model.predict(x1_test)

mse = mean_squared_error(y_test, y_pred)
print(f'Mean squared error: {mse}')

r2 = r2_score(y_test, y_pred)
print(f'R-squared: {r2}')
```

```
coefficient of determination: 0.6162667489541495
```

```
intercept: [8433.799658]
slope: [[23506.57981273]]
Mean squared error: 55347801.452357695
R-squared: 0.6330389537107518
```

The model has R-squared 0.6, which is slightly a better prediction closer to the middle value between 0 and 1. Here slope does not hold much information as the dependent variable is a binary variable. The mean squared error is equal to 55,347,801, a fairly large value. Figure 16 shows a regression line fitted to the data. Figure 16 also shows the inrease of the medical cost in the two category of smiking and non-smoking.

[ ]:
```
sns.regplot(x=x1_train, y=y_train, color='#1177FF')
plt.show()
print('Figure 16: Regression line for Medical Cost and Smoker')
```




```
Figure 16: Regression line for Medical Cost and Smoker
```

There is a clear pattern for medical costs for smokers and non-smokers. The regression plot in figure 16 shows the increase in medical costs for smoking individuals. Clearly, there are a significant amount of residuals.

Simple linear model to predict medical cost with BMI

[ ]:
```
x1 = df1_encode[['bmi']]
y = df1_encode[['medicalCost']]
x1_train, x1_test, y_train, y_test = train_test_split(
    x1, y, test_size=0.2, random_state=3)
```

```
model = LinearRegression()
model.fit(x1_train, y_train)
r_sq = model.score(x1_train, y_train)
print(f'coefficient of determination: {r_sq}')
print(f'intercept: {model.intercept_}')
print(f'slope: {model.coef_}')
y_pred = model.predict(x1_test)

mse = mean_squared_error(y_test, y_pred)
print(f'Mean squared error: {mse}')

r2 = r2_score(y_test, y_pred)
print(f'R-squared: {r2}')
```

```
coefficient of determination: 0.03789460176473547
intercept: [1310.83699573]
slope: [[387.33454902]]
Mean squared error: 144140190.02346116
R-squared: 0.04433719939408365
```

The model has R-squared 0.04, which suggests the model does not predict medical cost well as it is closer to 0 than 1. The slope shows a 387 increase in medical cost for a unit increase in BMI. The mean squared error is equal to 144,140,190, a reasonably large value. Figure 17 shows that there is a lot of observation lying fairly far away from the regression line toward the higher values of BMI.

[ ]:
```
sns.regplot(x=x1_train, y=y_train, color='purple')
plt.show()
print('Figure 17: Regression line for Medical Cost and BMI')
```

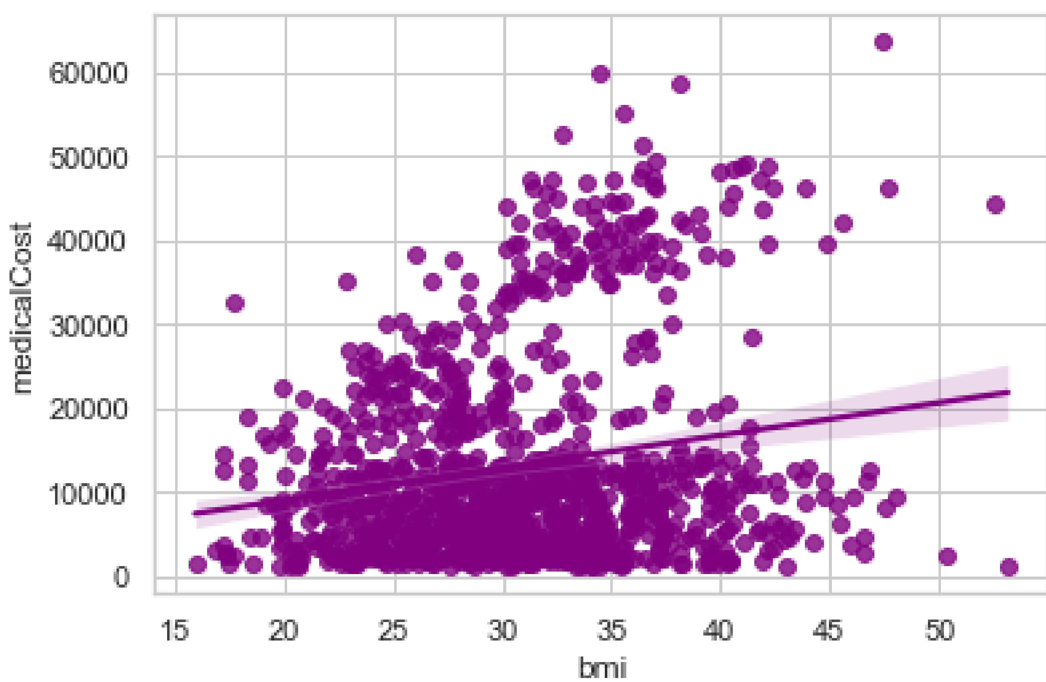


Figure 17: Regression line for Medical Cost and BMI

Figure 17 shows that when BMI increases, the residuals gets larger as the medical cost spreads in lager range.

Models with BMI and Age has much smaller R-squared value. The line in figure 16 has a higher angle with a slope value of 23506 than the linear model for BMI with a slope value of 387 and age with a slope value of 258. **Overall, the model with the smoker variable performs better** when compared R-squared value and mean squared error.

1.1.6 Multivariate regression models to predict medical cost

There are two multivariate models creatd with three best predictors and with all the vaariables.

Multivariate regression model to predict medical cost with age, smoker and bmi.

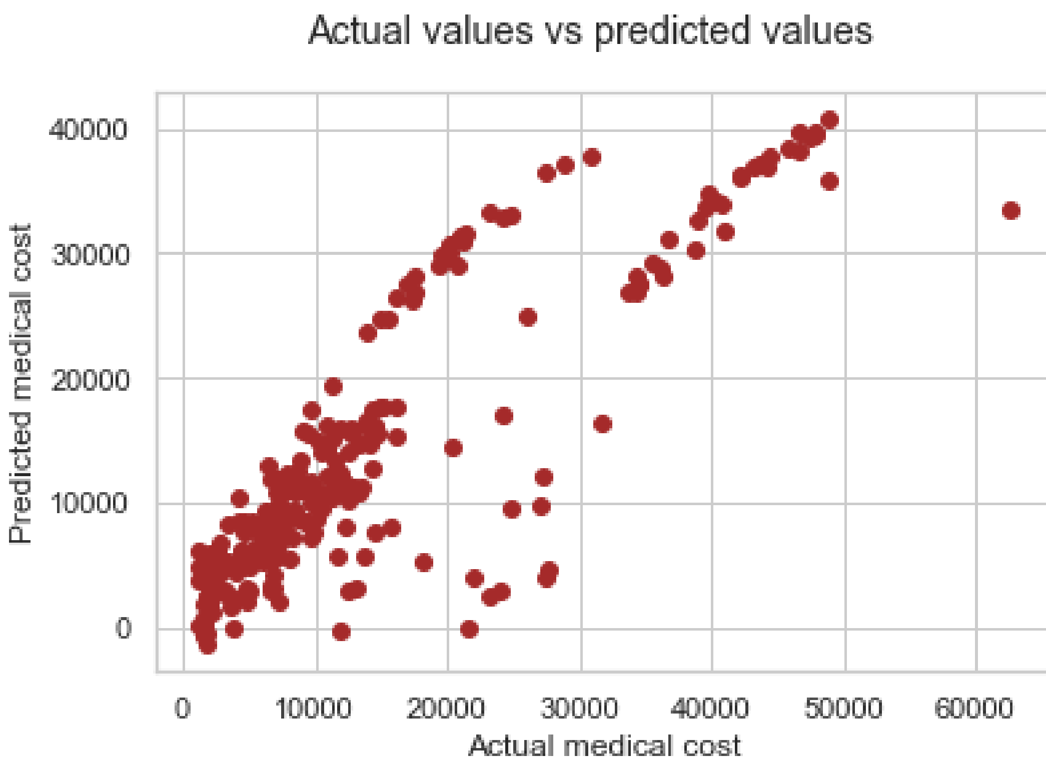
[ ]:
```
# Dropping all the variables except three highest correlated variables.
x1 = df1_encode.drop(columns=['sex', 'medicalCost', 'RE_northeast',
                     'RE_northwest', 'RE_southeast', 'RE_southwest',␣
 ↪'children'])
y = df1_encode[['medicalCost']]
x1_train, x1_test, y_train, y_test = train_test_split(
    x1, y, test_size=0.2, random_state=3)
model = LinearRegression()
model.fit(x1_train, y_train)
r_sq = model.score(x1_train, y_train)
print(f'coefficient of determination: {r_sq}')
print(f'intercept: {model.intercept_}')
print(f'slope: {model.coef_}')
y_pred = model.predict(x1_test)

mse = mean_squared_error(y_test, y_pred)
print(f'Mean squared error: {mse}')

r2 = r2_score(y_test, y_pred)
print(f'R-squared: {r2}')
```

```
coefficient of determination: 0.7487255284553438
intercept: [-12297.07065608]
slope: [[  265.48317257   333.28328133 23817.80914975]]
Mean squared error: 38904433.375912696
R-squared: 0.7420600059569823
```

The multivariate model with all three variables has a lower mean squared error than simple linear models with each of them. Where a model with age has 137,276,316, a model with a smoker has 55,347,801, the model with BMI has 144,140,190, and the model with all three variables has 38,904,433, which is a better value than the best simple leaner model.

R-squared value also shows a similar result with 0.74 for the multivariate model with three variables which is much closer to 1 than 0. Slopes for each variable stay closer to the linear models.

```
[ ]: fig, ax = plt.subplots()
     ax.scatter(y_test, y_pred, color='brown')
     fig.suptitle('Actual values vs predicted values')
     plt.ylabel('Predicted medical cost')
     plt.xlabel('Actual medical cost')
     plt.show()
     print('Figure 18: Actual value vs predicted value plot for multivariate model␣
      ↪with Age, BMI and Smoker variables as independent variables')
```

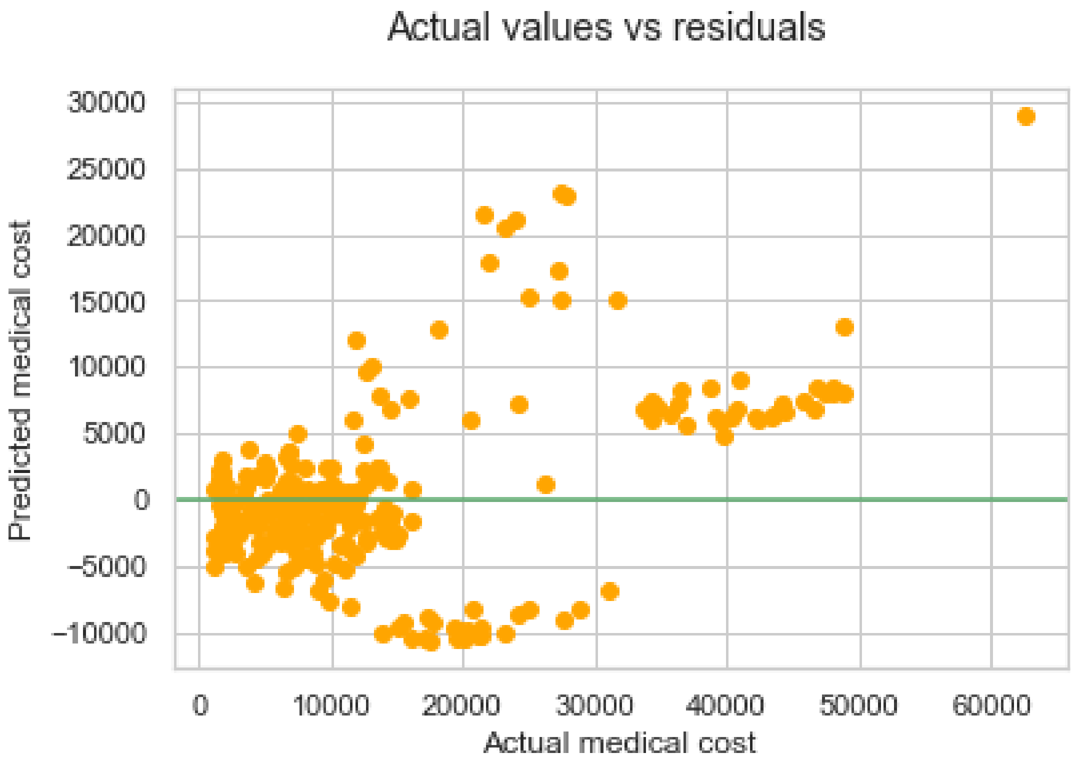


`Figure 18: Actual value vs predicted value plot for multivariate model with Age, BMI and Smoker variables as independent variables`

Figure 18 shows that higher values are predicted for higher actual values. However, in the range of 10000 to 30000 medical costs, there seems to have a wider range of expected values distributed from around zero to closer to 40000. These are the values that introduced more errors into the model. Lower values of medical costs also have a good prediction.

```
[ ]: fig, ax = plt.subplots()
     ax.scatter(y_test, (y_test - y_pred), color='orange')
     plt.axhline(y=0.0, color='g', linestyle='-')
```

```
fig.suptitle('Actual values vs residuals')
plt.ylabel('Predicted medical cost')
plt.xlabel('Actual medical cost')
plt.show()
print('Figure 19: Residual plot for multivariate model with Age, BMI and Smoker␣
 ↪variables as independent variables')
```




```
Figure 19: Residual plot for multivariate model with Age, BMI and Smoker
variables as independent variables
```

The residual plot in figure 19 also confirms the results of figure 18. In the mid-range, there is a higher variation of residual values. It is also clear from figure 19 that the values over 60000 have resulted in the most significant residual of the model.

[ ]:
```
residuals = (y_test - y_pred)

plt.hist(residuals, color='purple')
plt.show()
print('Figure 20: Histogram of residuals for multivariate model with Age, BMI␣
 ↪and Smoker variables as independent variables')
```

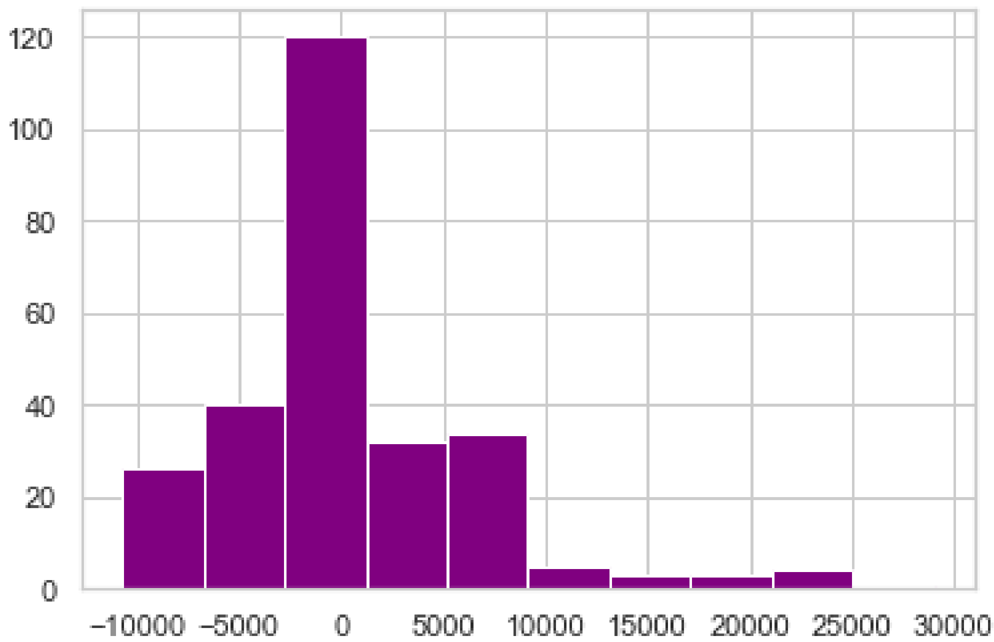


Figure 20: Histogram of residuals for multivariate model with Age, BMI and Smoker variables as independent variables

The histogram in figure 20 shows that the distribution of residuals is skewed. There are more zero or negative values than positive values. It is also clear there is a long tail towards the positive end, having larger positive residuals than negative residuals.

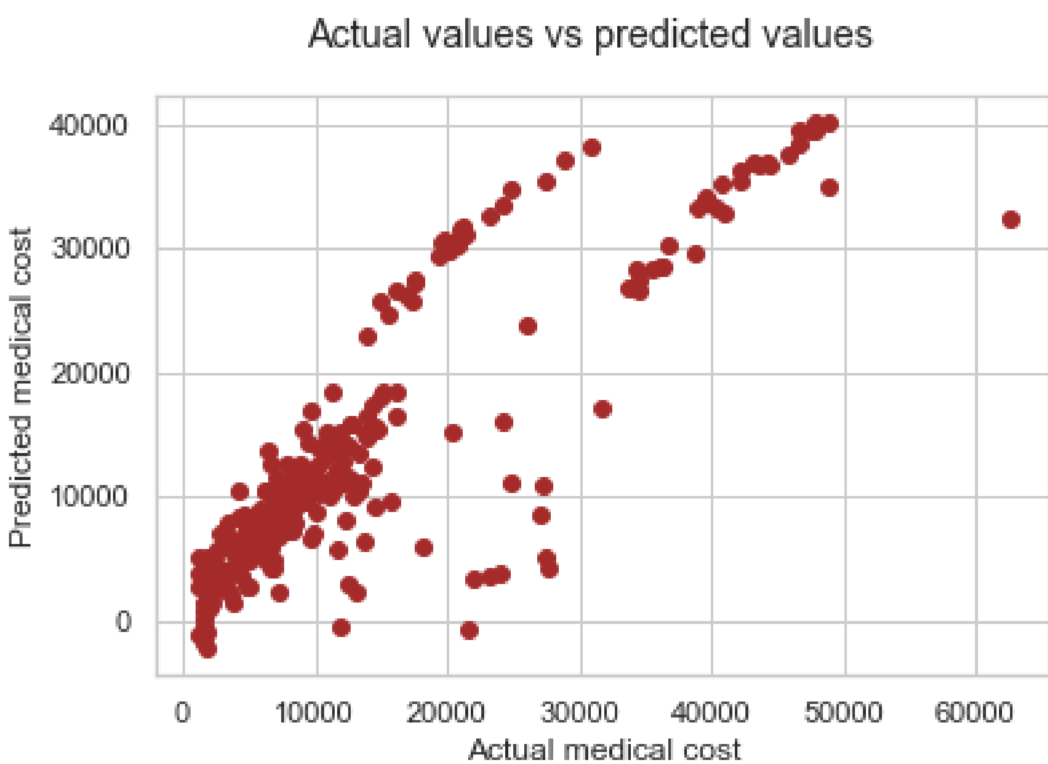
Multivariate regression model to predict medical cost all the variables.

[ ]:
```
x1 = df1_encode.drop(columns=['medicalCost'])
y = df1_encode[['medicalCost']]
x1_train, x1_test, y_train, y_test = train_test_split(
    x1, y, test_size=0.2, random_state=3)
model = LinearRegression()
model.fit(x1_train, y_train)
r_sq = model.score(x1_train, y_train)
print(f'coefficient of determination: {r_sq}')
print(f'intercept: {model.intercept_}')
print(f'slope: {model.coef_}')
y_pred = model.predict(x1_test)

mse = mean_squared_error(y_test, y_pred)
print(f'Mean squared error: {mse}')

r2 = r2_score(y_test, y_pred)
print(f'R-squared: {r2}')
```

```
coefficient of determination: 0.7534063569267673
intercept: [-13172.39719688]
slope: [[  262.31558491  -222.45944647   349.53918186   574.50846193
  23827.48548329   625.80325666   204.49787511  -537.19360189
   -293.10752988]]
Mean squared error: 39202908.26059814
R-squared: 0.7400810898464749
```

The model has a 0.74 R-squared error which shows a good prediction for the medical cost. The multivariate regression model with all the variables is performing closer to the multivariate model with the three best variables. The performance here is slightly reduced than the model with three variables when comparing the R-squared value and mean squared error.

[ ]:
```
fig, ax = plt.subplots()
ax.scatter(y_test, y_pred, color='brown')
plt.ylabel('Predicted medical cost')
plt.xlabel('Actual medical cost')
fig.suptitle('Actual values vs predicted values')
plt.show()
print('Figure 21: Actual value vs predicted value plot for multivariate model␣
 ↪with all the independent variables')
```




```
Figure 21: Actual value vs predicted value plot for multivariate model with all
the independent variables
```

[ ]:
```
fig, ax = plt.subplots()
ax.scatter(y_test, (y_test - y_pred), color='orange')
plt.axhline(y=0.0, color='g', linestyle='-')
fig.suptitle('Actual values vs residuals')
plt.show()
print('Figure 22: Residual plot for multivariate model with all the independent␣
↪variables')
```

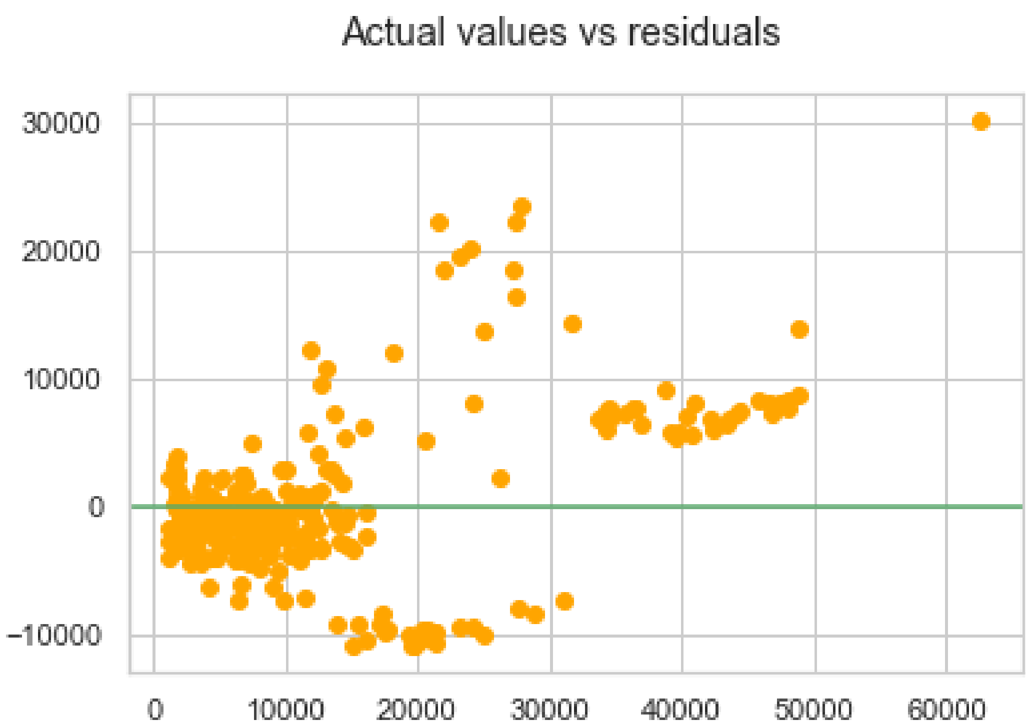


Figure 22: Residual plot for multivariate model with all the independent variables

[ ]:
```
residuals = (y_test - y_pred)

plt.hist(residuals, color='purple')
plt.show()
print('Figure 23: Histogram of residuals for multivariate model with all the␣
↪independent variables')
```

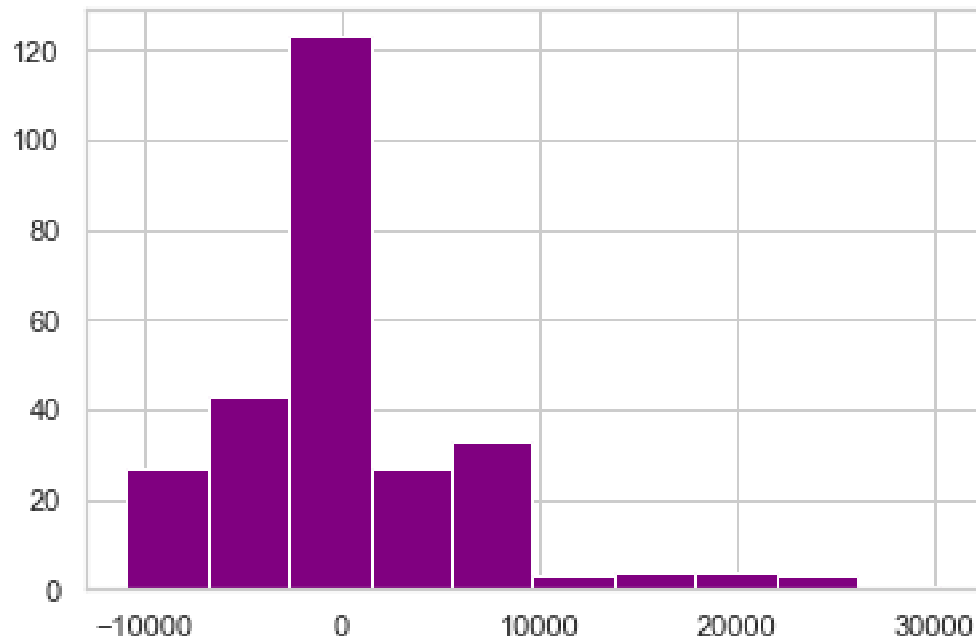


Figure 23: Histogram of residuals for multivariate model with all the independent variables

The actual value vs predicted value plot in the figure, actual values vs residuals in figure 22 and the distribution of the residuals in figure 23 show almost similar results as the respective plot for the multivariate model with the best three predicters. The highest positive error value seems slightly higher in the model with all the variables in it than in the model with only the three best predictors.

Overall, it is clear from the above results that the multivariate regression model with the three best predictors predicts medical cost better than all the other four models trained in this task. Given the time taken to train the model using all of the variables and best-correlated variables, and that compared with the accuracy of the prediction, the model with the best predictors chosen based on correlation seems the best choice.

---

2 Question 2. Census Income

2.0.1 Introduction

The dataset contains US census data, and the task is to predict whether a given individual earns more than $50000. The data set is labelled and includes two classes. Five machine learning models with different classifiers and two artificial neural network models with a different number of layers are used to predict the income of an individual. The list of variables in the dataset is:

- age: the age of an individual
- workclass: employment status of an individual
- fnlwgt: final weight. The number of people the census believes the entry represents

- education: the highest level of education achieved by an individual
- education-num: the highest level of education achieved in numerical form
- marital-status: marital status of an individual.
- occupation: the general type of occupation of an individual
- relationship: represents what this individual is relative to others
- sex: the biological sex of the individual
- capital-gain: capital gains for an individual
- capital-loss: capital loss for an individual
- hours-per-week: the hours an individual has reported to work per week
- native-country: country of origin for an individual
- label: whether or not an individual makes more than $50,000 annually.

2.0.2 Data Understanding and Preperration

The distribution of the data, type of the data, missing values, and a number of unique values in the data are analysed. Missing values are imputed based on the distribution of the data. Correlation is used to understand the relationship of the variables.

Lable encoding, One hot encoding is used to transform categorical data and scaling is done before using data in the machine learning models.

[ ]:
```
df2 = pd.read_csv('CensusDB.csv', na_values=['?'])
df2.head()
```

[ ]:
```
   age workclass  fnlwgt     education  education-num marital-status  \
0   90       NaN   77053       HS-grad              9        Widowed
1   82   Private  132870       HS-grad              9        Widowed
2   66       NaN  186061  Some-college             10        Widowed
3   54   Private  140359       7th-8th              4       Divorced
4   41   Private  264663  Some-college             10      Separated

          occupation   relationship     sex  capital-gain  capital-loss  \
0                NaN  Not-in-family  Female             0          4356
1    Exec-managerial  Not-in-family  Female             0          4356
2                NaN      Unmarried  Female             0          4356
3  Machine-op-inspct      Unmarried  Female             0          3900
4     Prof-specialty      Own-child  Female             0          3900

   hours-per-week native-country income
0              40  United-States  <=50K
1              18  United-States  <=50K
2              40  United-States  <=50K
3              40  United-States  <=50K
4              40  United-States  <=50K
```

[ ]:
```
print('Number of rows and columns in the dataset: ', df2.shape)
print('There are six continous variables and eight categorical variables.')
```

```
Number of rows and columns in the dataset:  (32561, 14)
```

There are six continous variables and eight categorical variables.

[ ]:
```
df2.isnull().sum()
```

[ ]:
```
age                  0
workclass         1836
fnlwgt               0
education            0
education-num        0
marital-status       0
occupation        1843
relationship         0
sex                  0
capital-gain         0
capital-loss         0
hours-per-week       0
native-country     583
income               0
dtype: int64
```

[ ]:
```
# Percentage of values missing in each column
for column in df2.columns:
    percentage = df2[column].isnull().mean()
    print(f'{column}: {round(percentage*100,4)}%')
```

```
age: 0.0%
workclass: 5.6386%
fnlwgt: 0.0%
education: 0.0%
education-num: 0.0%
marital-status: 0.0%
occupation: 5.6601%
relationship: 0.0%
sex: 0.0%
capital-gain: 0.0%
capital-loss: 0.0%
hours-per-week: 0.0%
native-country: 1.7905%
income: 0.0%
```

There are missing values present in the dataset. According to the distribution of the variables, missing values should be imputed as there are only three missing values per row at maximum. Dropping the row is a disadvantage to the analysis because it deletes the information of the other variables.

[ ]:
```
max_missing = 0
# Count of missing values across rows
for i in range(len(df2.index)):
```

```
    missing_current_row = df2.iloc[i].isnull().sum()
    if(max_missing < missing_current_row):
        max_missing = missing_current_row

print('maximum null values in a row : ', max_missing,
      '\nTherefore, dropping rows containing missing values is disadvantageous.␣
 ↪Dropping the entire rows not considered as it deletes data of the other 11␣
 ↪rows')
print()
```

```
maximum null values in a row :  3
Therefore, dropping rows containing missing values is disadvantageous. Dropping
the entire rows not considered as it deletes data of the other 11 rows
```

[ ]:
```
sns.countplot(x='income', palette='viridis', data=df2)
print('Figure 2.1: Number of observations representing each value of the income␣
 ↪label')
plt.title('Counplot for income')
plt.show()
```

```
Figure 2.1: Number of observations representing each value of the income label
```

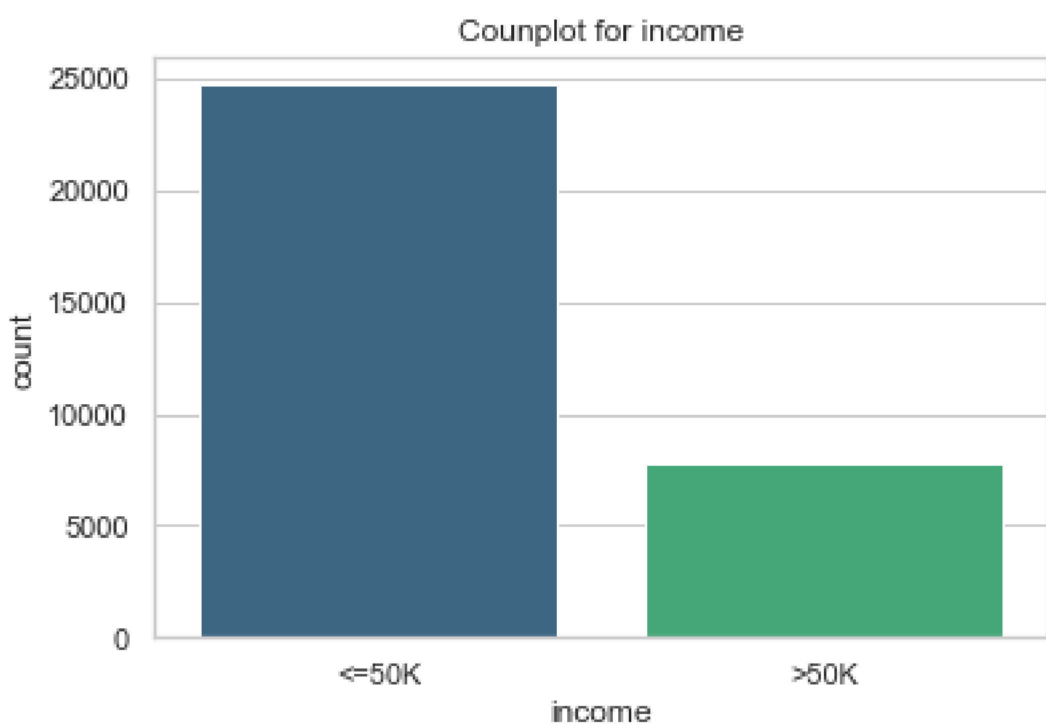


Figure 2.1 shows the target class does not have a balanced number of observations for each label

of the target class. The models should be evaluated depending on this to get better performance from the unbalanced dataset.

[ ]:
```
df2.describe()
```

[ ]:
```
                age        fnlwgt  education-num  capital-gain  capital-loss  \
count  32561.000000  3.256100e+04   32561.000000  32561.000000  32561.000000
mean      38.581647  1.897784e+05      10.080679   1077.648844     87.303830
std       13.640433  1.055500e+05       2.572720   7385.292085    402.960219
min       17.000000  1.228500e+04       1.000000      0.000000      0.000000
25%       28.000000  1.178270e+05       9.000000      0.000000      0.000000
50%       37.000000  1.783560e+05      10.000000      0.000000      0.000000
75%       48.000000  2.370510e+05      12.000000      0.000000      0.000000
max       90.000000  1.484705e+06      16.000000  99999.000000   4356.000000

       hours-per-week
count    32561.000000
mean        40.437456
std         12.347429
min          1.000000
25%         40.000000
50%         40.000000
75%         45.000000
max         99.000000
```

[ ]:
```
fig, ax = plt.subplots(2, 3, figsize=(15, 8))

plt.subplot(2, 3, 1)
plt.hist(df2.iloc[:, 0], rwidth=0.9)
plt.xlabel(df2.columns[0], fontsize=15)

plt.subplot(2, 3, 2)
plt.hist(df2.iloc[:, 2], rwidth=0.9)
plt.xlabel(df2.columns[2], fontsize=15)

plt.subplot(2, 3, 3)
plt.hist(df2.iloc[:, 4], rwidth=0.9)
plt.xlabel(df2.columns[4], fontsize=15)

plt.subplot(2, 3, 4)
plt.hist(df2.iloc[:, 9], rwidth=0.9)
plt.xlabel(df2.columns[9], fontsize=15)

plt.subplot(2, 3, 5)
plt.hist(df2.iloc[:, 10], rwidth=0.9)
plt.xlabel(df2.columns[10], fontsize=15)

plt.subplot(2, 3, 6)
```

```
plt.hist(df2.iloc[:, 11], rwidth=0.9)
plt.xlabel(df2.columns[11], fontsize=15)

plt.tight_layout()
plt.show()
print('Figure 2.2: Distribution of the continous variables')
```

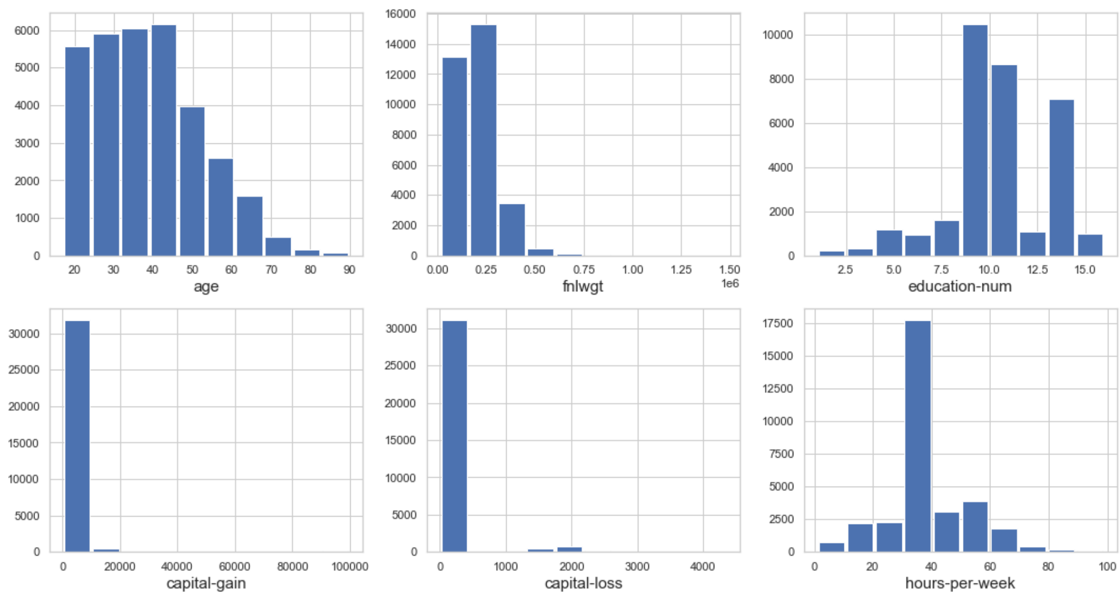
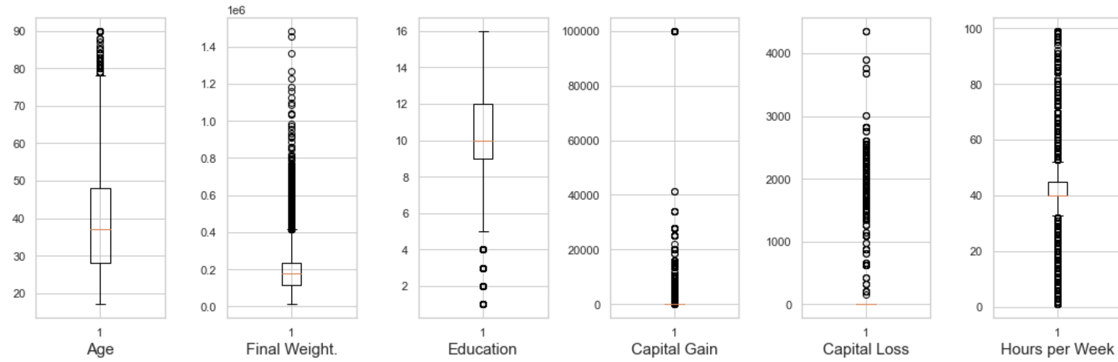


Figure 2.2: Distribution of the continous variables

All the distributions are uneven distributions. Especially, Capital gain and Capital loss are highly skewed as can be seen in the boxplot in Figure 2.2

[ ]:
```
# Boxplot of the continous variables
fig, ax = plt.subplots(1, 6, figsize=(15, 5))

plt.subplot(1, 6, 1)
plt.boxplot(df2[['age']])
plt.xlabel('Age', fontsize=15)

plt.subplot(1, 6, 2)
plt.boxplot(df2[['fnlwgt']])
plt.xlabel('Final Weight.', fontsize=15)

plt.subplot(1, 6, 3)
plt.boxplot(df2[['education-num']])
plt.xlabel('Education', fontsize=15)

plt.subplot(1, 6, 4)
```

```
plt.boxplot(df2[['capital-gain']])
plt.xlabel('Capital Gain', fontsize=15)

plt.subplot(1, 6, 5)
plt.boxplot(df2[['capital-loss']])
plt.xlabel('Capital Loss', fontsize=15)

plt.subplot(1, 6, 6)
plt.boxplot(df2[['hours-per-week']])
plt.xlabel('Hours per Week', fontsize=15)

plt.tight_layout()
plt.show()
print('Figure 2.3: Boxplot of the continous variables')
```




```
Figure 2.3: Boxplot of the continous variables
```

A boxplot is used to identify outliers. From figure 2.3, it is clear that all the continuous variables have outliers. Age and Final Weight have outliers at the higher end of the distribution. Education has outliers at the lower end. The other three variables have outliers on both sides.

This analysis suggests that the capital-gain variable has extreme values at 99999. Observations with these values are dropped as it seems to be erroneous data, and not clear how to validate the data with the given information.

[ ]:
```
df2.drop(df2[df2['capital-gain'] >= 60000].index, inplace=True)
```

[ ]:
```
freq_table = pd.crosstab(df2['workclass'], df2['income'])
freq_table
```

[ ]:
```
income          <=50K  >50K
workclass
Federal-gov       589   370
Local-gov        1476   611
Never-worked        7     0
```

```
Private           17733  4881
Self-emp-inc        494   586
Self-emp-not-inc   1817   695
State-gov           945   352
Without-pay          14     0
```

[ ]:
```python
sns.set_theme(style="whitegrid")
sns.countplot(y='workclass', hue='income', palette='rocket', data=df2)
plt.title('Countplot for workclass')
plt.show()
print('Figure 2.4: Countplot for Workclass')
```

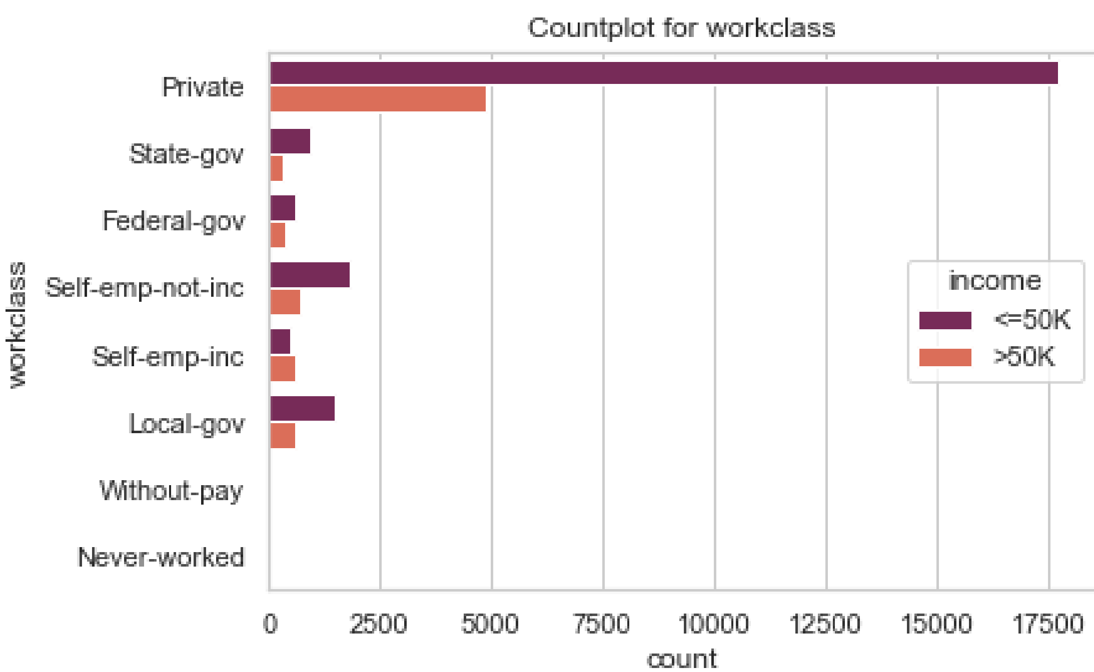


Figure 2.4: Countplot for Workclass

There are more low-income individuals, and fewer high-income individuals are visible in all the classes. In the private work-class category, the difference is significantly large.

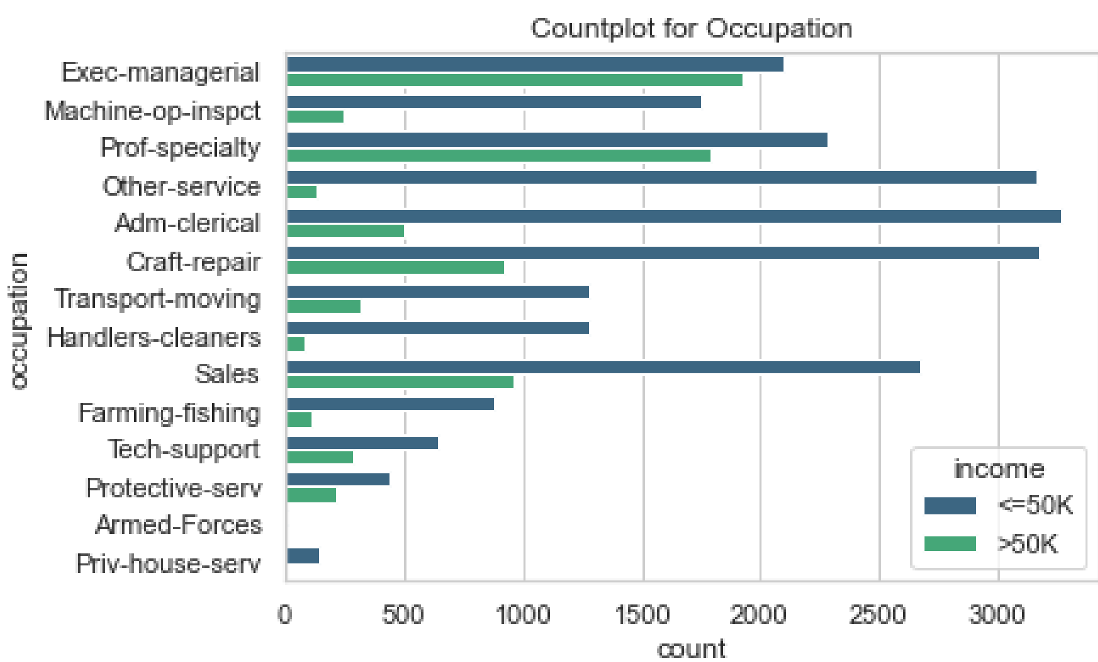
[ ]:
```python
df2['workclass'] = df2['workclass'].fillna(df2['workclass'].mode()[0])
```

[ ]:
```python
freq_table = pd.crosstab(df2['occupation'], df2['income'])
freq_table
```

[ ]:
```
income            <=50K  >50K
occupation
Adm-clerical       3263   501
Armed-Forces          8     1
```

```
Craft-repair         3170   921
Exec-managerial      2098  1926
Farming-fishing       879   115
Handlers-cleaners    1284    85
Machine-op-inspct    1752   249
Other-service        3158   135
Priv-house-serv       148     1
Prof-specialty       2281  1792
Protective-serv       438   210
Sales                2667   958
Tech-support          645   282
Transport-moving     1277   319
```

[ ]:
```
sns.countplot(y='occupation', hue='income', palette='viridis', data=df2)
plt.title('Countplot for Occupation')
plt.show()
print('Figure 2.5: Countplot for Occupation')
```




```
Figure 2.5: Countplot for Occupation
```

The same pattern of more low-income individuals and fewer high-income individuals is visible in all the classes. However, for Executive Managerial category and Professional Speciality categories have little difference in the two groups.

[ ]:
```
df2['occupation'] = df2['occupation'].fillna(df2['occupation'].mode()[0])
```

[ ]:
```
len(df2['native-country'].unique())
```

[ ]:
```
42
```

There are too many unique values in the native countries variable. In order to reduce dimensionality, their values are categorised based on geographical location.

[ ]:
```
freq_table = pd.crosstab(df2['native-country'], df2['income'])
freq_table
```

[ ]:
```
income                      <=50K  >50K
native-country
Cambodia                       12     7
Canada                         82    38
China                          55    20
Columbia                       57     2
Cuba                           70    25
Dominican-Republic             68     1
Ecuador                        24     4
El-Salvador                    97     9
England                        60    30
France                         17    12
Germany                        93    44
Greece                         21     8
Guatemala                      61     3
Haiti                          40     4
Holand-Netherlands              1     0
Honduras                       12     1
Hong                           14     6
Hungary                        10     3
India                          60    37
Iran                           25    18
Ireland                        19     5
Italy                          48    25
Jamaica                        71    10
Japan                          38    23
Laos                           16     2
Mexico                        610    32
Nicaragua                      32     2
Outlying-US(Guam-USVI-etc)     14     0
Peru                           29     2
Philippines                   137    60
Poland                         48    12
Portugal                       33     4
Puerto-Rico                   102    12
Scotland                        9     3
South                          64    15
```

```
Taiwan                          31    19
Thailand                        15     3
Trinadad&Tobago                 17     2
United-States                21999  7029
Vietnam                         62     5
Yugoslavia                      10     6
```

[ ]:
```
df2['native-country'] = df2['native-country'].fillna('Other')
```

The missing values in the native countries have been imputed with the value **other**. All the other wrong country names are categorised as 'other' in the next step, and other native countries are separated into groups depending on the region.

[ ]:
```
# Age grouping using mean values
df2.loc[df2['native-country'] == 'Cambodia', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'China', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'Vietnam', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'Thailand', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'Taiwan', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'Philippines', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'Japan', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'Hong', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'India', 'native-country'] = 'Asia'
df2.loc[df2['native-country'] == 'Iran', 'native-country'] = 'Asia'


df2.loc[df2['native-country'] == 'Portugal', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'Poland', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'Italy', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'Ireland', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] ==
        'Holand-Netherlands', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'Greece', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'Germany', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'France', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'England', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'Scotland', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'Yugoslavia', 'native-country'] = 'Europe'
df2.loc[df2['native-country'] == 'Hungary', 'native-country'] = 'Europe'


df2.loc[df2['native-country'] == 'Trinadad&Tobago',
        'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Puerto-Rico', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Peru', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Nicaragua', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Mexico', 'native-country'] = 'America'
```

```
df2.loc[df2['native-country'] == 'Jamaica', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Honduras', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Haiti', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Guatemala', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'El-Salvador', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Ecuador', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Dominican-Republic',
        'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Cuba', 'native-country'] = 'America'
df2.loc[df2['native-country'] == 'Columbia', 'native-country'] = 'America'

df2.loc[df2['native-country'] == 'South', 'native-country'] = 'Other'
df2.loc[df2['native-country'] == 'Laos', 'native-country'] = 'Other'
df2.loc[df2['native-country'] ==
        'Outlying-US(Guam-USVI-etc)', 'native-country'] = 'Other'
```

[ ]:
```
pd.crosstab(df2['native-country'], df2['income'])
```

[ ]:
```
income           <=50K  >50K
native-country
America           1290   109
Asia               449   198
Canada              82    38
Europe             369   152
Other              531   156
United-States    21999  7029
```

[ ]:
```
sns.countplot(x='native-country', hue='income', palette='cubehelix', data=df2)
plt.title('Countplot for native country')
plt.show()
print('Figure 2.6: Countplot for grouped Native Country')
```

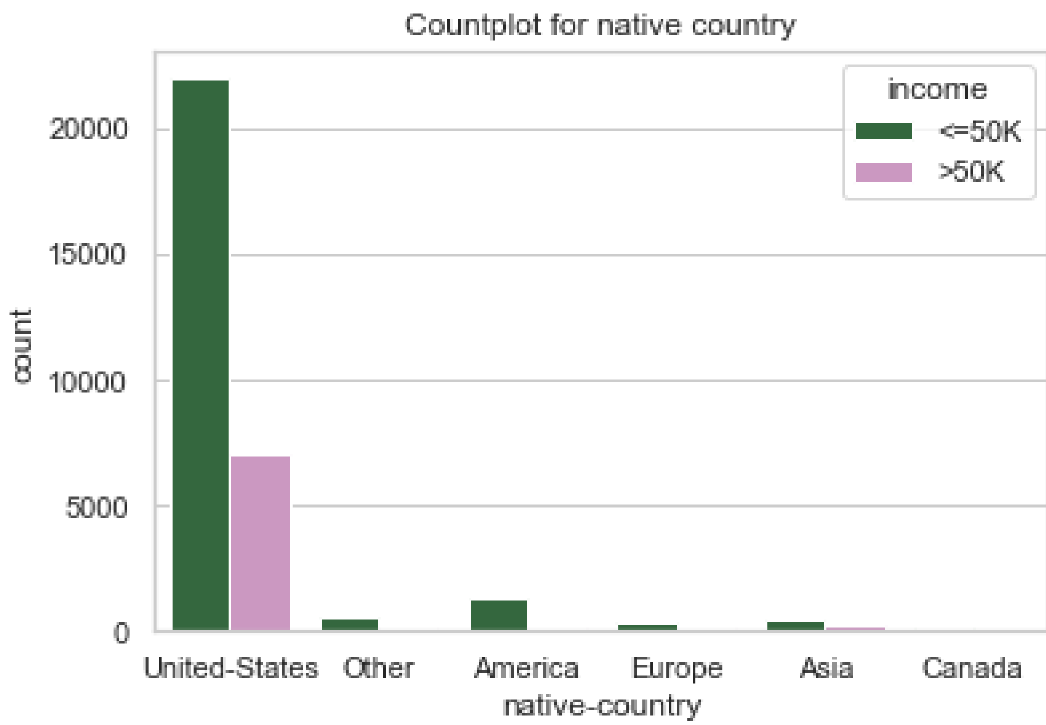


Figure 2.6: Countplot for grouped Native Country

The Native country has the most observations for the United States. There is only a small amount of observations ate recorded for other countries. The bar for lower income than 50000 dollars is prominent across all the countries.

Transforming categorical variables with lable encoding and OneHot encoding Lable encoding is used where ever possible to avoid increasing dimensionality. When there are more than two unique values in the column and no specific ordering, Dummy values are used.

[ ]:
```
# Lable encoding sex, income
# Because there are only two classes in the below two variables, label encoding␣
↪is used
le = LabelEncoder()

# Sex variable
le.fit(df2.sex.drop_duplicates())
df2.sex = le.transform(df2.sex)

# Smoker variable
le.fit(df2.income.drop_duplicates())
df2.income = le.transform(df2.income)
```

```
[ ]: # Dummy variable
     # Because there are sevaral values of native country, workclass,␣
      ↪marital-status, occupation and relationship, and has no ordering, OneHot␣
      ↪encoding is used
     df2 = pd.get_dummies(data=df2, prefix='country', prefix_sep='_', columns=[
                          'native-country'], drop_first=False, dtype='int8')
     df2 = pd.get_dummies(data=df2, prefix='wc', prefix_sep='_', columns=[
                          'workclass'], drop_first=False, dtype='int8')
     df2 = pd.get_dummies(data=df2, prefix='ms', prefix_sep='_', columns=[
                          'marital-status'], drop_first=False, dtype='int8')
     df2 = pd.get_dummies(data=df2, prefix='oc', prefix_sep='_', columns=[
                          'occupation'], drop_first=False, dtype='int8')
     df2 = pd.get_dummies(data=df2, prefix='re', prefix_sep='_', columns=[
                          'relationship'], drop_first=False, dtype='int8')
```

```
[ ]: # Dropp categorical values as they have transformed into other variables
     df2 = df2.drop(['education'], axis=1)
```

Correlation analysis

```
[ ]: plt.figure(figsize=(10, 5))
     sns.heatmap(df2[['age', 'sex', 'fnlwgt', 'education-num', 'capital-gain',␣
      ↪'capital-loss', 'hours-per-week', 'income']].corr(method='spearman'),
                 annot=True, fmt='.2f', cmap='PRGn')
     plt.title('Correlation plot for continuous variables')
     plt.show()
     print('Figure 2.7: Correlation plot for continuous variables')
```

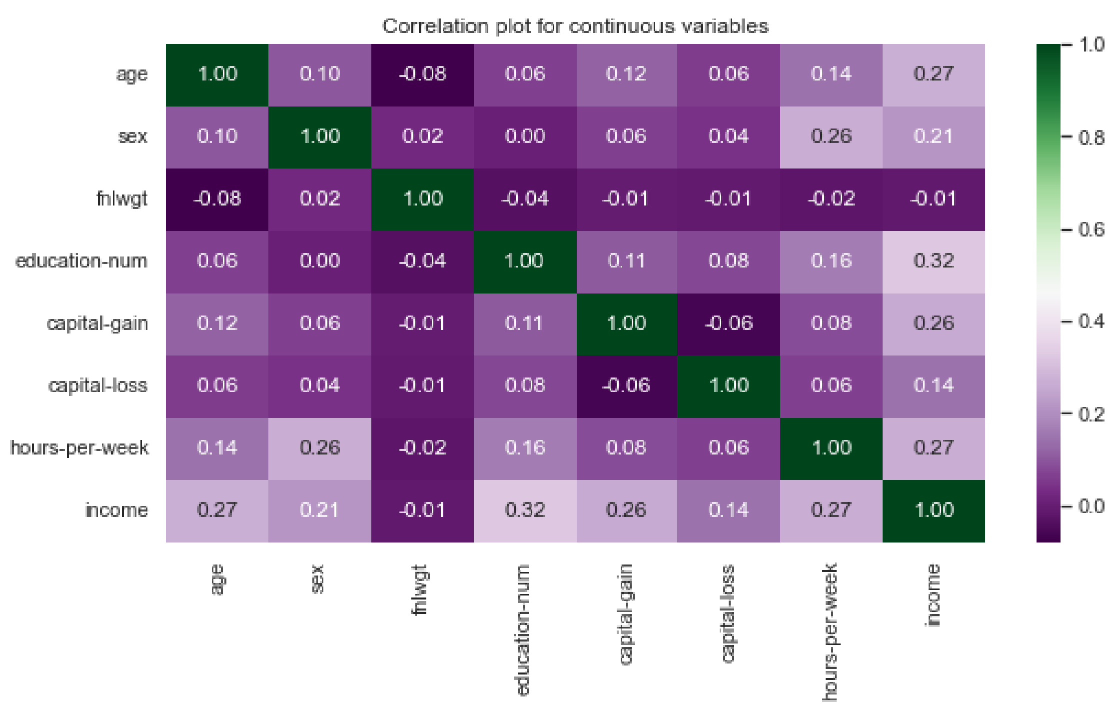


Figure 2.7: Correlation plot for continuous variables

```
[ ]: plt.figure(figsize=(10, 5))
     sns.heatmap(df2[['re_Husband', 're_Not-in-family', 're_Other-relative',␣
      ↪'re_Own-child', 're_Unmarried', 're_Wife', 'income']].
      ↪corr(method='spearman'),
                 annot=True, fmt='.2f', cmap='PRGn')
     plt.title('Correlation plot for Relationship variable')
     plt.show()
     print('Figure 2.8: Correlation plot for Relationshio variable')
```

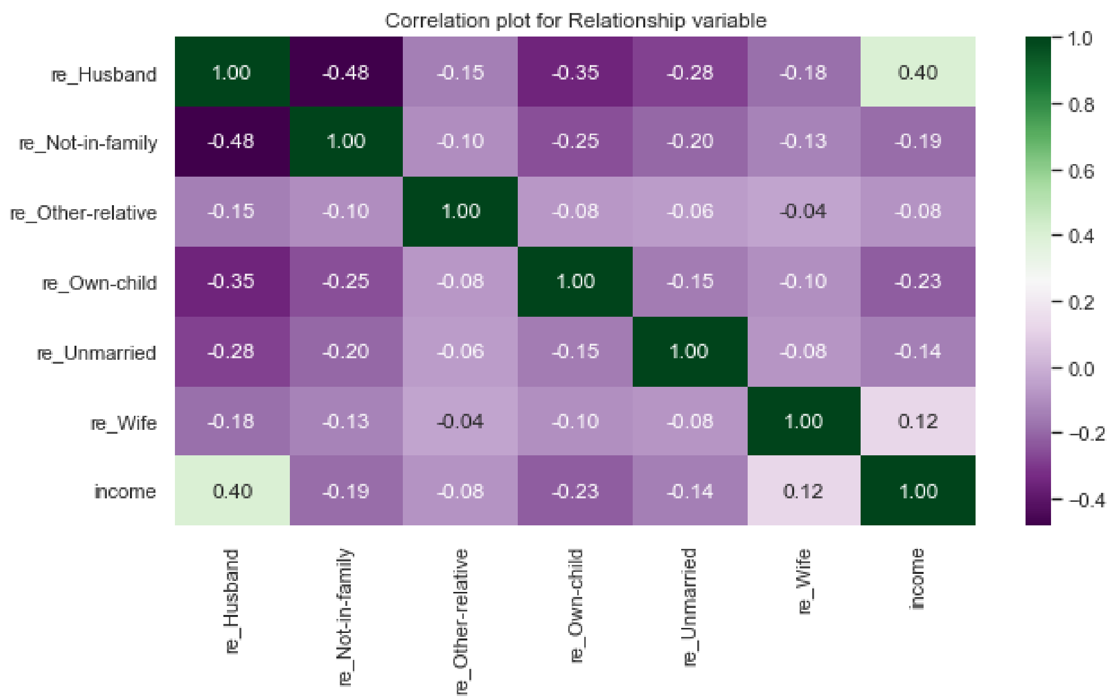


Figure 2.8: Correlation plot for Relationshio variable

```
[ ]: plt.figure(figsize=(10, 5))
     sns.heatmap(df2[['country_America', 'country_Asia', 'country_Canada',␣
      ↪'country_Europe', 'country_Other', 'country_United-States', 'income']].
      ↪corr(method='spearman'),
                 annot=True, fmt='.2f', cmap='PRGn')
     plt.title('Correlation plot for Native Country variable')
     plt.show()
     print('Figure 2.9: Correlation plot for Native County variable')
```

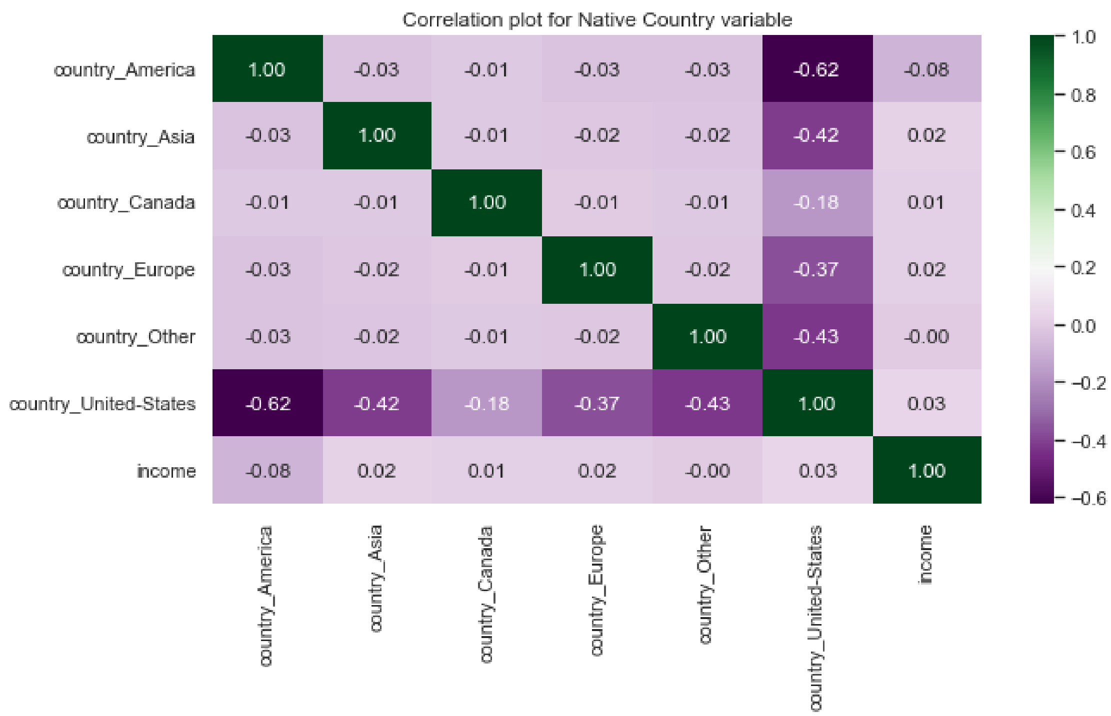


Figure 2.9: Correlation plot for Native County variable

```
[ ]: plt.figure(figsize=(10, 5))
     sns.heatmap(df2[['wc_Federal-gov', 'wc_Local-gov', 'wc_Never-worked',␣
      ↪'wc_Private', 'wc_Self-emp-inc', 'wc_Self-emp-not-inc', 'wc_State-gov',␣
      ↪'wc_Without-pay', 'income']].corr(method='spearman'),
                 annot=True, fmt='.2f', cmap='PRGn')
     plt.title('Correlation plot for Workclass variable')
     plt.show()
     print('Figure 2.10: Correlation plot for Workclass variable')
```

	wc_Federal-gov	wc_Local-gov	wc_Never-worked	wc_Private	wc_Self-emp-inc	wc_Self-emp-not-inc	wc_State-gov	wc_Without-pay	income
wc_Federal-gov	1.00	-0.05	-0.00	-0.31	-0.03	-0.05	-0.04	-0.00	0.06
wc_Local-gov	-0.05	1.00	-0.00	-0.46	-0.05	-0.08	-0.05	-0.01	0.03
wc_Never-worked	-0.00	-0.00	1.00	-0.03	-0.00	-0.00	-0.00	-0.00	-0.01
wc_Private	-0.31	-0.46	-0.03	1.00	-0.33	-0.51	-0.36	-0.04	-0.12
wc_Self-emp-inc	-0.03	-0.05	-0.00	-0.33	1.00	-0.05	-0.04	-0.00	0.13
wc_Self-emp-not-inc	-0.05	-0.08	-0.00	-0.51	-0.05	1.00	-0.06	-0.01	0.03
wc_State-gov	-0.04	-0.05	-0.00	-0.36	-0.04	-0.06	1.00	-0.00	0.02
wc_Without-pay	-0.00	-0.01	-0.00	-0.04	-0.00	-0.01	-0.00	1.00	-0.01
income	0.06	0.03	-0.01	-0.12	0.13	0.03	0.02	-0.01	1.00

Figure 2.10: Correlation plot for Workclass variable

[ ]:
```
plt.figure(figsize=(10, 5))
sns.heatmap(df2[['ms_Divorced', 'ms_Married-AF-spouse',␣
↪'ms_Married-civ-spouse', 'ms_Married-spouse-absent', 'ms_Never-married',␣
↪'ms_Separated', 'ms_Widowed', 'income']].corr(method='spearman'),
            annot=True, fmt='.2f', cmap='PRGn')
plt.title('Correlation plot for Married-status variable')
plt.show()
print('Figure 2.11: Correlation plot for Married-status variable')
```

Figure 2.11: Correlation plot for Married-status variable

[ ]:
```
plt.figure(figsize=(15, 8))
sns.heatmap(df2[['oc_Adm-clerical', 'oc_Armed-Forces', 'oc_Craft-repair',␣
↪'oc_Exec-managerial', 'oc_Farming-fishing', 'oc_Handlers-cleaners',
                 'oc_Machine-op-inspct', 'oc_Other-service',␣
↪'oc_Priv-house-serv', 'oc_Prof-specialty', 'oc_Protective-serv', 'oc_Sales',␣
↪'oc_Tech-support',
                 'oc_Transport-moving', 'income']].corr(method='spearman'),␣
↪annot=True, fmt='.2f', cmap='PRGn')
plt.title('Correlation plot for Occupation variable')
plt.show()
print('Figure 2.12: Correlation plot for Occupation variable')
```

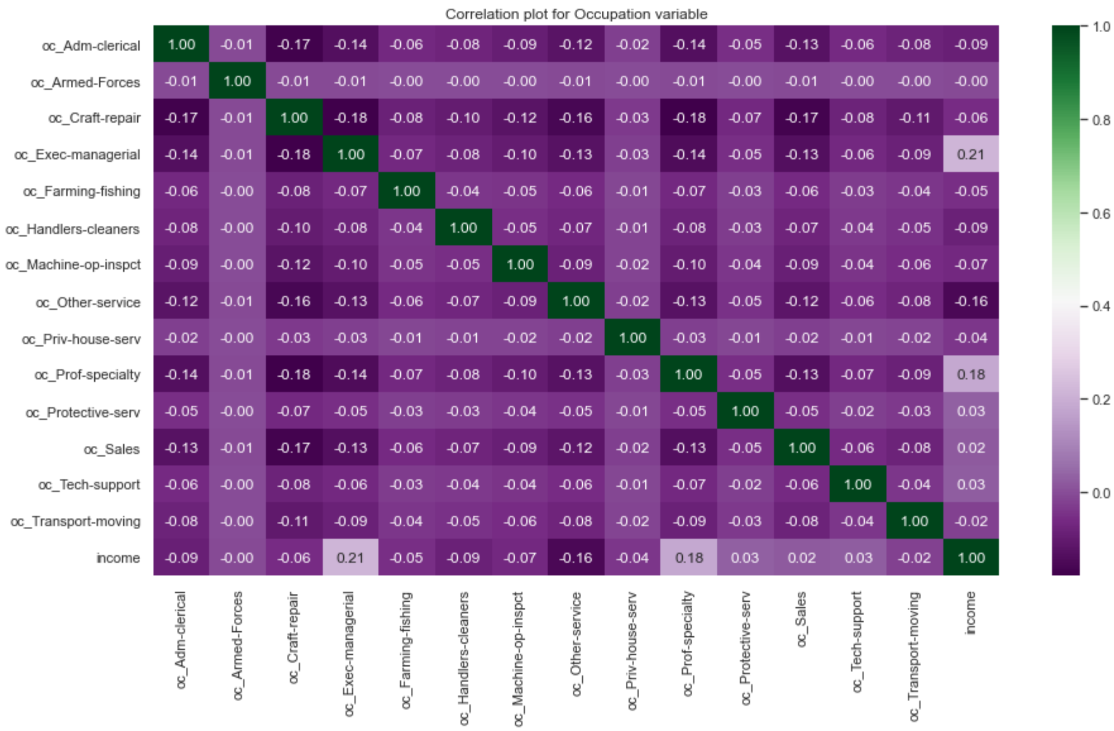


Figure 2.12: Correlation plot for Occupation variable

Correlation analysis shows that for the target variable, there is no strong correlation with any of the other variables. The maximum absolute values found in the correlation analysis are 0.44 for ms_Married-civ-spouse, 0.4 for re_Husband and 0.32 for education-num variables. All the variables are considered for the machine learning model because there are no prominent variables.

```
[ ]: # Separating dependent and independent variables
x2 = df2.drop(columns=['income'])
y2 = df2.income

# Scaling dependent variables using standard scaler
ssc = StandardScaler()
x2 = ssc.fit_transform(x2)

# Separate dataset to train and test sets with 80% to train and 20% to test
x2_train, x2_test, y2_train, y2_test = train_test_split(
    x2, y2, test_size=0.2, random_state=3)
```

2.0.3 Machine Learning model to predict whether an individual is going to earn more than $50,000 annually

There are four classification models, Logistic Regression, Support Vector Machine, Random Forest and Gaussian Naive Bayes and two Artificial Neural Network models.

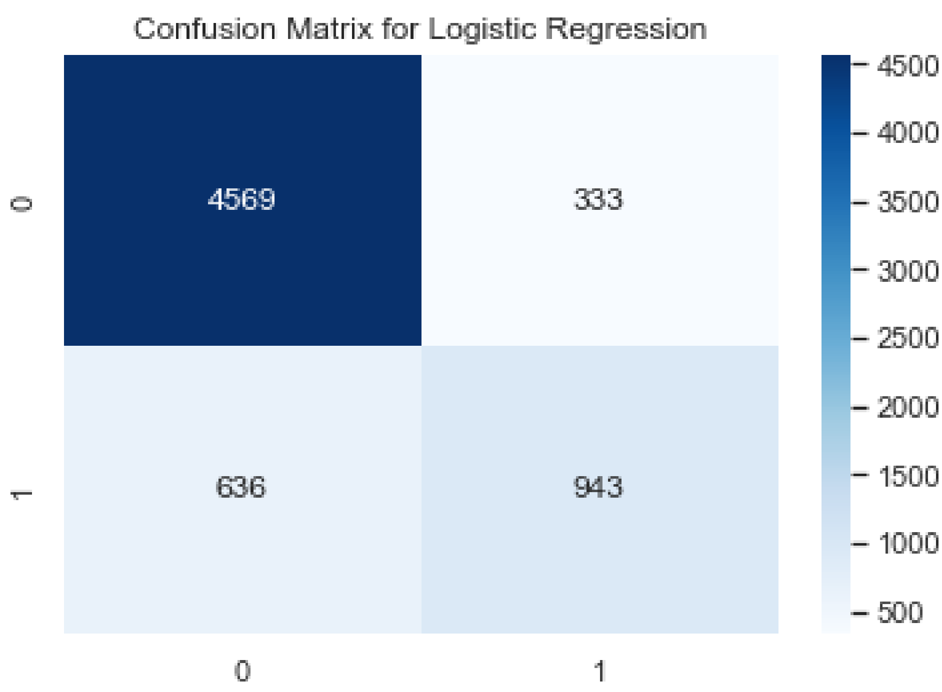
Classification models

Logistic Regression

```
[ ]: model_lr = LogisticRegression(random_state=0)
model_lr.fit(x2_train, y2_train)
pred_lr = model_lr.predict(x2_test)
matrix = confusion_matrix(y2_test, pred_lr)
sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
print(classification_report(y2_test, pred_lr))
plt.title('Confusion Matrix for Logistic Regression')
print('Figure 2.13: Confusion Matrix for Logistic Regression')
```

```
              precision    recall  f1-score   support

           0       0.88      0.93      0.90      4902
           1       0.74      0.60      0.66      1579

    accuracy                           0.85      6481
   macro avg       0.81      0.76      0.78      6481
weighted avg       0.84      0.85      0.84      6481
```

Figure 2.13: Confusion Matrix for Logistic Regression

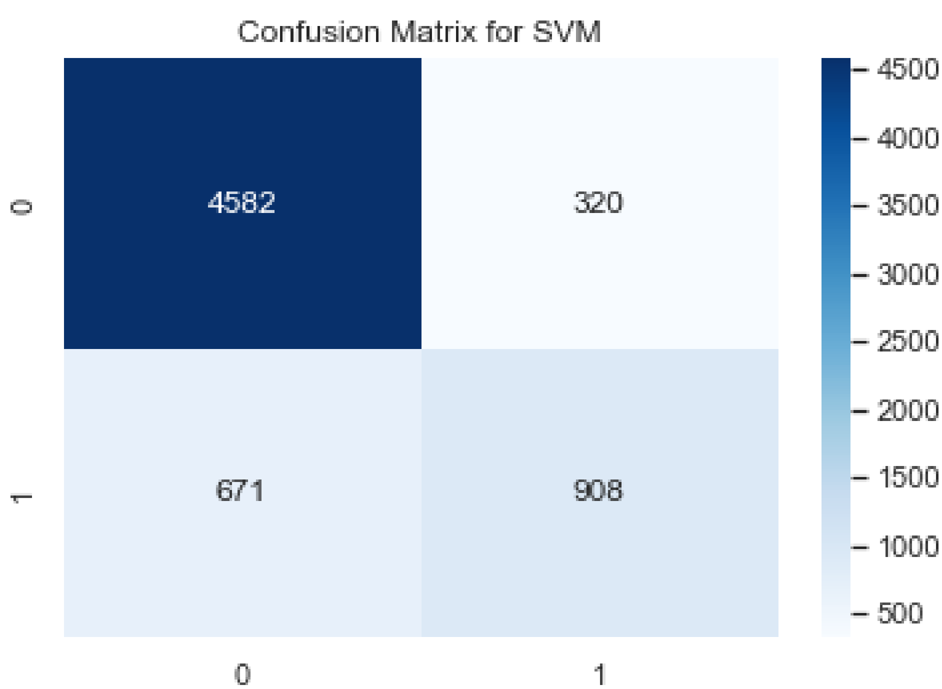


The Logistic Regression model has an accuracy of 0.85, which means that 85% of the sample has been correctly classified. The F1 score is 0.9 shows that for label one, classification is performing well. However, for label zero, just above average F1 score. High precision of 0.88 and recall of 0.9 shows that a high proportion of class one values of the output have been identified by the model correctly within the class and between classes. For the class, zero scores are a little lower.

Support Vector Machine

```
[ ]: model_svm = svm.SVC(kernel='poly')
     model_svm.fit(x2_train, y2_train)
     pred_svm = model_svm.predict(x2_test)
     matrix = confusion_matrix(y2_test, pred_svm)
     sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
     print(classification_report(y2_test, pred_svm))
     plt.title('Confusion Matrix for SVM')
     print('Figure 2.14: Confusion Matrix for Supported Vector Machine')
```

```
              precision    recall  f1-score   support

           0       0.87      0.93      0.90      4902
           1       0.74      0.58      0.65      1579

    accuracy                           0.85      6481
   macro avg       0.81      0.75      0.77      6481
weighted avg       0.84      0.85      0.84      6481

Figure 2.14: Confusion Matrix for Supported Vector Machine
```



The Supported Vector machine Model has an accuracy of 0.85, which means that 85% of the sample has been correctly classified. The F1 score is 0.9 shows that for class one, classification is performing well. However, for label zero, just above average F1 score. High precision of 0.87 and recall of 0.93 shows that a high proportion of class one values of the output have been identified by the model correctly within the class and between classes. For the class, zero scores are a little lower. All the model evaluation parameter values are approximately equal to the respective values from Logistic Regression.

Random Forest Classifier

[ ]:
```
model_rf = RandomForestClassifier()
model_rf.fit(x2_train, y2_train)
pred_rf = model_rf.predict(x2_test)
matrix = confusion_matrix(y2_test, pred_rf)
sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
print(classification_report(y2_test, pred_rf))
plt.title('Confusion Matrix for Random Forest classifier')
print('Figure 2.15: Confusion Matrix for Random Forest Classifier')
```

```
---------------------------------------------------------------------------
KeyboardInterrupt                         Traceback (most recent call last)
/var/folders/vj/796j6ms967z0rkptghjx57zm0000gn/T/ipykernel_65071/3143972477.py␣
 ↪in <module>
      1 model_rf = RandomForestClassifier()
----> 2 model_rf.fit(x2_train, y2_train)
      3 pred_rf = model_rf.predict(x2_test)
      4 matrix = confusion_matrix(y2_test, pred_rf)
      5 sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/sklearn/ensemble/
 ↪_forest.py in fit(self, X, y, sample_weight)
    448             # parallel_backend contexts set at a higher level,
    449             # since correctness does not rely on using threads.
--> 450             trees = Parallel(

    451                 n_jobs=self.n_jobs,
    452                 verbose=self.verbose,

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/joblib/parallel.py␣
 ↪in __call__(self, iterable)
   1042                 self._iterating = self._original_iterator is not None
   1043
-> 1044             while self.dispatch_one_batch(iterator):
   1045                 pass
   1046

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/joblib/parallel.py␣
 ↪in dispatch_one_batch(self, iterator)
    857                 return False
```

```
    858             else:
--> 859                 self._dispatch(tasks)
    860                 return True
    861 

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/joblib/parallel.py␣
 ↪in _dispatch(self, batch)
    775         with self._lock:
    776             job_idx = len(self._jobs)
--> 777             job = self._backend.apply_async(batch, callback=cb)
    778             # A job can complete so quickly than its callback is
    779             # called before we get here, causing self._jobs to

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/joblib/
 ↪_parallel_backends.py in apply_async(self, func, callback)
    206     def apply_async(self, func, callback=None):
    207         """Schedule a func to be run"""
--> 208         result = ImmediateResult(func)
    209         if callback:
    210             callback(result)

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/joblib/
 ↪_parallel_backends.py in __init__(self, batch)
    570         # Don't delay the application, to avoid keeping the input
    571         # arguments in memory
--> 572         self.results = batch()
    573 
    574     def get(self):

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/joblib/parallel.py␣
 ↪in __call__(self)
    260         # change the default number of processes to -1
    261         with parallel_backend(self._backend, n_jobs=self._n_jobs):
--> 262             return [func(*args, **kwargs)
    263                     for func, args, kwargs in self.items]
    264 

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/joblib/parallel.py␣
 ↪in <listcomp>(.0)
    260         # change the default number of processes to -1
    261         with parallel_backend(self._backend, n_jobs=self._n_jobs):
--> 262             return [func(*args, **kwargs)
    263                     for func, args, kwargs in self.items]
    264 

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/sklearn/utils/fixes
 ↪py in __call__(self, *args, **kwargs)
```

```
    214     def __call__(self, *args, **kwargs):
    215         with config_context(**self.config):
--> 216             return self.function(*args, **kwargs)
    217
    218

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/sklearn/ensemble/_forest.py in _parallel_build_trees(tree, forest, X, y, sample_weight, tree_idx, n_trees, verbose, class_weight, n_samples_bootstrap)
    183             curr_sample_weight *= compute_sample_weight("balanced", y, indices=indices)
    184
--> 185         tree.fit(X, y, sample_weight=curr_sample_weight, check_input=False)
    186     else:
    187         tree.fit(X, y, sample_weight=sample_weight, check_input=False)

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/sklearn/tree/_classes.py in fit(self, X, y, sample_weight, check_input, X_idx_sorted)
    935         """
    936
--> 937         super().fit(
    938             X,
    939             y,

~/opt/anaconda3/envs/HelloWorld/lib/python3.9/site-packages/sklearn/tree/_classes.py in fit(self, X, y, sample_weight, check_input, X_idx_sorted)
    418             )
    419
--> 420         builder.build(self.tree_, X, y, sample_weight)
    421
    422         if self.n_outputs_ == 1 and is_classifier(self):

KeyboardInterrupt:
```

The Random Forest classifier has an accuracy of 0.85, which means that 85% of the sample has been correctly classified. The F1 score is 0.9 shows that for class one, classification is performing well. However, for label zero, just above average F1 score. High precision of 0.88 and recall of 0.93 shows that a high proportion of class one values of the output have been identified by the model correctly within the class and between classes. For the class, zero scores are a little lower. All the model evaluation parameter values are approximately equal to the respective values from Logistic Regression and Supported Vector Machine.

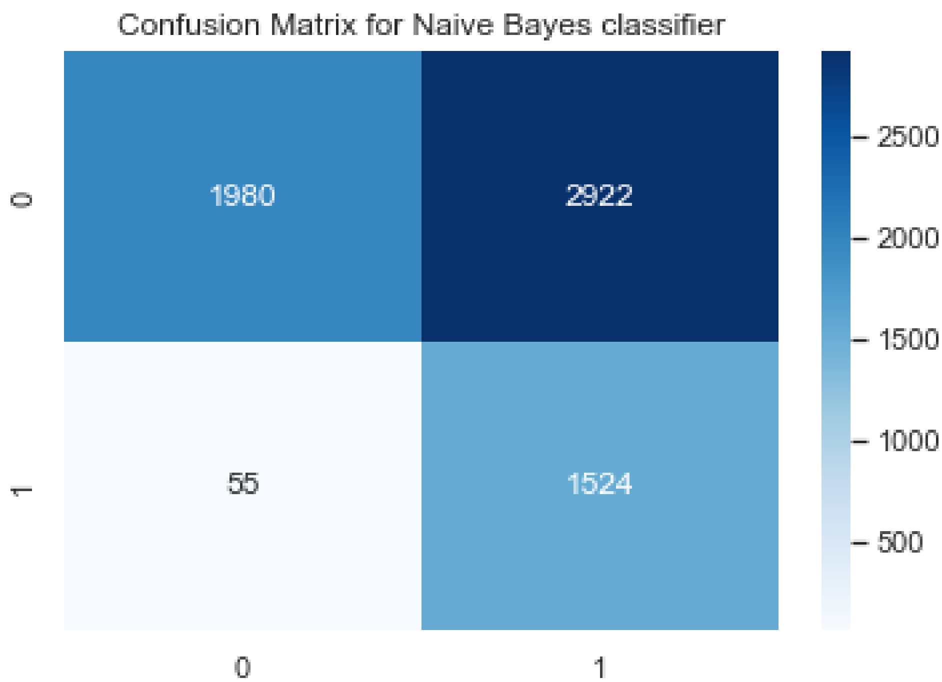
[ ]:
```
# Separating dependent and independent variables
x2 = df2.drop(columns=['income'])
y2 = df2.income
```

```
# Scaling dependent variables using standard scaler
x2 = StandardScaler().fit_transform(x2)

# Separate dataset to train and test sets with 80% to train and 20% to test
x2_train, x2_test, y2_train, y2_test = train_test_split(
    x2, y2, test_size=0.2, random_state=3)
```

Naive Bayes Classifier

[ ]:
```
model_gnb = GaussianNB()
model_gnb.fit(x2_train, y2_train)
pred_gnb = model_gnb.predict(x2_test)
matrix = confusion_matrix(y2_test, pred_gnb)
sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
print(classification_report(y2_test, pred_gnb))
plt.title('Confusion Matrix for Naive Bayes classifier')
print('Figure 2.16: Confusion Matrix for Naive Bayes Classifier')
```

```
              precision    recall  f1-score   support

           0       0.97      0.40      0.57      4902
           1       0.34      0.97      0.51      1579

    accuracy                           0.54      6481
   macro avg       0.66      0.68      0.54      6481
weighted avg       0.82      0.54      0.56      6481

Figure 2.16: Confusion Matrix for Naive Bayes Classifier
```

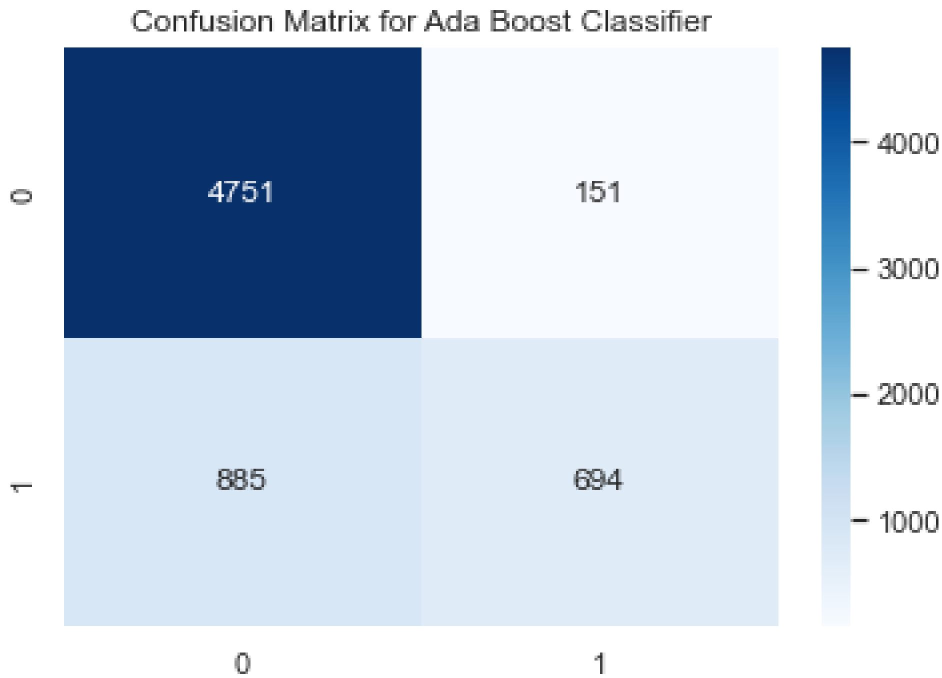


The Gaussian Naive Bayes Model has an accuracy of 0.54, which means that only 54% of the sample has been correctly classified. F1 score of 0.57 and 0.51 for class one and zero shows that when considering both output cases, classification only has an average performance. A high value of 0.97 precision shows that the model is performing better for one output label. However, the low value of precision of 0.34 suggests that for the other class, the model is not performing well. The confusion matrix shows there are 2922 wrong classifications for class label 1. The low recall value for class one and low precision for class zero explains the average accuracy of the model.

[ ]:
```
model = AdaBoostClassifier(learning_rate=0.15, n_estimators=25)
model.fit(x2_train, y2_train)
y_pred = model.predict(x2_test)
print(classification_report(y2_test, y_pred))
matrix = confusion_matrix(y2_test, y_pred)
sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
plt.title('Confusion Matrix for Ada Boost Classifier')
print('Figure 2.17: Confusion Matrix for Ada Boost Classifier')
```

```
              precision    recall  f1-score   support

           0       0.84      0.97      0.90      4902
           1       0.82      0.44      0.57      1579

    accuracy                           0.84      6481
   macro avg       0.83      0.70      0.74      6481
weighted avg       0.84      0.84      0.82      6481
```

Figure 2.17: Confusion Matrix for Ada Boost Classifier



The Ada Boost classifier Model has an accuracy of 0.84, which means that only 84% of the sample has been correctly classified. F1 score of 0.9 for class one and 0.57 for class zero shows that the performance difference in the two classes observed in Logistic regression, SVM and Random Forrest, is the same in this model. A high value of 0.84 and 0.82 for class one and class zero, respectively, shows that the model performs better when identifying the true positives model performes better. However, a low value of recall of 0.34 for class zero suggests that the proportion of actual positives is not high. The confusion matrix shows there are 2922 wrong classifications for class label 1.

When comparing classification models, four models are performing well, and one model, the Naive Bayes model, is not performing well for one output label of the target class, reducing the accuracy of that model. F1 score is almost the same for the first three models, Logistic Regression, Supported Vector Machine and Random Forest, fairly good for AdaBoost Classifier. However, the average for the Naive Bayes model. Accuracy is better in Logistic Regression, Random Forest and Supported Vector Machine. The naive Bayes classifier has the highest precision value of .97 for class one and the highest recall of .97 for class zero, even though all the other metrics have low values. Ada Boost classifier also has 0.97 recall for class one. The Random Forest classier has the highest performance, even though it is only a slight difference from the other two top classifiers.

Artificial Neural Network models Two Artificial Neural Network models have been trained. One with the input layer, two hidden layers, and the output layer. And another with the input layer, one hidden layer, and the output layer. Models are also different in the number of nodes in the hidden layers.

Artificial Neural Network model one

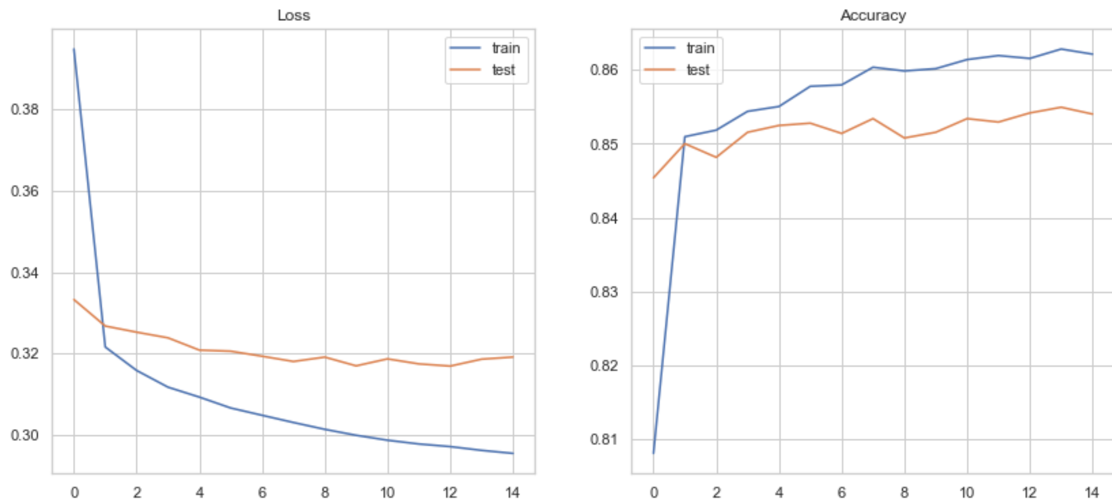
```
[ ]: # Initialise ANN
model_ann1 = tf.keras.models.Sequential()
# Add two hidden layers
model_ann1.add(tf.keras.layers.Dense(units=20, activation='relu'))
model_ann1.add(tf.keras.layers.Dense(units=10, activation='relu'))
# Add output layer
model_ann1.add(tf.keras.layers.Dense(units=1, activation='sigmoid'))

model_ann1.compile(
    optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

history = model_ann1.fit(x2_train, y2_train, validation_data=(
    x2_test, y2_test), batch_size=50, epochs=15)
loss, acc = model_ann1.evaluate(x2_test, y2_test)
print('Accuracy: %f' % (acc*100))
```

```
Epoch 1/15

2022-07-24 22:55:58.266084: I tensorflow/core/platform/cpu_feature_guard.cc:193]
This TensorFlow binary is optimized with oneAPI Deep Neural Network Library
(oneDNN) to use the following CPU instructions in performance-critical
operations:  AVX2 FMA
To enable them in other operations, rebuild TensorFlow with the appropriate
compiler flags.

519/519 [==============================] - 1s 2ms/step - loss: 0.3949 -
accuracy: 0.8080 - val_loss: 0.3332 - val_accuracy: 0.8454
Epoch 2/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3215 -
accuracy: 0.8510 - val_loss: 0.3267 - val_accuracy: 0.8500
Epoch 3/15
519/519 [==============================] - 1s 2ms/step - loss: 0.3158 -
accuracy: 0.8519 - val_loss: 0.3252 - val_accuracy: 0.8482
Epoch 4/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3116 -
accuracy: 0.8544 - val_loss: 0.3238 - val_accuracy: 0.8516
Epoch 5/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3092 -
accuracy: 0.8551 - val_loss: 0.3208 - val_accuracy: 0.8525
Epoch 6/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3065 -
accuracy: 0.8578 - val_loss: 0.3205 - val_accuracy: 0.8528
Epoch 7/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3047 -
accuracy: 0.8580 - val_loss: 0.3193 - val_accuracy: 0.8514
Epoch 8/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3029 -
```

```
accuracy: 0.8604 - val_loss: 0.3180 - val_accuracy: 0.8534
Epoch 9/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3012 -
accuracy: 0.8599 - val_loss: 0.3190 - val_accuracy: 0.8508
Epoch 10/15
519/519 [==============================] - 1s 1ms/step - loss: 0.2998 -
accuracy: 0.8602 - val_loss: 0.3169 - val_accuracy: 0.8516
Epoch 11/15
519/519 [==============================] - 1s 1ms/step - loss: 0.2986 -
accuracy: 0.8614 - val_loss: 0.3186 - val_accuracy: 0.8534
Epoch 12/15
519/519 [==============================] - 1s 1ms/step - loss: 0.2976 -
accuracy: 0.8620 - val_loss: 0.3174 - val_accuracy: 0.8530
Epoch 13/15
519/519 [==============================] - 1s 1ms/step - loss: 0.2970 -
accuracy: 0.8616 - val_loss: 0.3168 - val_accuracy: 0.8542
Epoch 14/15
519/519 [==============================] - 1s 1ms/step - loss: 0.2961 -
accuracy: 0.8629 - val_loss: 0.3185 - val_accuracy: 0.8550
Epoch 15/15
519/519 [==============================] - 1s 1ms/step - loss: 0.2953 -
accuracy: 0.8622 - val_loss: 0.3191 - val_accuracy: 0.8540
203/203 [==============================] - 0s 664us/step - loss: 0.3191 -
accuracy: 0.8540
Accuracy: 85.403490
```

[ ]:
```
f = plt.figure(figsize=(14, 6))
plt.subplot(121)
plt.title('Loss')
plt.plot(history.history['loss'], label='train')
plt.plot(history.history['val_loss'], label='test')
plt.legend()

plt.subplot(122)
plt.title('Accuracy')
plt.plot(history.history['accuracy'], label='train')
plt.plot(history.history['val_accuracy'], label='test')
plt.legend()

print('Figure 2.18: Performance of ANN')
```

```
Figure 2.18: Performance of ANN
```



Artificial Neural Network model two

[ ]:
```
# Initialise ANN
model_ann2 = tf.keras.models.Sequential()
# Add a hidden layer
model_ann2.add(tf.keras.layers.Dense(units=15, activation='relu'))
# Add output layer
model_ann2.add(tf.keras.layers.Dense(units=1, activation='sigmoid'))

model_ann2.compile(
    optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

history = model_ann2.fit(x2_train, y2_train, validation_data=(
    x2_test, y2_test), batch_size=30, epochs=20)
loss, acc = model_ann2.evaluate(x2_test, y2_test)
print('Accuracy: %f' % (acc*100))
```

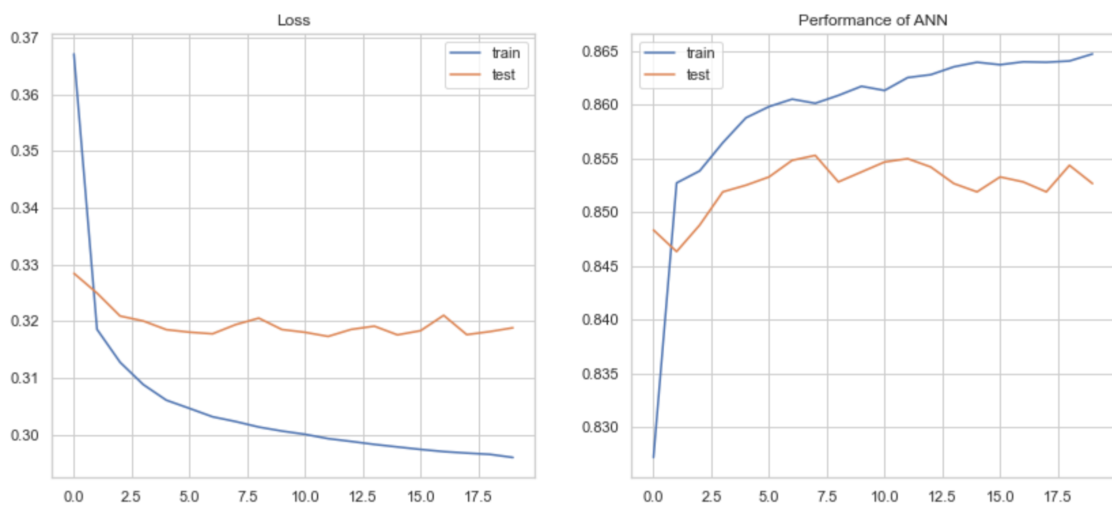
```
Epoch 1/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3671 -
accuracy: 0.8272 - val_loss: 0.3284 - val_accuracy: 0.8483
Epoch 2/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3185 -
accuracy: 0.8527 - val_loss: 0.3249 - val_accuracy: 0.8463
Epoch 3/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3127 -
accuracy: 0.8538 - val_loss: 0.3209 - val_accuracy: 0.8488
Epoch 4/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3088 -
accuracy: 0.8564 - val_loss: 0.3200 - val_accuracy: 0.8519
Epoch 5/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3060 -
```

```
accuracy: 0.8588 - val_loss: 0.3185 - val_accuracy: 0.8525
Epoch 6/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3046 -
accuracy: 0.8598 - val_loss: 0.3180 - val_accuracy: 0.8533
Epoch 7/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3031 -
accuracy: 0.8605 - val_loss: 0.3178 - val_accuracy: 0.8548
Epoch 8/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3023 -
accuracy: 0.8601 - val_loss: 0.3194 - val_accuracy: 0.8553
Epoch 9/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3013 -
accuracy: 0.8608 - val_loss: 0.3205 - val_accuracy: 0.8528
Epoch 10/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3006 -
accuracy: 0.8617 - val_loss: 0.3185 - val_accuracy: 0.8537
Epoch 11/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3000 -
accuracy: 0.8613 - val_loss: 0.3180 - val_accuracy: 0.8547
Epoch 12/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2993 -
accuracy: 0.8625 - val_loss: 0.3173 - val_accuracy: 0.8550
Epoch 13/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2988 -
accuracy: 0.8628 - val_loss: 0.3185 - val_accuracy: 0.8542
Epoch 14/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2982 -
accuracy: 0.8635 - val_loss: 0.3191 - val_accuracy: 0.8526
Epoch 15/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2978 -
accuracy: 0.8639 - val_loss: 0.3176 - val_accuracy: 0.8519
Epoch 16/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2974 -
accuracy: 0.8637 - val_loss: 0.3183 - val_accuracy: 0.8533
Epoch 17/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2970 -
accuracy: 0.8640 - val_loss: 0.3210 - val_accuracy: 0.8528
Epoch 18/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2967 -
accuracy: 0.8639 - val_loss: 0.3176 - val_accuracy: 0.8519
Epoch 19/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2965 -
accuracy: 0.8640 - val_loss: 0.3181 - val_accuracy: 0.8543
Epoch 20/20
865/865 [==============================] - 1s 1ms/step - loss: 0.2959 -
accuracy: 0.8647 - val_loss: 0.3188 - val_accuracy: 0.8526
203/203 [==============================] - 0s 673us/step - loss: 0.3188 -
accuracy: 0.8526
```

Accuracy: 85.264617

```
[ ]: f = plt.figure(figsize=(14, 6))

     plt.subplot(121)
     plt.title('Loss')
     plt.plot(history.history['loss'], label='train')
     plt.plot(history.history['val_loss'], label='test')
     plt.legend()

     plt.subplot(122)
     plt.title('Accuracy')
     plt.plot(history.history['accuracy'], label='train')
     plt.plot(history.history['val_accuracy'], label='test')
     plt.legend()
     plt.title('Performance of ANN')
     print('Figure 2.19: Performance of ANN')
```

Figure 2.19: Performance of ANN



Both Artificial Neural Network (ANN) models are performing with an accuracy of 85% to 86%, which can be considered good performance for an ANN model. The accuracy of the model_ann1 oscillates between 85% and 85.5%.

2.0.4 Optimisation

- Top three models from the classification are further optimised.

Step 1 The First attempt to optimise models is made by dropping low correlated variables from the input data.

```
[ ]: # Drop variables with correlation between 0.1 and -0.1 from dataset and select␣
     ↪dependent variables
     x2 = df2.drop(columns=['income', 'fnlwgt', 're_Other-relative',␣
     ↪'wc_Federal-gov', 'wc_Local-gov', 'wc_Never-worked', 'wc_Self-emp-not-inc',␣
     ↪'wc_State-gov', 'wc_Without-pay',
                            'ms_Married-AF-spouse', 'ms_Married-spouse-absent',␣
     ↪'ms_Separated', 'ms_Widowed', 'country_America', 'country_Asia',␣
     ↪'country_Canada', 'country_Europe', 'country_Other',
                            'country_United-States', 'oc_Adm-clerical',␣
     ↪'oc_Armed-Forces', 'oc_Craft-repair', 'oc_Farming-fishing',␣
     ↪'oc_Handlers-cleaners', 'oc_Machine-op-inspct', 'oc_Priv-house-serv',
                            'oc_Protective-serv', 'oc_Sales', 'oc_Tech-support',␣
     ↪'oc_Transport-moving'])
     y = df2.income

     # Scaling dependent variables using standard scaler
     ssc = StandardScaler()
     x2 = ssc.fit_transform(x2)

     # Separate dataset to train and test sets with 80% to train and 20% to test
     x2_train, x2_test, y2_train, y2_test = train_test_split(
         x2, y2, test_size=0.2, random_state=3)
```

```
[ ]: model_lr_1 = LogisticRegression(random_state=0)
     model_lr_1.fit(x2_train, y2_train)
     pred_lr_op = model_lr_1.predict(x2_test)

     print(classification_report(y2_test, pred_lr_op))
     matrix = confusion_matrix(y2_test, pred_lr_op)
     sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
     plt.title('Confusion Matrix for Loggistic Reggression')
     plt.show()

     print('Figure 2.20: Confusion Matrix for Logistic Reggression')
```

```
              precision    recall  f1-score   support

           0       0.87      0.93      0.90      4902
           1       0.74      0.57      0.64      1579

    accuracy                           0.84      6481
   macro avg       0.80      0.75      0.77      6481
weighted avg       0.84      0.84      0.84      6481
```

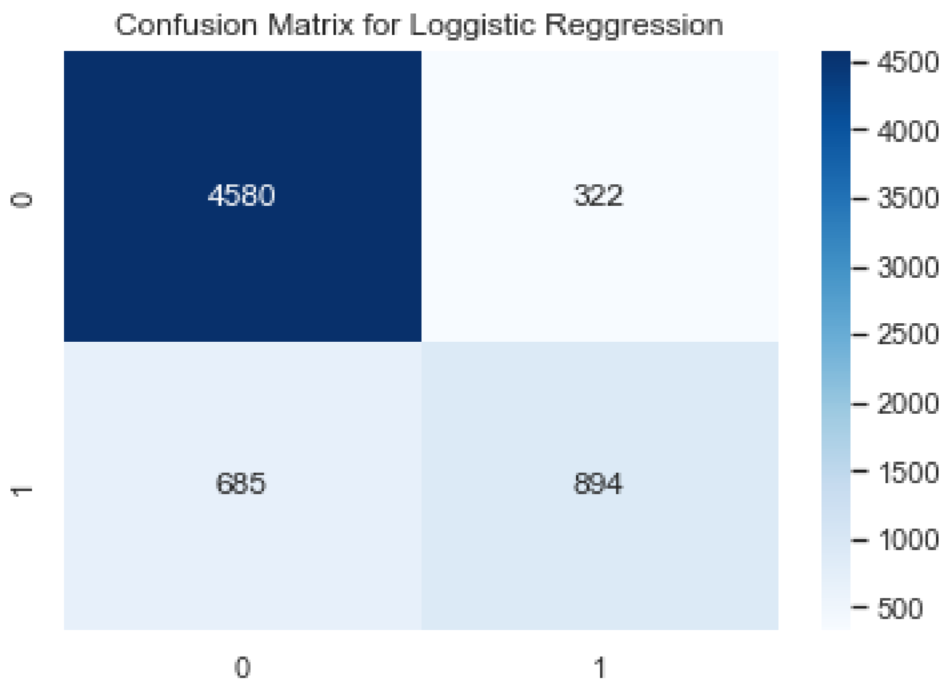


Figure 2.20: Confusion Matrix for Logistic Reggression

```
[ ]: model_svm_1 = svm.SVC(kernel='poly')
     model_svm_1.fit(x2_train, y2_train)
     pred_svm_op = model_svm_1.predict(x2_test)

     print(classification_report(y2_test, pred_svm_op))
     matrix = confusion_matrix(y2_test, pred_svm_op)
     sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
     plt.title('Confusion Matrix for SVM Classifier')
     plt.show()
     print('Figure 2.21: Confusion Matrix for SVM Classifier')
```

```
              precision    recall  f1-score   support

           0       0.86      0.95      0.90      4902
           1       0.77      0.54      0.63      1579

    accuracy                           0.85      6481
   macro avg       0.81      0.74      0.77      6481
weighted avg       0.84      0.85      0.84      6481
```

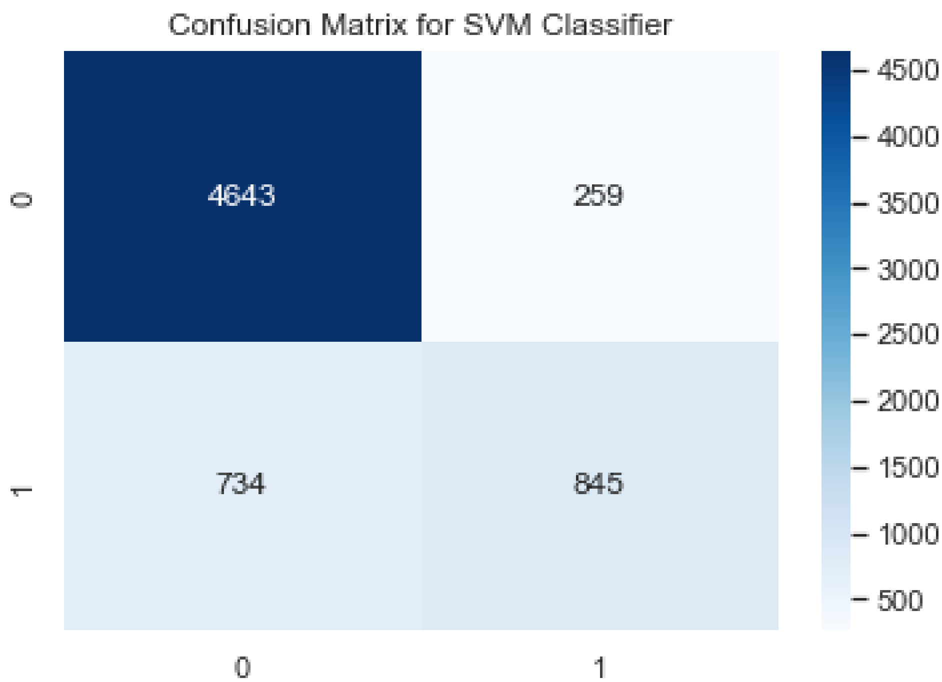


Figure 2.21: Confusion Matrix for SVM Classifier

```
[ ]: model_rf_1 = RandomForestClassifier()
model_rf_1.fit(x2_train, y2_train)
pred_rf_op = model_rf_1.predict(x2_test)

print(classification_report(y2_test, pred_rf_op))
matrix = confusion_matrix(y2_test, pred_rf_op)
sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
plt.title('Confusion Matrix for Random Forest Classifier')
plt.show()
print('Figure 2.22: Confusion Matrix for Random Forest Classifier')
```

```
              precision    recall  f1-score   support

           0       0.88      0.92      0.90      4902
           1       0.72      0.61      0.66      1579

    accuracy                           0.85      6481
   macro avg       0.80      0.77      0.78      6481
weighted avg       0.84      0.85      0.84      6481
```

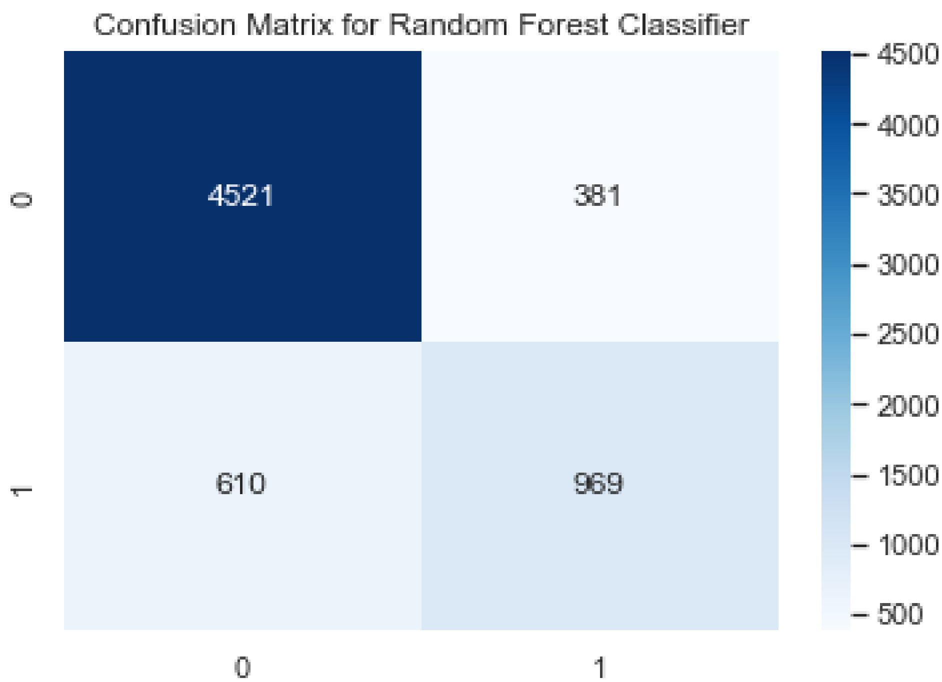


Figure 2.22: Confusion Matrix for Random Forest Classifier

```
[ ]: # Initialise ANN
model_ann1 = tf.keras.models.Sequential()
# Add two hidden layers
model_ann1.add(tf.keras.layers.Dense(units=20, activation='relu'))
model_ann1.add(tf.keras.layers.Dense(units=10, activation='relu'))
# Add output layer
model_ann1.add(tf.keras.layers.Dense(units=1, activation='sigmoid'))

model_ann1.compile(
    optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

history = model_ann1.fit(x2_train, y2_train, validation_data=(
    x2_test, y2_test), batch_size=50, epochs=15)
loss, acc = model_ann1.evaluate(x2_test, y2_test)
print('Accuracy: %f' % (acc*100))
```

```
Epoch 1/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3752 -
accuracy: 0.8255 - val_loss: 0.3320 - val_accuracy: 0.8460
Epoch 2/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3216 -
accuracy: 0.8464 - val_loss: 0.3273 - val_accuracy: 0.8465
Epoch 3/15
```

```
519/519 [==============================] - 1s 1ms/step - loss: 0.3174 -
accuracy: 0.8487 - val_loss: 0.3257 - val_accuracy: 0.8462
Epoch 4/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3153 -
accuracy: 0.8498 - val_loss: 0.3241 - val_accuracy: 0.8494
Epoch 5/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3133 -
accuracy: 0.8511 - val_loss: 0.3250 - val_accuracy: 0.8466
Epoch 6/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3120 -
accuracy: 0.8524 - val_loss: 0.3265 - val_accuracy: 0.8494
Epoch 7/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3111 -
accuracy: 0.8522 - val_loss: 0.3227 - val_accuracy: 0.8466
Epoch 8/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3104 -
accuracy: 0.8537 - val_loss: 0.3224 - val_accuracy: 0.8482
Epoch 9/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3095 -
accuracy: 0.8546 - val_loss: 0.3220 - val_accuracy: 0.8493
Epoch 10/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3092 -
accuracy: 0.8547 - val_loss: 0.3230 - val_accuracy: 0.8497
Epoch 11/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3088 -
accuracy: 0.8547 - val_loss: 0.3212 - val_accuracy: 0.8483
Epoch 12/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3081 -
accuracy: 0.8548 - val_loss: 0.3234 - val_accuracy: 0.8508
Epoch 13/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3076 -
accuracy: 0.8556 - val_loss: 0.3209 - val_accuracy: 0.8496
Epoch 14/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3072 -
accuracy: 0.8554 - val_loss: 0.3236 - val_accuracy: 0.8499
Epoch 15/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3067 -
accuracy: 0.8559 - val_loss: 0.3211 - val_accuracy: 0.8502
203/203 [==============================] - 0s 669us/step - loss: 0.3211 -
accuracy: 0.8502
Accuracy: 85.017747
```

[ ]:
```
# Initialise ANN
model_ann2 = tf.keras.models.Sequential()
# Add a hidden layer
model_ann2.add(tf.keras.layers.Dense(units=15, activation='relu'))
# Add output layer
```

```
model_ann2.add(tf.keras.layers.Dense(units=1, activation='sigmoid'))

model_ann2.compile(
    optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

history = model_ann2.fit(x2_train, y2_train, validation_data=(
    x2_test, y2_test), batch_size=30, epochs=20)
loss, acc = model_ann2.evaluate(x2_test, y2_test)
print('Accuracy: %f' % (acc*100))
```

```
Epoch 1/20
865/865 [==============================] - 2s 1ms/step - loss: 0.4315 -
accuracy: 0.7889 - val_loss: 0.3375 - val_accuracy: 0.8446
Epoch 2/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3266 -
accuracy: 0.8465 - val_loss: 0.3308 - val_accuracy: 0.8462
Epoch 3/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3215 -
accuracy: 0.8475 - val_loss: 0.3291 - val_accuracy: 0.8460
Epoch 4/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3183 -
accuracy: 0.8497 - val_loss: 0.3283 - val_accuracy: 0.8466
Epoch 5/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3162 -
accuracy: 0.8509 - val_loss: 0.3260 - val_accuracy: 0.8466
Epoch 6/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3147 -
accuracy: 0.8503 - val_loss: 0.3260 - val_accuracy: 0.8471
Epoch 7/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3134 -
accuracy: 0.8520 - val_loss: 0.3236 - val_accuracy: 0.8497
Epoch 8/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3125 -
accuracy: 0.8519 - val_loss: 0.3231 - val_accuracy: 0.8491
Epoch 9/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3121 -
accuracy: 0.8524 - val_loss: 0.3229 - val_accuracy: 0.8508
Epoch 10/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3115 -
accuracy: 0.8524 - val_loss: 0.3232 - val_accuracy: 0.8503
Epoch 11/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3115 -
accuracy: 0.8526 - val_loss: 0.3236 - val_accuracy: 0.8505
Epoch 12/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3107 -
accuracy: 0.8536 - val_loss: 0.3229 - val_accuracy: 0.8511
Epoch 13/20
```

```
865/865 [==============================] - 1s 1ms/step - loss: 0.3103 -
accuracy: 0.8537 - val_loss: 0.3243 - val_accuracy: 0.8500
Epoch 14/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3100 -
accuracy: 0.8541 - val_loss: 0.3231 - val_accuracy: 0.8486
Epoch 15/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3096 -
accuracy: 0.8543 - val_loss: 0.3215 - val_accuracy: 0.8506
Epoch 16/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3093 -
accuracy: 0.8540 - val_loss: 0.3231 - val_accuracy: 0.8513
Epoch 17/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3090 -
accuracy: 0.8540 - val_loss: 0.3218 - val_accuracy: 0.8506
Epoch 18/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3087 -
accuracy: 0.8551 - val_loss: 0.3214 - val_accuracy: 0.8497
Epoch 19/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3086 -
accuracy: 0.8554 - val_loss: 0.3213 - val_accuracy: 0.8500
Epoch 20/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3080 -
accuracy: 0.8554 - val_loss: 0.3214 - val_accuracy: 0.8497
203/203 [==============================] - 0s 662us/step - loss: 0.3214 -
accuracy: 0.8497
Accuracy: 84.971458
```

This step did not increase the performance of the models, and for Random Forest and ANN models, it decreased the accuracy slightly. Therefore, this step is not carried forward. All the features are used in the model training.

Step 2 Different scaling methods are used to transform data to check whether the performance can be increased.

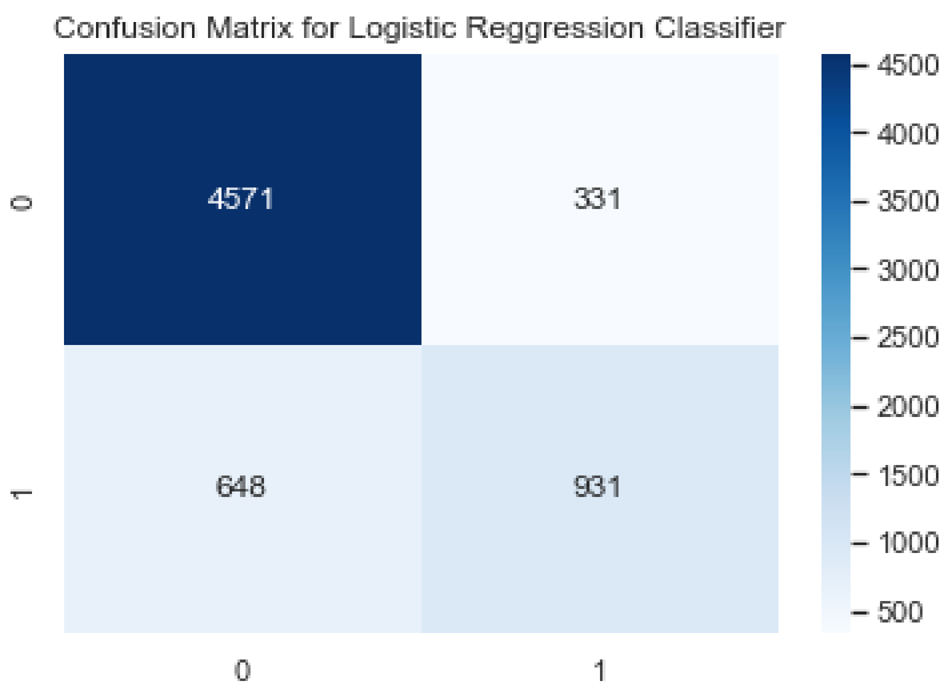
[ ]:
```python
# Select dependent variables
x2 = df2.drop(columns=['income', 'fnlwgt'])
y = df2.income

# RobustScaler, MinMaxScaler,Normalizer was tried
#x2 = StandardScaler().fit_transform(x2)
#x2 = MinMaxScaler().fit_transform(x2)
#x2 =  Normalizer().fit_transform(x2)

# Scaling dependent variables using minmax scaler
x2 = MinMaxScaler().fit_transform(x2)

# Separate dataset to train and test sets with 80% to train and 20% to test
x2_train, x2_test, y2_train, y2_test = train_test_split(
```

```
    x2, y2, test_size=0.2, random_state=3)
```

[ ]:
```
model_lr = LogisticRegression(random_state=0, max_iter=1000)
model_lr.fit(x2_train, y2_train)
pred_lr_op = model_lr.predict(x2_test)

print(classification_report(y2_test, pred_lr_op))
matrix = confusion_matrix(y2_test, pred_lr_op)
sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
plt.title('Confusion Matrix for Logistic Reggression Classifier')
print('Figure 2.23: Confusion Matrix for Logistic Reggression Classifier')
```

```
              precision    recall  f1-score   support

           0       0.88      0.93      0.90      4902
           1       0.74      0.59      0.66      1579

    accuracy                           0.85      6481
   macro avg       0.81      0.76      0.78      6481
weighted avg       0.84      0.85      0.84      6481
```

Figure 2.23: Confusion Matrix for Logistic Reggression Classifier

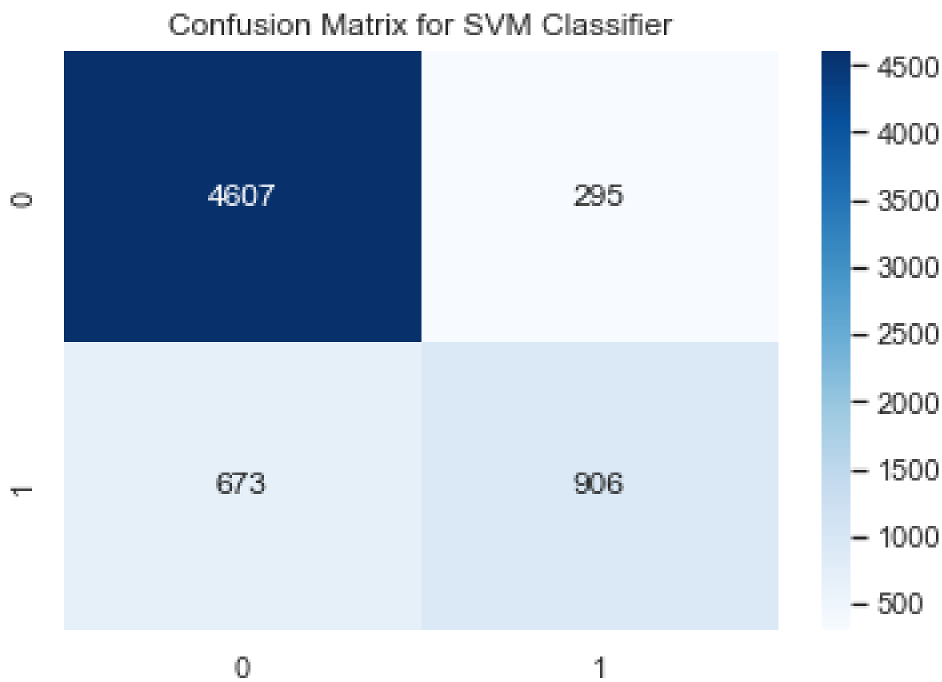


[ ]:

```
model_svm = svm.SVC(kernel='poly')
model_svm.fit(x2_train, y2_train)
pred_svm_op = model_svm.predict(x2_test)

print(classification_report(y2_test, pred_svm_op))
matrix = confusion_matrix(y2_test, pred_svm_op)
sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
plt.title('Confusion Matrix for SVM Classifier')
print('Figure 2.24: Confusion Matrix for SVM Classifier')
```

```
              precision    recall  f1-score   support

           0       0.87      0.94      0.90      4902
           1       0.75      0.57      0.65      1579

    accuracy                           0.85      6481
   macro avg       0.81      0.76      0.78      6481
weighted avg       0.84      0.85      0.84      6481
```

Figure 2.24: Confusion Matrix for SVM Classifier

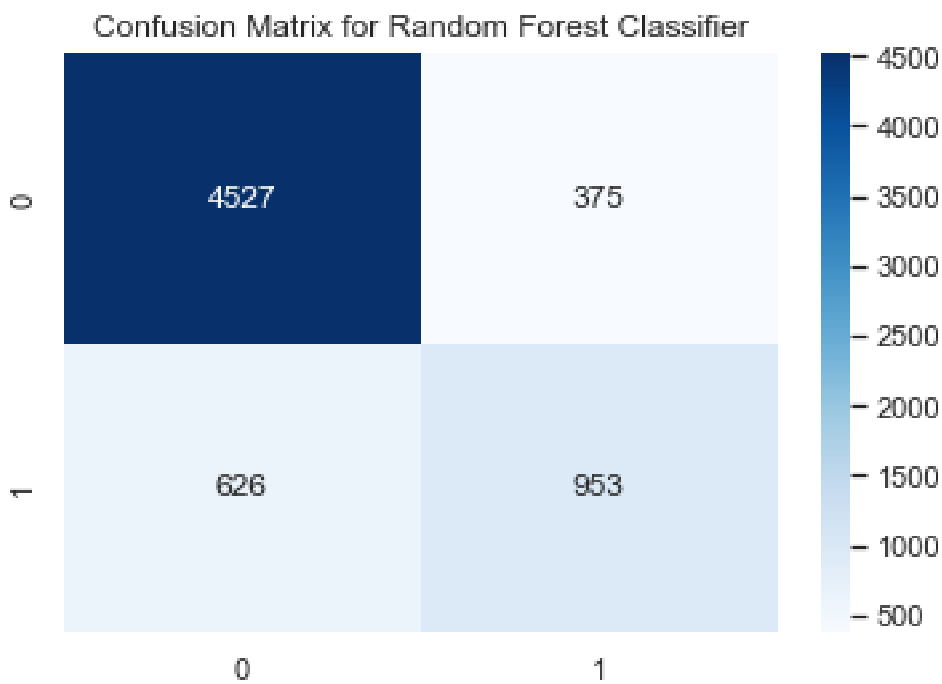


[ ]:

```
model_rf = RandomForestClassifier()
model_rf.fit(x2_train, y2_train)
pred_rf_op = model_rf.predict(x2_test)
```

```python
print(classification_report(y2_test, pred_rf_op))
matrix = confusion_matrix(y2_test, pred_rf_op)
sns.heatmap(matrix, annot=True, fmt='d', cmap="Blues")
plt.title('Confusion Matrix for Random Forest Classifier')
print('Figure 2.25: Confusion Matrix for Random Forest Classifier')
```

```
              precision    recall  f1-score   support

           0       0.88      0.92      0.90      4902
           1       0.72      0.60      0.66      1579

    accuracy                           0.85      6481
   macro avg       0.80      0.76      0.78      6481
weighted avg       0.84      0.85      0.84      6481

Figure 2.25: Confusion Matrix for Random Forest Classifier
```




```python
[ ]: # Initialise ANN
model_ann1 = tf.keras.models.Sequential()
# Add two hidden layers
model_ann1.add(tf.keras.layers.Dense(units=20, activation='relu'))
model_ann1.add(tf.keras.layers.Dense(units=10, activation='relu'))
# Add output layer
model_ann1.add(tf.keras.layers.Dense(units=1, activation='sigmoid'))
```

```python
model_ann1.compile(
    optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

history = model_ann1.fit(x2_train, y2_train, validation_data=(
    x2_test, y2_test), batch_size=50, epochs=15)
loss, acc = model_ann1.evaluate(x2_test, y2_test)
print('Accuracy: %f' % (acc*100))
```

```
Epoch 1/15
519/519 [==============================] - 1s 1ms/step - loss: 0.4275 -
accuracy: 0.7948 - val_loss: 0.3654 - val_accuracy: 0.8354
Epoch 2/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3436 -
accuracy: 0.8394 - val_loss: 0.3335 - val_accuracy: 0.8482
Epoch 3/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3259 -
accuracy: 0.8474 - val_loss: 0.3294 - val_accuracy: 0.8500
Epoch 4/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3199 -
accuracy: 0.8510 - val_loss: 0.3245 - val_accuracy: 0.8514
Epoch 5/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3185 -
accuracy: 0.8510 - val_loss: 0.3226 - val_accuracy: 0.8485
Epoch 6/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3175 -
accuracy: 0.8517 - val_loss: 0.3234 - val_accuracy: 0.8489
Epoch 7/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3163 -
accuracy: 0.8532 - val_loss: 0.3223 - val_accuracy: 0.8486
Epoch 8/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3155 -
accuracy: 0.8525 - val_loss: 0.3227 - val_accuracy: 0.8480
Epoch 9/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3139 -
accuracy: 0.8538 - val_loss: 0.3209 - val_accuracy: 0.8508
Epoch 10/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3138 -
accuracy: 0.8541 - val_loss: 0.3233 - val_accuracy: 0.8493
Epoch 11/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3129 -
accuracy: 0.8536 - val_loss: 0.3227 - val_accuracy: 0.8511
Epoch 12/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3120 -
accuracy: 0.8559 - val_loss: 0.3220 - val_accuracy: 0.8474
Epoch 13/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3107 -
```

```
accuracy: 0.8544 - val_loss: 0.3217 - val_accuracy: 0.8486
Epoch 14/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3101 -
accuracy: 0.8548 - val_loss: 0.3236 - val_accuracy: 0.8502
Epoch 15/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3095 -
accuracy: 0.8553 - val_loss: 0.3204 - val_accuracy: 0.8528
203/203 [==============================] - 0s 664us/step - loss: 0.3204 -
accuracy: 0.8528
Accuracy: 85.280049
```

[ ]:
```
# Initialise ANN
model_ann2 = tf.keras.models.Sequential()
# Add a hidden layer
model_ann2.add(tf.keras.layers.Dense(units=15, activation='relu'))
# Add output layer
model_ann2.add(tf.keras.layers.Dense(units=1, activation='sigmoid'))

model_ann2.compile(
    optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

history = model_ann2.fit(x2_train, y2_train, validation_data=(
    x2_test, y2_test), batch_size=30, epochs=20)
loss, acc = model_ann2.evaluate(x2_test, y2_test)
print('Accuracy: %f' % (acc*100))
```

```
Epoch 1/20
865/865 [==============================] - 1s 1ms/step - loss: 0.4022 -
accuracy: 0.8120 - val_loss: 0.3632 - val_accuracy: 0.8351
Epoch 2/20
865/865 [==============================] - 1s 2ms/step - loss: 0.3481 -
accuracy: 0.8372 - val_loss: 0.3417 - val_accuracy: 0.8420
Epoch 3/20
865/865 [==============================] - 1s 2ms/step - loss: 0.3341 -
accuracy: 0.8450 - val_loss: 0.3310 - val_accuracy: 0.8483
Epoch 4/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3260 -
accuracy: 0.8499 - val_loss: 0.3264 - val_accuracy: 0.8503
Epoch 5/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3218 -
accuracy: 0.8510 - val_loss: 0.3269 - val_accuracy: 0.8511
Epoch 6/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3194 -
accuracy: 0.8507 - val_loss: 0.3248 - val_accuracy: 0.8491
Epoch 7/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3186 -
accuracy: 0.8514 - val_loss: 0.3231 - val_accuracy: 0.8520
Epoch 8/20
```

```
865/865 [==============================] - 1s 1ms/step - loss: 0.3170 -
accuracy: 0.8525 - val_loss: 0.3222 - val_accuracy: 0.8477
Epoch 9/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3159 -
accuracy: 0.8531 - val_loss: 0.3214 - val_accuracy: 0.8471
Epoch 10/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3153 -
accuracy: 0.8514 - val_loss: 0.3213 - val_accuracy: 0.8497
Epoch 11/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3146 -
accuracy: 0.8538 - val_loss: 0.3208 - val_accuracy: 0.8476
Epoch 12/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3140 -
accuracy: 0.8543 - val_loss: 0.3226 - val_accuracy: 0.8476
Epoch 13/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3133 -
accuracy: 0.8546 - val_loss: 0.3214 - val_accuracy: 0.8479
Epoch 14/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3130 -
accuracy: 0.8554 - val_loss: 0.3214 - val_accuracy: 0.8511
Epoch 15/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3121 -
accuracy: 0.8547 - val_loss: 0.3200 - val_accuracy: 0.8505
Epoch 16/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3114 -
accuracy: 0.8553 - val_loss: 0.3201 - val_accuracy: 0.8496
Epoch 17/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3107 -
accuracy: 0.8549 - val_loss: 0.3195 - val_accuracy: 0.8496
Epoch 18/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3104 -
accuracy: 0.8559 - val_loss: 0.3209 - val_accuracy: 0.8522
Epoch 19/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3098 -
accuracy: 0.8554 - val_loss: 0.3191 - val_accuracy: 0.8482
Epoch 20/20
865/865 [==============================] - 1s 1ms/step - loss: 0.3093 -
accuracy: 0.8555 - val_loss: 0.3207 - val_accuracy: 0.8517
203/203 [==============================] - 0s 927us/step - loss: 0.3207 -
accuracy: 0.8517
Accuracy: 85.172039
```

In this step, it is clear the initial data transform method, Standard Scaler, is the best way to scale data as other scaling methods did not increase performance. Moreover, some scaling methods have decreased model performance.

2.0.5 Hyper parameter tuning

The exhaustive search method Grid Search is used to find the best parameters for an estimator from the specified parameter values. These parameters are defined in the model and not directly learnt with the estimator. Here Grid Search is used to avoid missing out on any good values from the specified parameters. In the GridSearchCV, cross-validation is also used to find the best values from the parameter grid.

Tuning the hyper-parameters of Logistic Regression For Penalty, l1, l2, and a combination of the two methods, elastic-net is used as parameters. Solvers lbfgs, newton-CG, sag, saga, and liblinear is used with supported penalty methods. Max iter values 1000 and 200, tolerance values of 0.001 and 0.01 and C values of 2, 4 and 5 are used to make the parameter space.

[ ]:
```
# Separating dependent and independent variables
x2 = df2.drop(columns=['income'])
y2 = df2.income

# Scaling dependent variables using standard scaler
x2 = StandardScaler().fit_transform(x2)

# Separate dataset to train and test sets with 80% to train and 20% to test
x2_train, x2_test, y2_train, y2_test = train_test_split(
    x2, y2, test_size=0.2, random_state=3)
```

[ ]:
```
# Depending on the supported solvers for penalty parameter, different set of␣
 ↪parameter grids are defined
param_grid = [
    {'penalty': ['l2'],
     'solver': ['lbfgs', 'newton-cg', 'sag', 'saga'],
     'max_iter': [1000, 2000],
     'tol':[0.001, 0.01],
     'C':[2.0, 4.0, 0.5]
     },
    {'penalty': ['l1'],
     'solver': ['saga', 'liblinear'],
     'max_iter': [1000, 2000],
     'tol':[0.001, 0.01],
     'C':[2.0, 4.0, 0.5]
     },
    {'penalty': ['elasticnet'],
     'solver': ['saga'],
     'max_iter': [1000, 2000],
     'tol':[0.001, 0.01],
     'C':[2.0, 4.0, 5.0, ]
     }
]
clf = GridSearchCV(estimator=model_lr, param_grid=param_grid)
best_model = clf.fit(x2_train, y2_train)
```

```
print('The best score across ALL searched params:\n', best_model.best_score_)
print('The best parameters across ALL searched params:\n', best_model.
 ↪best_params_)
```

```
Best Penalty: l1
Best C: 0.5
The best score across ALL searched params:
 0.8514716894650999
The best parameters across ALL searched params:
 {'C': 0.5, 'max_iter': 1000, 'penalty': 'l1', 'solver': 'saga', 'tol': 0.01}
```

[ ]:
```
best_predicted_values = best_model.predict(x2_test)
accuracy_score(best_predicted_values, y2_test)
```

[ ]: 0.8503317389291776

The accuracy of the Logistic regression is not improved after hyper-parameter tuning. The default parameters also have the same accuracy of 85% as the best model.

Tuning the hyper-parameters of Suported Vector Machine Here, linear, rbf and poly kernels and C values of 1 and 10 are used to make the parameter grid.

[ ]:
```
parameters = {'kernel': ('linear', 'rbf'), 'C': [1, 10]}
svc = svm.SVC()
# Run the grid search
clf = GridSearchCV(estimator=svc, param_grid=parameters)
best_model = clf.fit(x2_train, y2_train)
print('The best score across ALL searched params:\n', clf.best_score_)
print('The best parameters across ALL searched params:\n', clf.best_params_)
```

```
The best score across ALL searched params:
 0.8523207004416825
The best parameters across ALL searched params:
 {'C': 1, 'kernel': 'rbf'}
```

[ ]:
```
best_predicted_values = best_model.predict(x2_test)
accuracy_score(best_predicted_values, y2_test)
```

[ ]: 0.852029007869156

Similar to Logistic Regression, the Supported vector machine also achieved higher accuracy after hyper-parameter tuning.

Tuning the hyper-parameters of Random Forest Classifier The number of estimators, Selection criterion Gini and entropy, and different values of max depth and minimum sample split is used to make the parameter grid.

[ ]:
```
# Hyperparameter Optimization
parameters = {
    'n_estimators': [50, 100, 300, 400],
    'criterion': ['entropy', 'gini'],
    'max_depth': [30, 40, 50],
    'min_samples_split': [20, 25, 50]
}

# Run the grid search
grid_obj = GridSearchCV(estimator=model_rf, param_grid=parameters)
grid_obj = grid_obj.fit(x2_train, y2_train)

# Set the clf to the best combination of parameters
clf = grid_obj.best_estimator_

# Train the model using the training sets
clf.fit(x2_train, y2_train)

print('The best score across ALL searched params:\n', grid_obj.best_score_)
print('The best parameters across ALL searched params:\n', grid_obj.
 ↪best_params_)
```

```
The best score across ALL searched params:
 0.865939006750241
The best parameters across ALL searched params:
 {'criterion': 'gini', 'max_depth': 40, 'min_samples_split': 50, 'n_estimators':
50}
```

[ ]:
```
best_predicted_values = clf.predict(x2_test)
accuracy_score(best_predicted_values, y2_test)
```

[ ]:
```
0.8620583243326647
```

The Random Forest model has improved its accuracy after the hyper-parameter tuning from 85 to 86.

Manual hyper-parameters tuning the for Artificial Neural Network Models

[ ]:
```
# Initialise ANN
model_ann1 = tf.keras.models.Sequential()
# Add two hidden layers
model_ann1.add(tf.keras.layers.Dense(units=35, activation='softmax'))
model_ann1.add(tf.keras.layers.Dropout(.1, input_shape=(2,)))
# Add output layer
model_ann1.add(tf.keras.layers.Dense(units=1, activation='sigmoid'))

model_ann1.compile(
    optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
```

```python
history = model_ann1.fit(x2_train, y2_train, validation_data=(
    x2_test, y2_test), batch_size=50, epochs=15)
loss, acc = model_ann1.evaluate(x2_test, y2_test)
print('Accuracy: %f' % (acc*100))
```

```
Epoch 1/15
519/519 [==============================] - 1s 1ms/step - loss: 0.5468 -
accuracy: 0.7852 - val_loss: 0.4564 - val_accuracy: 0.8389
Epoch 2/15
519/519 [==============================] - 1s 1ms/step - loss: 0.4188 -
accuracy: 0.8370 - val_loss: 0.3893 - val_accuracy: 0.8479
Epoch 3/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3778 -
accuracy: 0.8411 - val_loss: 0.3628 - val_accuracy: 0.8511
Epoch 4/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3610 -
accuracy: 0.8434 - val_loss: 0.3505 - val_accuracy: 0.8519
Epoch 5/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3499 -
accuracy: 0.8452 - val_loss: 0.3434 - val_accuracy: 0.8516
Epoch 6/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3442 -
accuracy: 0.8455 - val_loss: 0.3390 - val_accuracy: 0.8511
Epoch 7/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3393 -
accuracy: 0.8461 - val_loss: 0.3353 - val_accuracy: 0.8494
Epoch 8/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3357 -
accuracy: 0.8451 - val_loss: 0.3321 - val_accuracy: 0.8503
Epoch 9/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3321 -
accuracy: 0.8459 - val_loss: 0.3294 - val_accuracy: 0.8505
Epoch 10/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3288 -
accuracy: 0.8477 - val_loss: 0.3278 - val_accuracy: 0.8499
Epoch 11/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3264 -
accuracy: 0.8483 - val_loss: 0.3260 - val_accuracy: 0.8499
Epoch 12/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3240 -
accuracy: 0.8470 - val_loss: 0.3249 - val_accuracy: 0.8519
Epoch 13/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3221 -
accuracy: 0.8482 - val_loss: 0.3233 - val_accuracy: 0.8536
Epoch 14/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3201 -
```

```
accuracy: 0.8491 - val_loss: 0.3221 - val_accuracy: 0.8525
Epoch 15/15
519/519 [==============================] - 1s 1ms/step - loss: 0.3185 -
accuracy: 0.8498 - val_loss: 0.3215 - val_accuracy: 0.8513
203/203 [==============================] - 0s 682us/step - loss: 0.3215 -
accuracy: 0.8513
Accuracy: 85.125750
```

Results

- Using different optimisers resulted accuracy:
  - sgd ~ 75
  - Adadelta ~ 67
  - Ftrl ~ 75
  - Nadam ~ 85
- Using tanh, selu, and exponential activation functions resutled accuracy around 85

Try	Layer 1	Layer 2	Accuracy
1	units=15 activation = relu	units=5 activation = relu	85.0
—	—	—	—
2	units=25 activation = relu	units=15 activation = relu	85.1
—	—	—	—
3	units=30 activation = relu	units=10 activation = relu	85.1
—	—	—	—
4	units=30 activation = softmax	units=10 activation = softmax	85.3
—	—	—	—
5	units=35 activation = softmax	units=15 activation = softmax	85.4
—	—	—	—
6	units=35 activation = softmax	units=10 activation = softmax	85.7
—	—	—	—
7	units=35 activation = softmax	units=10 activation = softmax	85.7

All the different parameter changes only incresed accuracy slightly for this model. Even one layer changing to **dropout** layer did not help to increase accuracy.

[ ]:
```python
# Initialise ANN
model_ann2 = tf.keras.models.Sequential()
# Add a hidden layer
model_ann2.add(tf.keras.layers.Dense(units=35, activation='softmax'))
# Add output layer
model_ann2.add(tf.keras.layers.Dense(units=1, activation='sigmoid'))

model_ann2.compile(
    optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])

history = model_ann2.fit(x2_train, y2_train, validation_data=(
    x2_test, y2_test), batch_size=25, epochs=20)
```

```python
loss, acc = model_ann2.evaluate(x2_test, y2_test)
print('Accuracy: %f' % (acc*100))
```

```
Epoch 1/20
1037/1037 [==============================] - 2s 1ms/step - loss: 0.4925 -
accuracy: 0.7939 - val_loss: 0.3950 - val_accuracy: 0.8491
Epoch 2/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3631 -
accuracy: 0.8504 - val_loss: 0.3518 - val_accuracy: 0.8514
Epoch 3/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3372 -
accuracy: 0.8525 - val_loss: 0.3388 - val_accuracy: 0.8513
Epoch 4/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3261 -
accuracy: 0.8539 - val_loss: 0.3320 - val_accuracy: 0.8508
Epoch 5/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3197 -
accuracy: 0.8553 - val_loss: 0.3285 - val_accuracy: 0.8522
Epoch 6/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3153 -
accuracy: 0.8571 - val_loss: 0.3260 - val_accuracy: 0.8559
Epoch 7/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3120 -
accuracy: 0.8579 - val_loss: 0.3249 - val_accuracy: 0.8559
Epoch 8/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3094 -
accuracy: 0.8591 - val_loss: 0.3234 - val_accuracy: 0.8559
Epoch 9/20
1037/1037 [==============================] - 2s 2ms/step - loss: 0.3074 -
accuracy: 0.8587 - val_loss: 0.3225 - val_accuracy: 0.8562
Epoch 10/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3054 -
accuracy: 0.8599 - val_loss: 0.3221 - val_accuracy: 0.8559
Epoch 11/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3039 -
accuracy: 0.8607 - val_loss: 0.3219 - val_accuracy: 0.8559
Epoch 12/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3022 -
accuracy: 0.8611 - val_loss: 0.3214 - val_accuracy: 0.8554
Epoch 13/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.3009 -
accuracy: 0.8620 - val_loss: 0.3210 - val_accuracy: 0.8557
Epoch 14/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.2999 -
accuracy: 0.8616 - val_loss: 0.3217 - val_accuracy: 0.8543
Epoch 15/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.2990 -
```

```
accuracy: 0.8618 - val_loss: 0.3202 - val_accuracy: 0.8539
Epoch 16/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.2977 -
accuracy: 0.8617 - val_loss: 0.3201 - val_accuracy: 0.8522
Epoch 17/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.2970 -
accuracy: 0.8623 - val_loss: 0.3206 - val_accuracy: 0.8536
Epoch 18/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.2962 -
accuracy: 0.8627 - val_loss: 0.3207 - val_accuracy: 0.8520
Epoch 19/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.2954 -
accuracy: 0.8627 - val_loss: 0.3204 - val_accuracy: 0.8505
Epoch 20/20
1037/1037 [==============================] - 1s 1ms/step - loss: 0.2948 -
accuracy: 0.8629 - val_loss: 0.3209 - val_accuracy: 0.8525
203/203 [==============================] - 0s 993us/step - loss: 0.3209 -
accuracy: 0.8525
Accuracy: 85.249192
```

Results

- Using different optimisers resulted accuracy:
  - sgd ~ 85
  - Adadelta ~ 72
  - Ftrl ~ 85
  - Nadam ~ 85
- Using tanh, selu, and exponential activation functions resutled accuracy around 83 ~ 85

Try	Layer 1	Accuracy
1	units=15 activation = relu	85.0
—	—	—
2	units=25 activation = relu	85.3
—	—	—
3	units=30 activation = relu	85.1
—	—	—
4	units=30 activation = softmax	85.3
—	—	—
5	units=35 activation = softmax	85.3
—	—	—
6	units=25 activation = softmax	85.4

All the different parameter changes only incresed accuracy slightly for this model

2.1 Conclusion

Five classification models and two Artificial Neural Network models were used to predict individuals' annual income based on US census data. Then the first three classification models and two ANN models were chosen based on the performance of predicting data to further tuning. Those five selected models are further tuned using feature selection, different methods of data cleaning and hyperparameter tuning. The highest accuracy is 86% from the Random Forest Classifier. Most of the other models also performed around 85% at their best.

Overall, there is no significant difference when considering the best performance for the top five models. However, the Random Forest Classifier is more accurate in predicting if an individual gets an annual income of $50000 or more. The Random Forest model is robust to outliers, and it has shown unchanging accuracy of over 85% despite changes to the model parameters, scaling methods and feature selection. In comparison, other models had an accuracy range from ~50% to 85%.

2.1.1 Referencese

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