# The Impact of Medicine to your Wallet

Today we will explore a data set dedicated to the cost of treatment of different patients. The cost of treatment depends on many factors: diagnosis, type of clinic, city of residence, age and so on. We have no data on the diagnosis of patients.

But we have other information that can help us to make a conclusion about the health of patients and practice regression analysis. In any case, I wish you to be healthy! Let's look at our data.

## | Domain Knowledge

1. **`Age`**: Age is a significant factor in health insurance as older individuals are generally at a higher risk of health issues compared to younger individuals. Therefore, age often correlates with higher insurance charges.
2. **`Sex`**: Gender can play a role in health insurance costs. Some studies suggest that women tend to use more health care services, especially during childbearing years. However, the impact of gender on health insurance charges can vary depending on other factors.
3. **`BMI (Body Mass Index)`**: BMI is a measure that attempts to quantify an individual's tissue mass. It's widely used as a simple method to assess whether a person has a healthy body weight for a given height. High BMI values are often associated with higher risk of chronic diseases like heart disease, diabetes, and certain types of cancer, which can lead to higher health care costs.
4. **`Children`**: The number of dependents a person has can influence health insurance costs. More dependents usually mean higher insurance charges because more individuals are covered under the same plan.
5. **`Smoker`**: Smoking is a significant risk factor for many health conditions, including heart disease, stroke, and cancer. Smokers often face higher health insurance charges due to these increased health risks.
6. **`Region`**: The region where the beneficiary lives can also affect health insurance charges. This could be due to variations in cost of living, health care costs, and health behaviors across different regions.
7. **`Charges`**: This is the individual medical costs billed by health insurance. It's the dependent variable in this dataset, and it's influenced by all the other factors. Understanding the relationships between the independent variables (age, sex, bmi, children, smoker, region) and charges is the main goal of this analysis.

## | Import libraries

```
import pandas as pd
import numpy as np
import matplotlib

import matplotlib.pyplot as plt
import seaborn as sns

sns.set_style("dark")
matplotlib.style.use('seaborn-notebook')
%matplotlib inline

import warnings
warnings.filterwarnings('ignore')

from IPython.core.interactiveshell import InteractiveShell
InteractiveShell.ast_node_interactivity = 'all'

# Suppress Scientific Notation in Pandas
pd.set_option('display.float_format', '{:.2f}'.format)

# for HD visualizations
%config InlineBackend.figure_format='retina'

from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import LabelEncoder

# Evaluation
from sklearn import metrics
from sklearn.metrics import roc_curve
from sklearn.metrics import r2_score, mean_absolute_error,
mean_squared_error
from sklearn.metrics import recall_score, confusion_matrix,
precision_score, f1_score, accuracy_score, classification_report
```

```
C:\Users\prave\AppData\Local\Temp\ipykernel_16016\3204938556.py:9:
MatplotlibDeprecationWarning: The seaborn styles shipped by Matplotlib
are deprecated since 3.6, as they no longer correspond to the styles
shipped by seaborn. However, they will remain available as 'seaborn-
v0_8-<style>'. Alternatively, directly use the seaborn API instead.
  matplotlib.style.use('seaborn-notebook')
```

```
insurance_df = pd.read_csv(r"C:\Data\insurance.csv")
```

```
insurance_df.head(3)
```

```
   age     sex   bmi  children smoker     region  charges
0   19  female 27.90         0    yes  southwest 16884.92
1   18    male 33.77         1     no  southeast  1725.55
2   28    male 33.00         3     no  southeast  4449.46
```

```
insurance_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1338 entries, 0 to 1337
Data columns (total 7 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       1338 non-null   int64  
 1   sex       1338 non-null   object 
 2   bmi       1338 non-null   float64
 3   children  1338 non-null   int64  
 4   smoker    1338 non-null   object 
 5   region    1338 non-null   object 
 6   charges   1338 non-null   float64
dtypes: float64(2), int64(2), object(3)
memory usage: 73.3+ KB
```

! image-2.png

## | Handling Duplicates

```
# Handle duplicates
duplicate_rows_data = insurance_df[insurance_df.duplicated()]
print("number of duplicate rows: ", duplicate_rows_data.shape)
```

```
number of duplicate rows:  (1, 7)
```

```
insurance_df[insurance_df.duplicated()]
```

```
     age   sex    bmi  children smoker     region  charges
581   19  male 30.59         0     no  northwest  1639.56
```

```
insurance_df = insurance_df.drop_duplicates()
```

## | Uniqueness

```
# Loop through each column and count the number of distinct values
for column in insurance_df.columns:
    num_distinct_values = len(insurance_df[column].unique())
    print(f"{column}: {num_distinct_values} distinct values")
```

```
age: 47 distinct values
sex: 2 distinct values
bmi: 548 distinct values
children: 6 distinct values
smoker: 2 distinct values
region: 4 distinct values
charges: 1337 distinct values
```

## | Missing Values

```
# Missing or Null values
insurance_df.isna().sum()
```

```
age         0
sex         0
bmi         0
children    0
smoker      0
region      0
charges     0
dtype: int64
```

## | Describe the Data

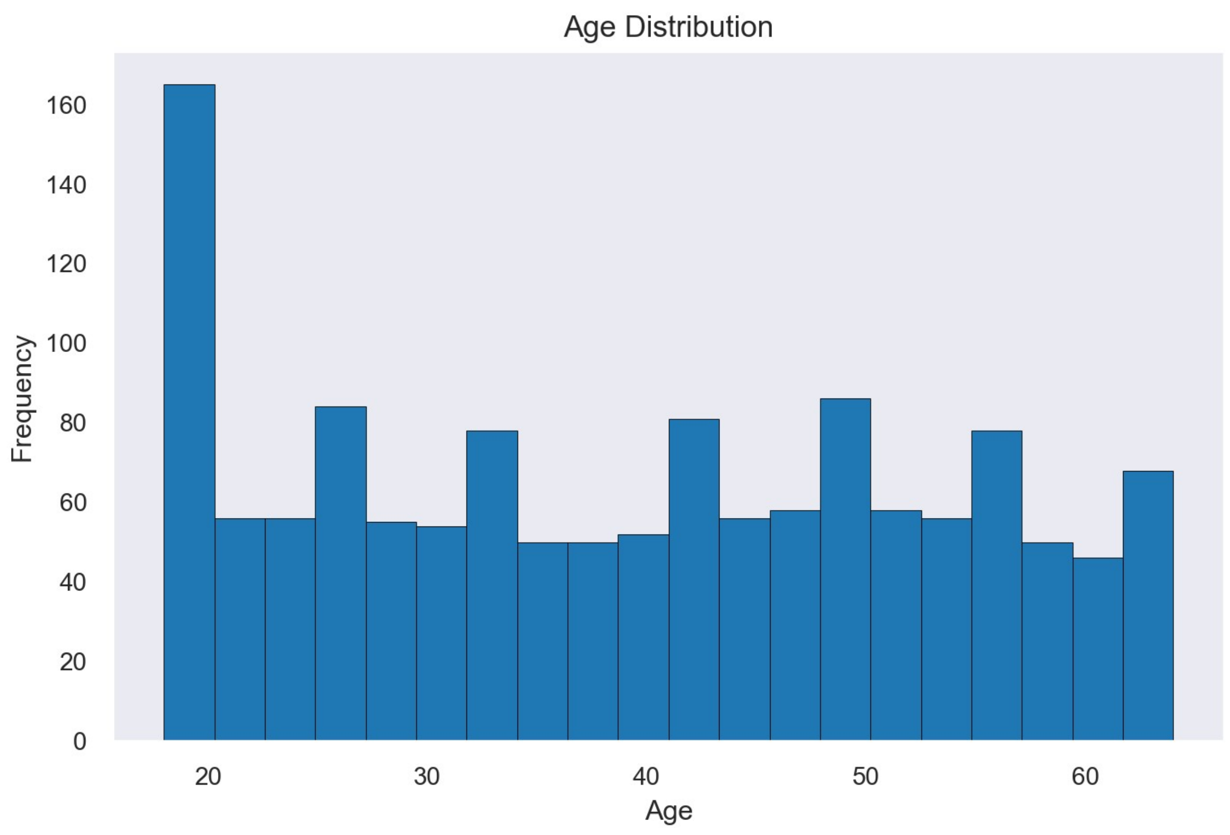
```
insurance_df.describe().style.format("{:.2f}")
```

```
<pandas.io.formats.style.Styler at 0x1647b55cf40>
```

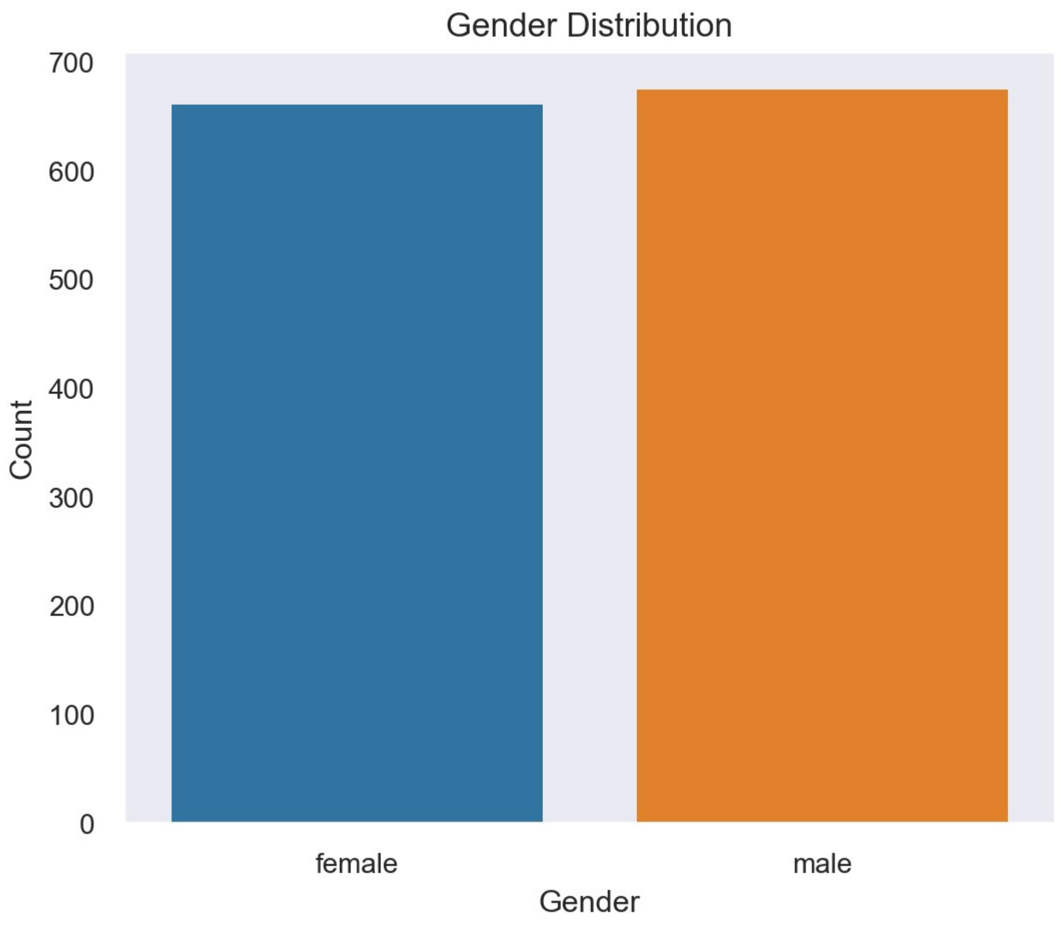
image.png

# Univariate analysis

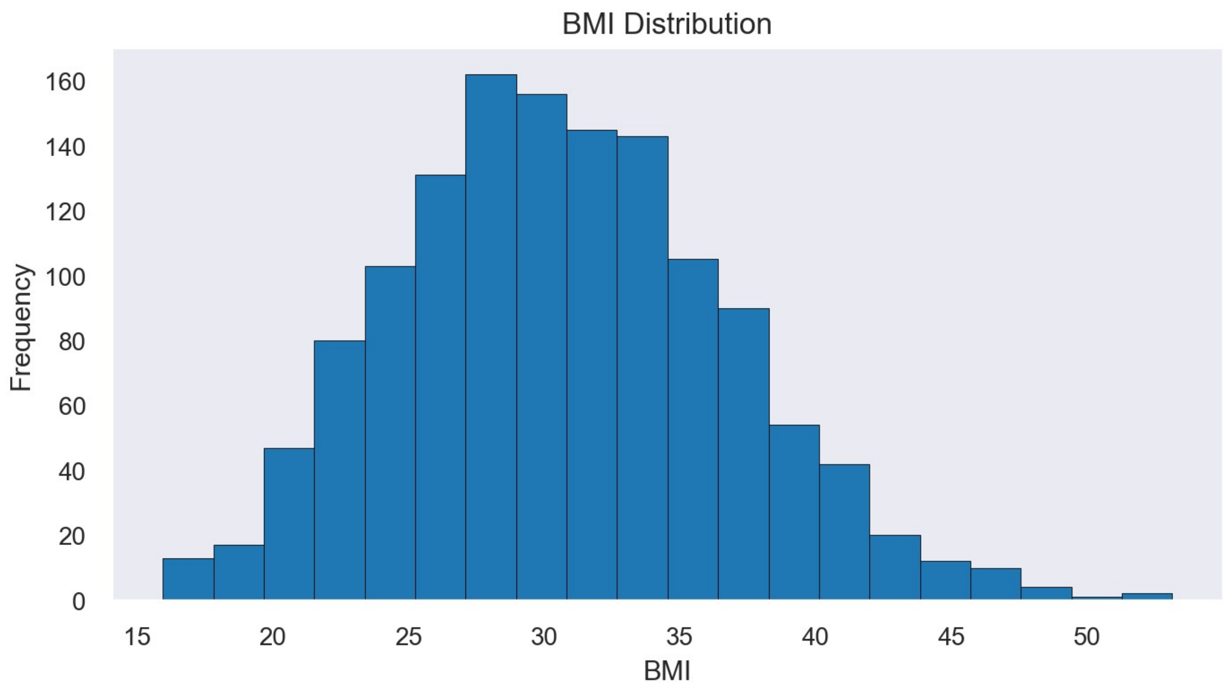
```
# Histogram of age distribution
plt.figure(figsize=(8, 5))
plt.hist(insurance_df['age'], bins=20, edgecolor='black')
plt.xlabel('Age')
plt.ylabel('Frequency')
plt.title('Age Distribution')
plt.show();
```



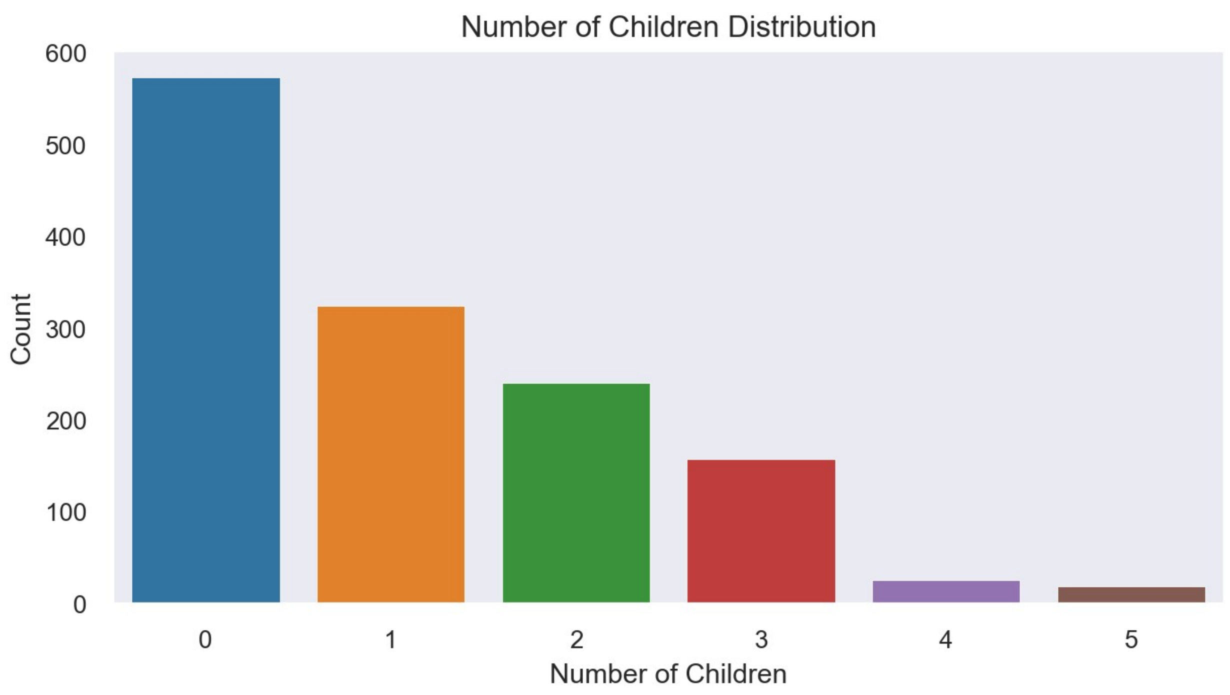
```
# Bar plot of gender distribution
plt.figure(figsize=(6,5))
sns.countplot(data = insurance_df, x ='sex')
plt.xlabel('Gender')
plt.ylabel('Count')
plt.title('Gender Distribution')
plt.show();
```



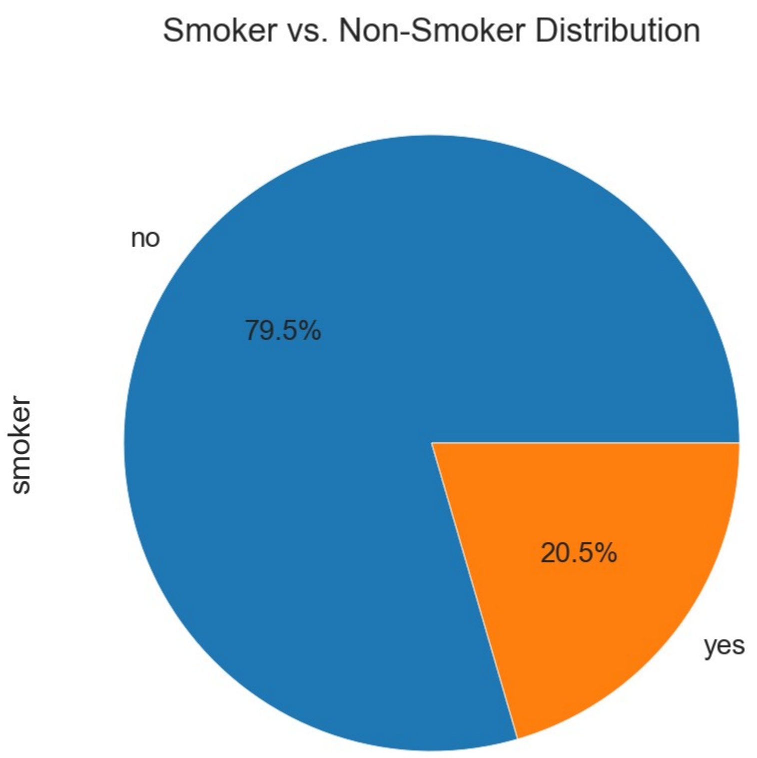
```
# Histogram of BMI values
plt.figure(figsize=(8, 4))
plt.hist(insurance_df['bmi'], bins=20, edgecolor='black')
plt.xlabel('BMI')
plt.ylabel('Frequency')
plt.title('BMI Distribution')
plt.show();
```



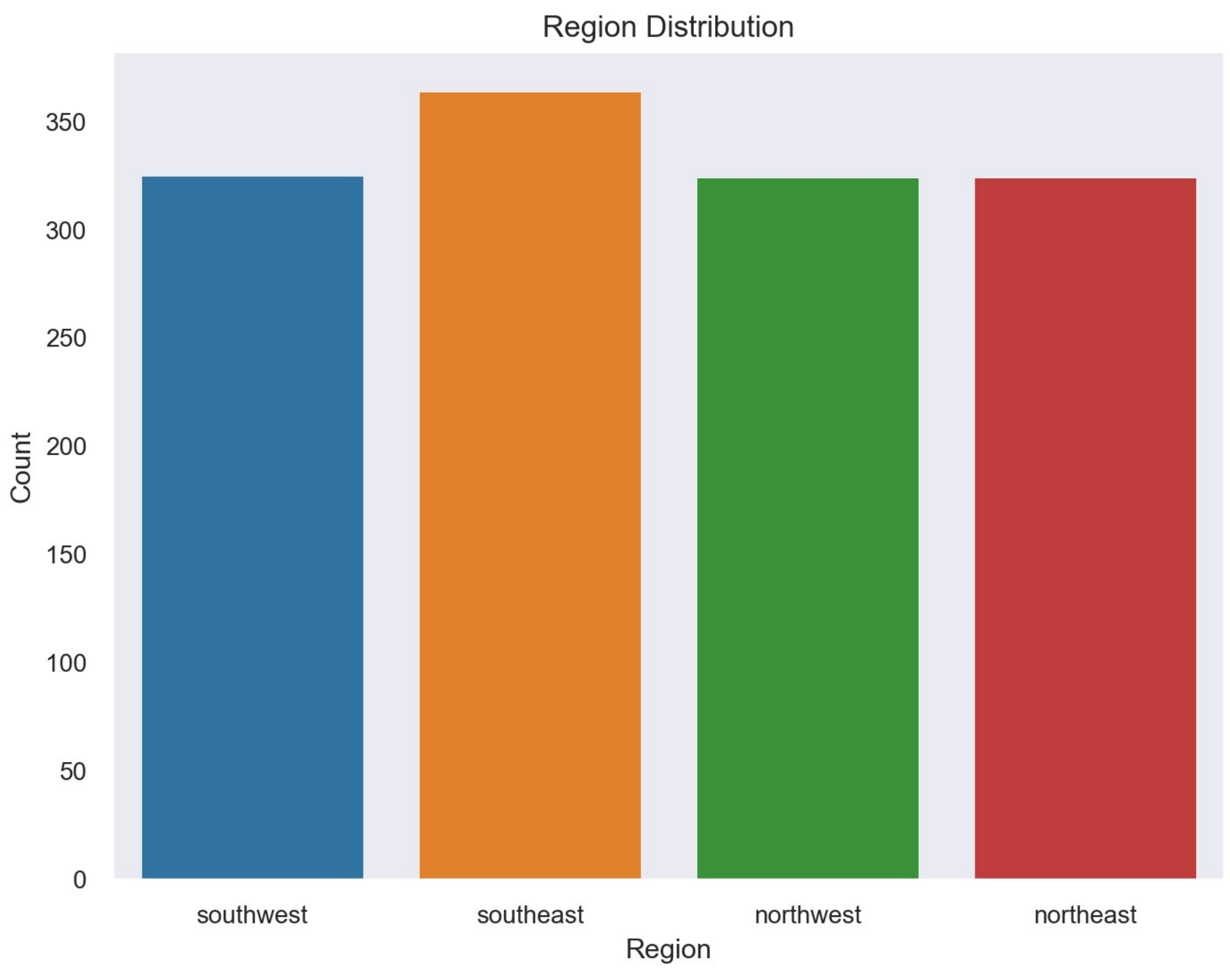
```python
# Visualization : Bar plot of the number of children/dependents
plt.figure(figsize=(8,4))
sns.countplot(data = insurance_df, x='children')
plt.xlabel('Number of Children')
plt.ylabel('Count')
plt.title('Number of Children Distribution')
plt.show();
```



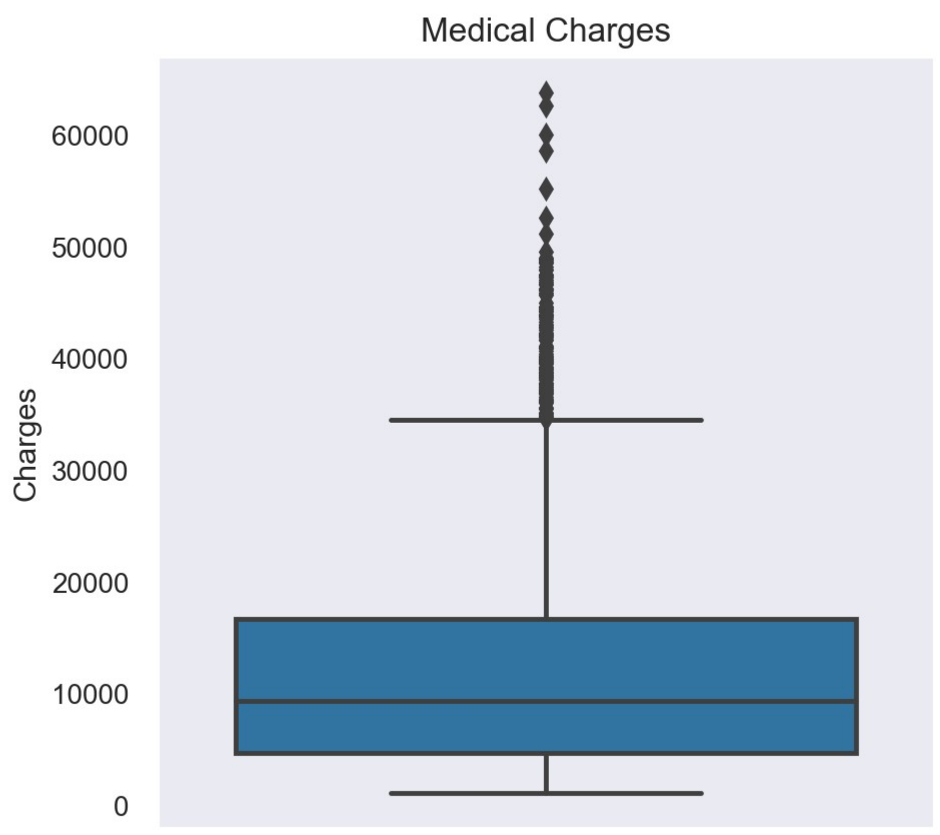
```
# Pie chart of smoker vs. non-smoker distribution
plt.figure(figsize=(5,5))
insurance_df['smoker'].value_counts().plot(kind='pie', autopct='%1.1f%
%')
plt.title('Smoker vs. Non-Smoker Distribution')
plt.show();
```



```python
# Bar plot of region distribution
plt.figure(figsize=(8, 6))
sns.countplot(data = insurance_df, x='region')
plt.xlabel('Region')
plt.ylabel('Count')
plt.title('Region Distribution')
plt.show();
```

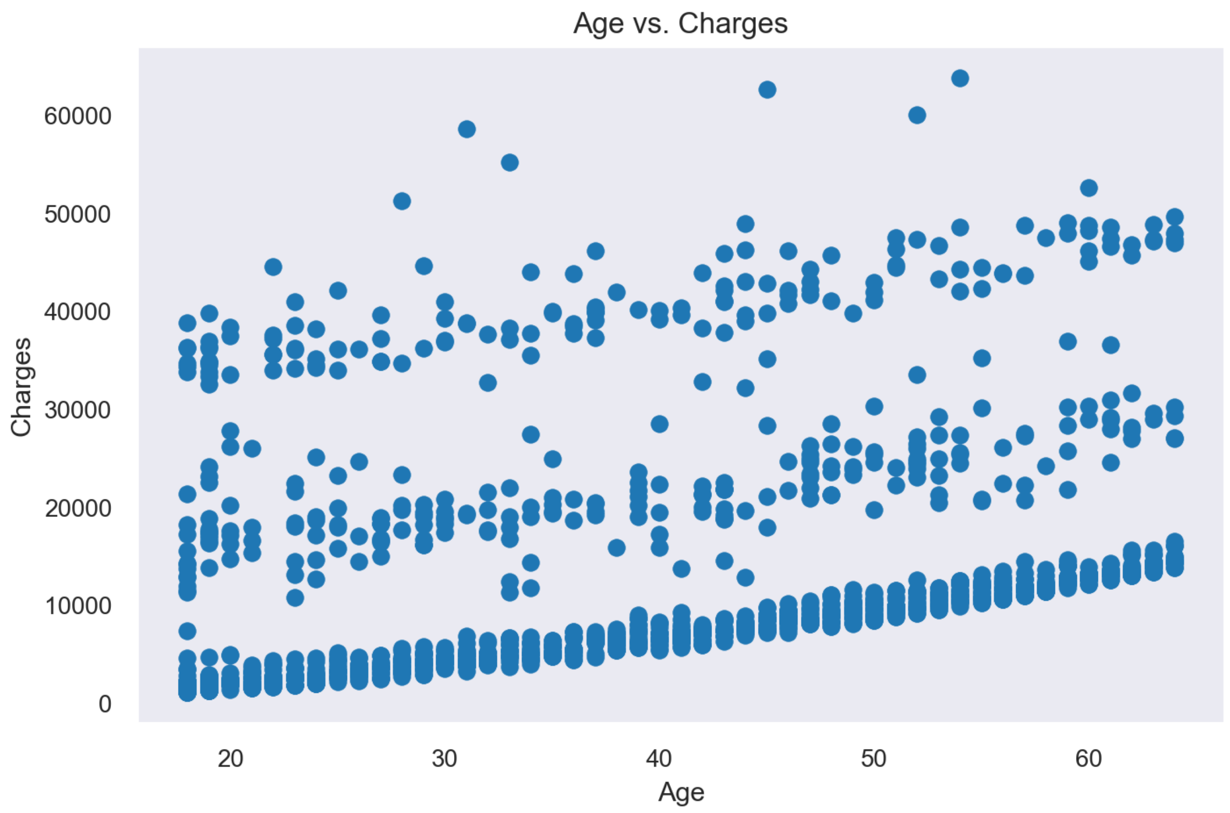


```
# Box plot of medical charges
plt.figure(figsize=(5,5))
sns.boxplot(data = insurance_df, y='charges')
plt.ylabel('Charges')
plt.title('Medical Charges')
plt.show();
```

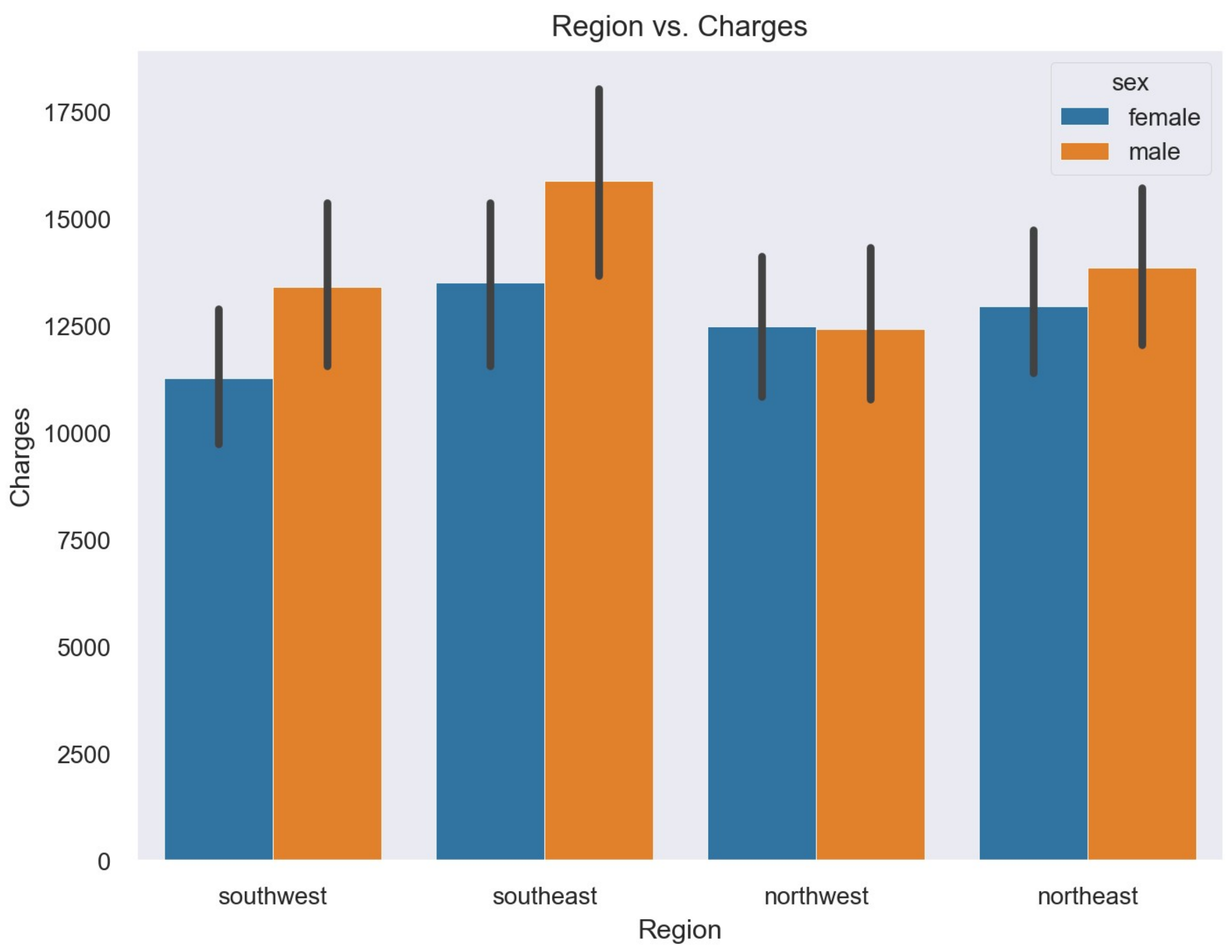


## Bi-Variate Analysis

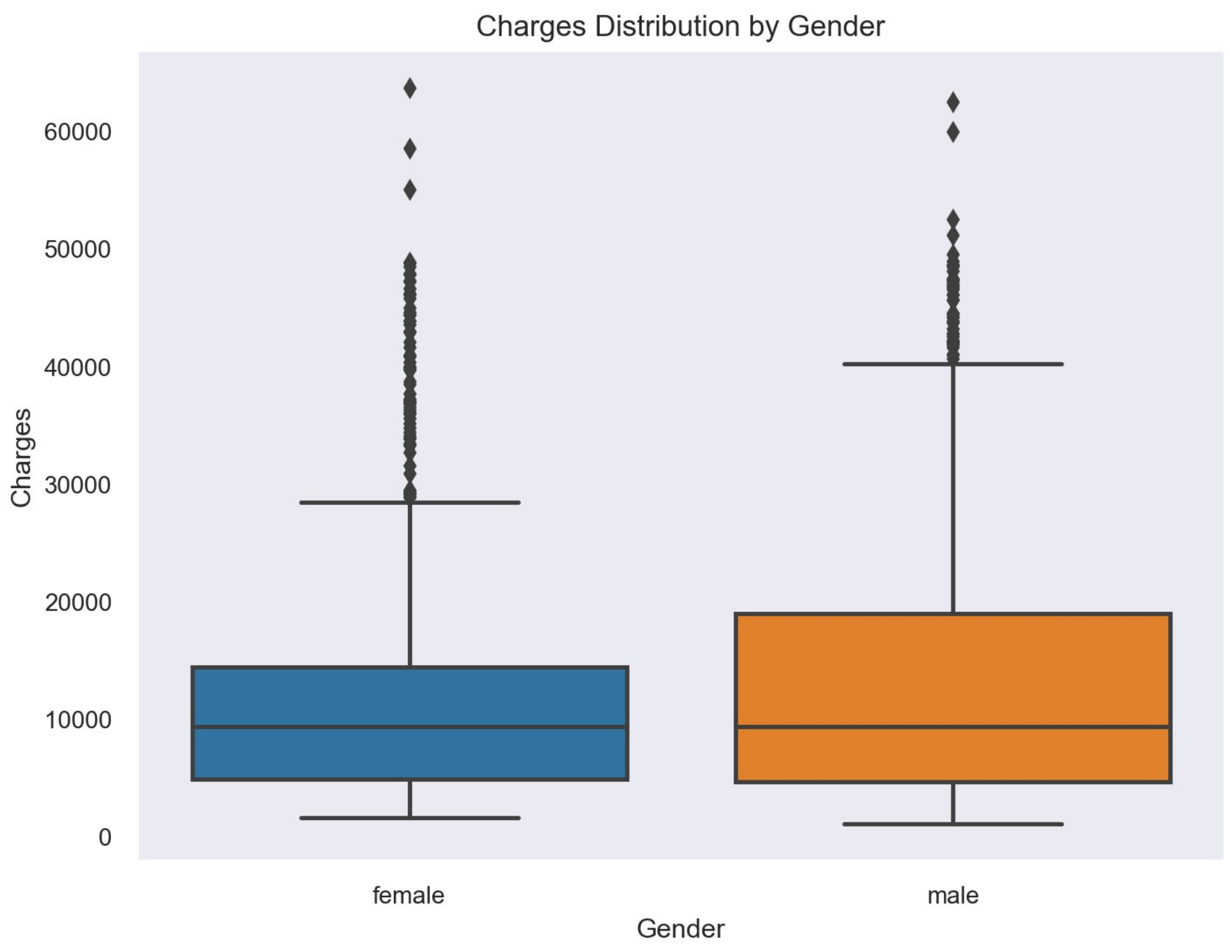
```python
# Scatter plot of age vs. charges
plt.figure(figsize=(8,5))
plt.scatter(insurance_df['age'], insurance_df['charges'])
plt.xlabel('Age')
plt.ylabel('Charges')
plt.title('Age vs. Charges')
plt.show();
```



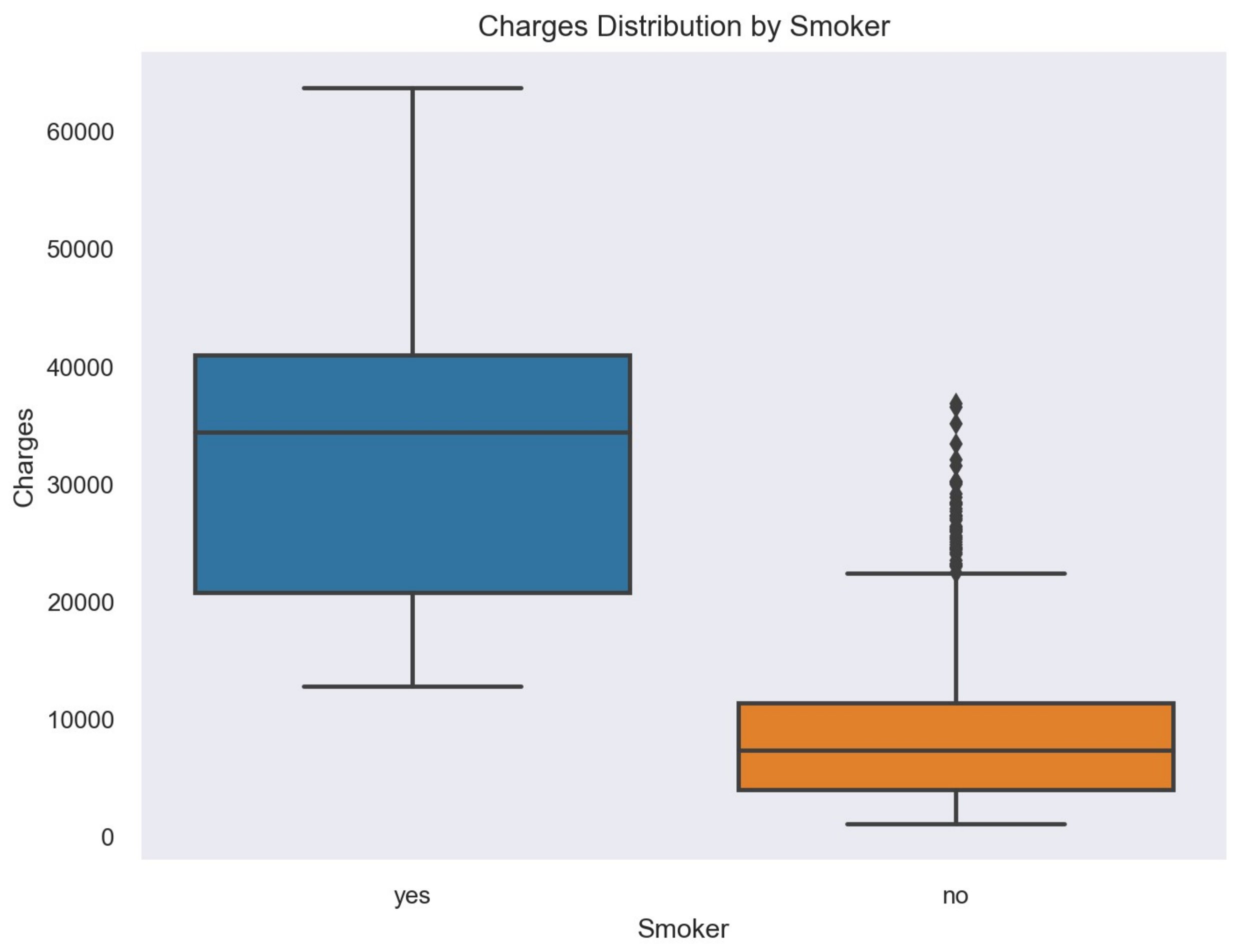
```
# Stacked bar plot of region vs. charges
plt.figure(figsize=(8, 6))
sns.barplot(data = insurance_df, x='region', y='charges', hue='sex')
plt.xlabel('Region')
plt.ylabel('Charges')
plt.title('Region vs. Charges')
plt.show();
```



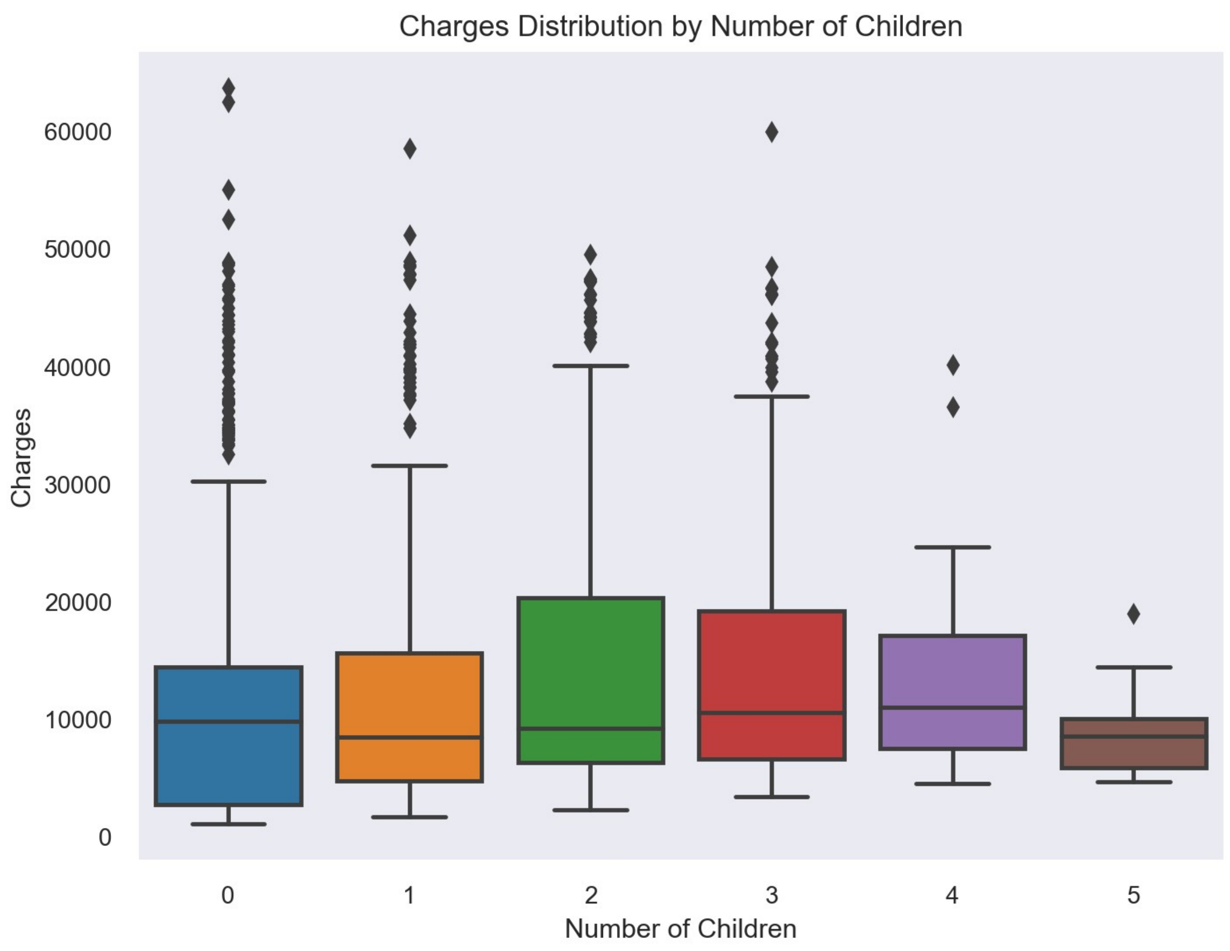
```
# Box plot of charges grouped by gender
plt.figure(figsize=(8, 6))
sns.boxplot(data=insurance_df, x='sex', y='charges')
plt.xlabel('Gender')
plt.ylabel('Charges')
plt.title('Charges Distribution by Gender')
plt.show();
```



```
# Box plot of charges grouped by smoker vs. non-smoker
plt.figure(figsize=(8, 6))
sns.boxplot(data=insurance_df, x='smoker', y='charges')
plt.xlabel('Smoker')
plt.ylabel('Charges')
plt.title('Charges Distribution by Smoker')
plt.show();
```



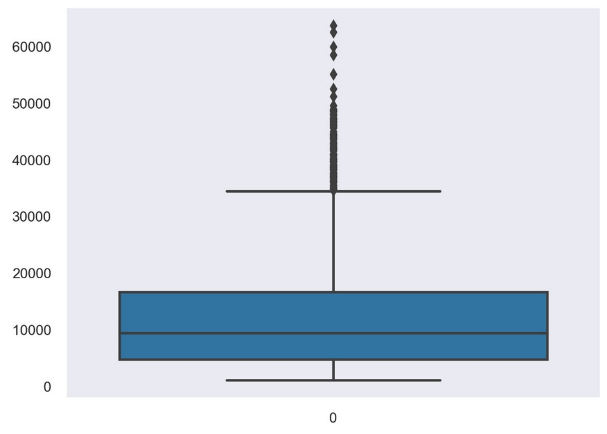
```
# Box plot of charges grouped by the number of children
plt.figure(figsize=(8, 6))
sns.boxplot(data=insurance_df, x='children', y='charges')
plt.xlabel('Number of Children')
plt.ylabel('Charges')
plt.title('Charges Distribution by Number of Children')
plt.show();
```

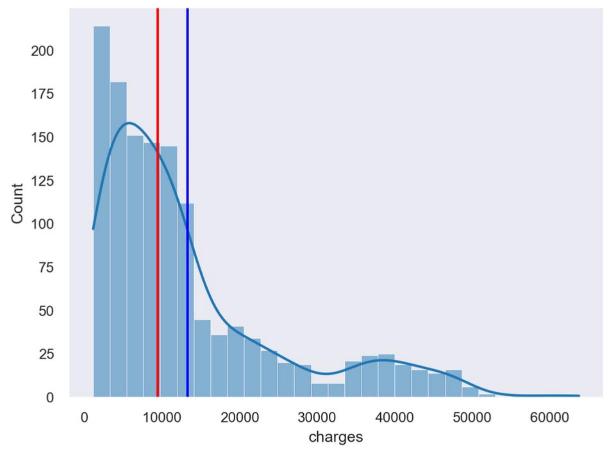


```
plt.figure(figsize=(15,5))

plt.subplot(121)
sns.boxplot(insurance_df.charges)

plt.subplot(122)
sns.histplot(insurance_df.charges.astype(float), kde = True)
plt.axvline(insurance_df.charges.astype(float).mean(), color = 'blue')
plt.axvline(insurance_df.charges.astype(float).median(), color =
'red');
```

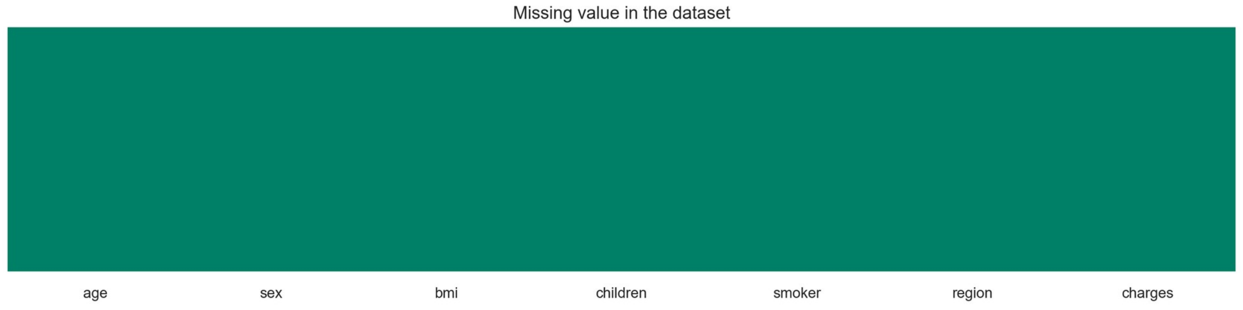




```
insurance_df.groupby('children').agg(['mean','min','max'])['charges']
```

```
              mean     min      max
children
0         12384.70 1121.87 63770.43
1         12731.17 1711.03 58571.07
2         15073.56 2304.00 49577.66
3         15355.32 3443.06 60021.40
4         13850.66 4504.66 40182.25
5          8786.04 4687.80 19023.26
```

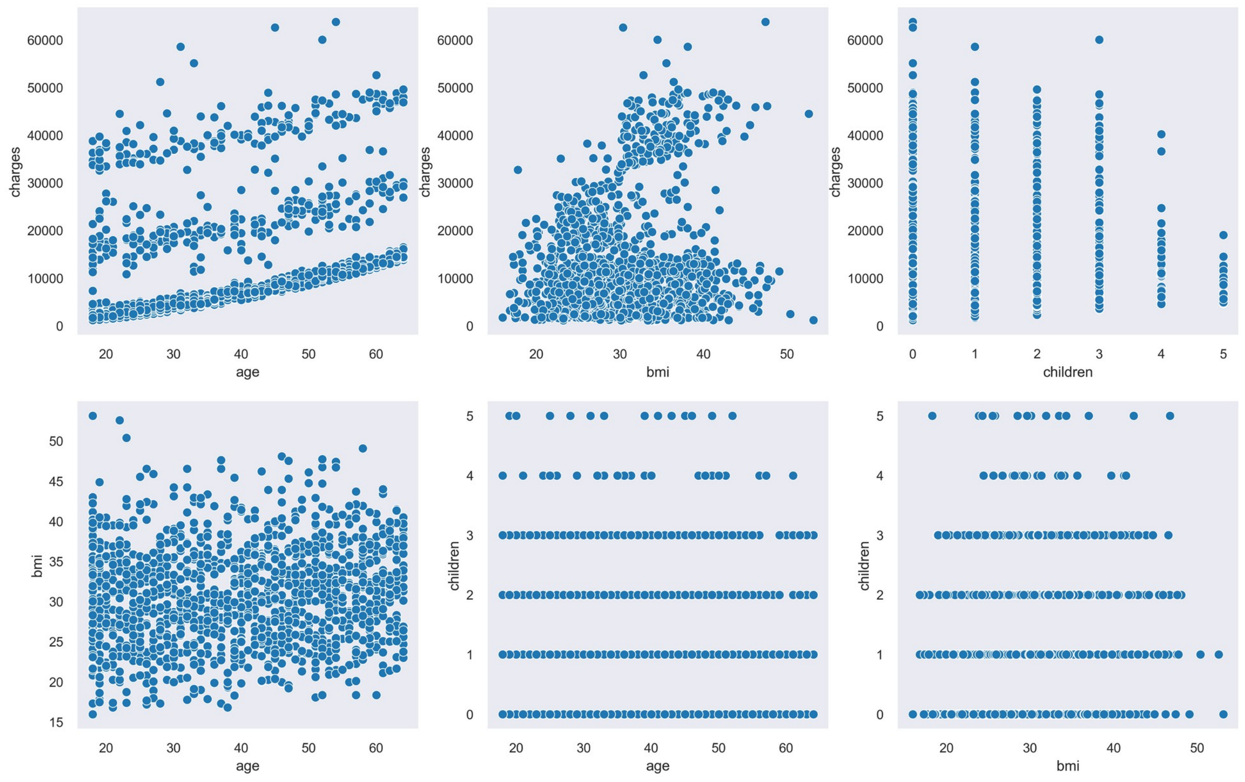
```
# Outliers
plt.figure(figsize=(15,3))
sns.heatmap(insurance_df.isnull(),cbar=False,cmap='summer',yticklabels
=False)
plt.title('Missing value in the dataset');
```



There is no missing values in data set

```
plt.figure(figsize=(16,10), dpi = 200)
plt.subplot(231)
sns.scatterplot(data = insurance_df, x ='age', y = 'charges')
plt.subplot(232)
sns.scatterplot(data =insurance_df, x = 'bmi', y = 'charges')
plt.subplot(233)
```

```
sns.scatterplot(data =insurance_df, x = 'children', y = 'charges')
plt.subplot(234)
sns.scatterplot(data =insurance_df, x = 'age', y = 'bmi')
plt.subplot(235)
sns.scatterplot(data =insurance_df, x = 'age', y = 'children')
plt.subplot(236)
sns.scatterplot(data =insurance_df, x = 'bmi', y = 'children');
```



! image.png

## Data Preprocessing

### | Encoding

Machine learning algorithms cannot work with categorical data directly, categorical data must be converted to number.

### | Label Encoding

Label encoding refers to transforming the word labels into numerical form so that the algorithms can understand how to operate on them.

### | One Hot encoding

A One hot encoding is a representation of categorical variable as binary vectors.It allows the representation of categorical data to be more expresive. This first requires that the categorical values be mapped to integer values, that is label encoding. Then, each integer value is represented as a binary vector that is all zero values except the index of the integer, which is marked with a 1.

```
X = insurance_df[['age','sex','bmi','smoker','children']]
y = insurance_df['charges']

X.head()
y.head()
```

```
   age     sex   bmi  smoker  children
0   19  female 27.90     yes         0
1   18    male 33.77      no         1
2   28    male 33.00      no         3
3   33    male 22.70      no         0
4   32    male 28.88      no         0
```

```
0   16884.92
1    1725.55
2    4449.46
3   21984.47
4    3866.86
Name: charges, dtype: float64
```

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size =
0.25, random_state = 100)

print(X_train.shape, y_train.shape)
print(X_test.shape, y_test.shape)
```

```
(1002, 5) (1002,)
(335, 5) (335,)
```

## Seperating Categorical and numerical

```
X_train.head()
```

```
      age     sex   bmi  smoker  children
1000   30    male 22.99     yes         2
885    32    male 28.93     yes         1
517    45    male 30.50      no         2
1132   57    male 40.28      no         0
1188   43  female 25.27     yes         1
```

```
X_train_cat = X_train.select_dtypes(include=['object'])

X_train_cat.head()
```

```
         sex smoker
1000    male    yes
```

```
885      male    yes
517      male     no
1132     male     no
1188   female    yes

X_train_num = X_train.select_dtypes(include=['int64', 'float64'])

X_train_num.head()

      age   bmi  children
1000   30 22.99         2
885    32 28.93         1
517    45 30.50         2
1132   57 40.28         0
1188   43 25.27         1
```

## Scaling the Numerical features

```
X_train_num.head()

      age   bmi  children
1000   30 22.99         2
885    32 28.93         1
517    45 30.50         2
1132   57 40.28         0
1188   43 25.27         1

# scaling the numerical features
from sklearn.preprocessing import StandardScaler

scaler = StandardScaler()

# column names are (annoyingly) lost after Scaling
# (i.e. the dataframe is converted to a numpy ndarray)

X_train_num_rescaled = pd.DataFrame(scaler.fit_transform(X_train_num),
                                    columns = X_train_num.columns,
                                    index = X_train_num.index)

X_train_num_rescaled.head()

       age   bmi  children
1000 -0.64 -1.23      0.79
885  -0.50 -0.27     -0.07
517   0.42 -0.01      0.79
1132  1.27  1.58     -0.92
1188  0.28 -0.86     -0.07

X_train_num.describe()
```

```
          age     bmi  children
count 1002.00 1002.00   1002.00
mean    39.08   30.57      1.08
std     14.10    6.14      1.18
min     18.00   15.96      0.00
25%     26.00   26.08      0.00
50%     39.00   30.30      1.00
75%     51.00   34.80      2.00
max     64.00   53.13      5.00
```

```
print("Number of Numerical Features:", scaler.n_features_in_)
print("Mean of each column:", scaler.mean_)
print("Std of each column:", np.sqrt(scaler.var_))
```

```
Number of Numerical Features: 3
Mean of each column: [39.08283433 30.57117265  1.07684631]
Std of each column: [14.09138002  6.14168693  1.17572029]
```

## Applying OneHotEncoding on Categorical Columns

```
X_train_cat['sex'].value_counts(normalize=True)
```

```
male     0.51
female   0.49
Name: sex, dtype: float64
```

```
X_train_cat['smoker'].value_counts(normalize=True)
```

```
no    0.79
yes   0.21
Name: smoker, dtype: float64
```

```
from sklearn.preprocessing import OneHotEncoder

encoder = OneHotEncoder(drop='first', sparse=False)

# column names are (annoyingly) lost after OneHotEncoding
# (i.e. the dataframe is converted to a numpy ndarray)

X_train_cat_ohe = pd.DataFrame(encoder.fit_transform(X_train_cat),

columns=encoder.get_feature_names_out(X_train_cat.columns),
                               index = X_train_cat.index)

X_train_cat_ohe.head()
```

```
      sex_male  smoker_yes
1000      1.00        1.00
885       1.00        1.00
517       1.00        0.00
```

```
1132      1.00        0.00
1188      0.00        1.00
```

## Concatinating the Encoded Categorical Features and Rescaled Numerical Features

```
X_train_transformed = pd.concat([X_train_num_rescaled,
X_train_cat_ohe], axis=1)

X_train_transformed.head()

       age   bmi  children  sex_male  smoker_yes
1000 -0.64 -1.23      0.79      1.00        1.00
885  -0.50 -0.27     -0.07      1.00        1.00
517   0.42 -0.01      0.79      1.00        0.00
1132  1.27  1.58     -0.92      1.00        0.00
1188  0.28 -0.86     -0.07      0.00        1.00
```

## Preparing Test Data

```
X_test.head()

     age     sex   bmi smoker  children
12    23    male 34.40     no         0
306   28  female 27.50     no         2
318   44  female 27.64     no         0
816   24  female 24.23     no         0
157   18    male 25.18    yes         0

X_test.info()

<class 'pandas.core.frame.DataFrame'>
Int64Index: 335 entries, 12 to 625
Data columns (total 5 columns):
 #   Column    Non-Null Count  Dtype  
---  ------    --------------  -----  
 0   age       335 non-null    int64  
 1   sex       335 non-null    object 
 2   bmi       335 non-null    float64
 3   smoker    335 non-null    object 
 4   children  335 non-null    int64  
dtypes: float64(1), int64(2), object(2)
memory usage: 15.7+ KB

X_test_cat = X_test.select_dtypes(include=['object'])

X_test_cat.head()


X_test_num = X_test.select_dtypes(include=['int64', 'float64'])
```

```
X_test_num.head()
```

```
        sex smoker
12     male     no
306  female     no
318  female     no
816  female     no
157    male    yes
```

```
     age   bmi  children
12    23 34.40         0
306   28 27.50         2
318   44 27.64         0
816   24 24.23         0
157   18 25.18         0
```

```
X_test_cat_ohe = pd.DataFrame(encoder.transform(X_test_cat),

columns=encoder.get_feature_names_out(X_test_cat.columns),
                               index = X_test_cat.index)

X_test_cat_ohe.head()
```

```
     sex_male  smoker_yes
12       1.00        0.00
306      0.00        0.00
318      0.00        0.00
816      0.00        0.00
157      1.00        1.00
```

```
X_test_num_rescaled = pd.DataFrame(scaler.transform(X_test_num),
                                   columns = X_test_num.columns,
                                   index = X_test_num.index)

X_test_num_rescaled.head()
```

```
      age   bmi  children
12  -1.14  0.62     -0.92
306 -0.79 -0.50      0.79
318  0.35 -0.48     -0.92
816 -1.07 -1.03     -0.92
157 -1.50 -0.88     -0.92
```

```
X_test_transformed = pd.concat([X_test_num_rescaled, X_test_cat_ohe],
axis=1)

X_test_transformed.head()
```

```
      age   bmi  children  sex_male  smoker_yes
12  -1.14  0.62     -0.92      1.00        0.00
```

```
306 -0.79 -0.50      0.79      0.00         0.00
318  0.35 -0.48     -0.92      0.00         0.00
816 -1.07 -1.03     -0.92      0.00         0.00
157 -1.50 -0.88     -0.92      1.00         1.00
```

## Variance inflation factor

```
from patsy import dmatrices
from statsmodels.stats.outliers_influence import
variance_inflation_factor

vif = pd.DataFrame()
vif['VIF'] = [variance_inflation_factor(X_train_transformed.values, i)
for i in range(X_train_transformed.shape[1])]
vif['variable'] = X_train_transformed.columns

vif
```

```
   VIF    variable
0 1.01         age
1 1.01         bmi
2 1.00    children
3 1.16    sex_male
4 1.15  smoker_yes
```

```
vif = pd.DataFrame()
vif['VIF'] = [variance_inflation_factor(X_test_transformed.values, i)
for i in range(X_test_transformed.shape[1])]
vif['variable'] = X_test_transformed.columns

vif
```

```
   VIF    variable
0 1.04         age
1 1.04         bmi
2 1.01    children
3 1.19    sex_male
4 1.19  smoker_yes
```

## | Model Building

### Linear Regression

```
from sklearn.linear_model import LinearRegression
LR_regressor = LinearRegression()
LR_regressor.fit(X_train_transformed, y_train)
```

```
LinearRegression()

y_test_pred = LR_regressor.predict(X_test_transformed)

#Testing the model accuracy

r2   = r2_score(y_test, y_test_pred)              # Getting the R-
squared (R²)
mae  = mean_absolute_error(y_test, y_test_pred)  # Getting the Mean
Absolute Error
mse  = mean_squared_error(y_test, y_test_pred)   # Getting the Mean
Squared Error
rmse = np.sqrt(mse)                               # Getting the Root
Mean Squared Error


#Defining a DataFrame
results = pd.DataFrame([['Linear Regression', r2*100, mae, mse,
rmse]],
                    columns=['Model', 'R-squared (R²)', 'Mean Absolute
Error', 'Mean Squared Error', 'Root Mean Squared Error'])

#Printing the Model Results with different Metrics
results

               Model  R-squared (R²)  Mean Absolute Error   Mean
Squared Error  \
0  Linear Regression           75.40              3938.02
31503873.50

   Root Mean Squared Error
0                  5612.83

print('Linear Regression Train Score is : ' ,
LR_regressor.score(X_train_transformed, y_train))
print('Linear Regression Test Score is : ' ,
LR_regressor.score(X_test_transformed, y_test))

Linear Regression Train Score is :  0.7477013745713325
Linear Regression Test Score is :  0.7540307970555084
```

## Residuals (Difference between y_test and y_pred)

```
test_residual= y_test - y_test_pred

medical_LR = pd.DataFrame({'Actual': y_test, 'Predicted': y_test_pred,
'diff':(abs(y_test-y_test_pred))})

medical_LR.head()
```

```
      Actual  Predicted     diff
12   1826.84    4798.71  2971.87
306 20177.67    5005.99 15171.68
318  7421.19    8305.25   884.06
816  2842.76    1823.34  1019.42
157 15518.18   24129.98  8611.80
```

## KNN Regression

```
from sklearn.neighbors import KNeighborsRegressor
KNN_regressor = KNeighborsRegressor()
KNN_regressor.fit(X_train_transformed, y_train)
```

```
KNeighborsRegressor()
```

```
y_test_pred = KNN_regressor.predict(X_test_transformed)

#Testing the model accuracy

r2   = r2_score(y_test, y_test_pred)             # Getting the R-
squared (R²)
mae  = mean_absolute_error(y_test, y_test_pred)  # Getting the Mean
Absolute Error
mse  = mean_squared_error(y_test, y_test_pred)   # Getting the Mean
Squared Error
rmse = np.sqrt(mse)                              # Getting the Root
Mean Squared Error


#Defining a DataFrame
knn_results = pd.DataFrame([['KNN Regression', r2*100, mae, mse,
rmse]],
                    columns=['Model', 'R-squared (R²)', 'Mean Absolute
Error', 'Mean Squared Error', 'Root Mean Squared Error'])

#Printing the Model Results with different Metrics
results = results.append(knn_results , ignore_index=True)
results
```

```
               Model  R-squared (R²)  Mean Absolute Error  Mean
Squared Error  \
0  Linear Regression           75.40              3938.02
31503873.50
1     KNN Regression           79.97              3006.35
25660048.66

   Root Mean Squared Error
0                  5612.83
1                  5065.57
```

```
print('KNN Regression Train Score is : ' ,
KNN_regressor.score(X_train_transformed, y_train))
print('KNN Regression Test Score is : ' ,
KNN_regressor.score(X_test_transformed, y_test))

KNN Regression Train Score is :  0.8386114862600965
KNN Regression Test Score is :  0.7996569622824252
```

## Residuals (Difference between y_test and y_pred)

```
test_residual= y_test - y_test_pred

medical_knn = pd.DataFrame({'Actual': y_test, 'Predicted':
y_test_pred, 'diff':(abs(y_test-y_test_pred))})

medical_knn.head()

      Actual  Predicted     diff
12   1826.84    1652.96   173.88
306 20177.67    4587.75 15589.92
318  7421.19    6863.31   557.89
816  2842.76    7573.04  4730.28
157 15518.18   19947.37  4429.19
```

## Decision Tree Regression

```
from sklearn.tree import DecisionTreeRegressor

DT_regressor = DecisionTreeRegressor()
DT_regressor.fit(X_train_transformed, y_train)

DecisionTreeRegressor()

y_test_pred = DT_regressor.predict(X_test_transformed)

#Testing the model accuracy

r2   = r2_score(y_test, y_test_pred)            # Getting the R-
squared (R²)
mae  = mean_absolute_error(y_test, y_test_pred)  # Getting the Mean
Absolute Error
mse  = mean_squared_error(y_test, y_test_pred)   # Getting the Mean
Squared Error
rmse = np.sqrt(mse)                              # Getting the Root
Mean Squared Error


#Defining a DataFrame
dt_results = pd.DataFrame([['Decison-tree Regression', r2*100, mae,
mse, rmse]],
                    columns=['Model', 'R-squared (R²)', 'Mean Absolute
Error', 'Mean Squared Error', 'Root Mean Squared Error'])

#Printing the Model Results with different Metrics
results = results.append(dt_results , ignore_index=True)
results
```

```
                     Model  R-squared (R²)  Mean Absolute Error  \
0        Linear Regression           75.40              3938.02
1           KNN Regression           79.97              3006.35
2  Decison-tree Regression           58.68              3648.23

   Mean Squared Error  Root Mean Squared Error
0         31503873.50                  5612.83
1         25660048.66                  5065.57
2         52924035.93                  7274.89
```

```
print('Decision Regression Train Score is : ' ,
DT_regressor.score(X_train_transformed, y_train))
print('Decision Regression Test Score is : ' ,
DT_regressor.score(X_test_transformed, y_test))
```

```
Decision Regression Train Score is :  0.9988021709249079
Decision Regression Test Score is :  0.5867910358585947
```

## Residuals (Difference between y_test and y_pred)

```
test_residual= y_test - y_test_pred

medical_DT = pd.DataFrame({'Actual': y_test, 'Predicted': y_test_pred,
'diff':(abs(y_test-y_test_pred))})

medical_DT.head()
```

```
      Actual  Predicted     diff
12   1826.84    1837.28    10.44
306 20177.67    4340.44 15837.23
318  7421.19    7626.99   205.80
816  2842.76   22395.74 19552.98
157 15518.18   16232.85   714.67
```

## Hyperparametric Tuning for Decision Tree

```
from sklearn.model_selection import RandomizedSearchCV

parameters={"splitter":["best","random"],
            "max_depth" : [1,3,5,7,9],
           "min_samples_leaf":[1,2,3,4,5,],
           "max_features":["auto","sqrt"],
           "max_leaf_nodes":[5,10,15] }
```

```
hyper_tuning = RandomizedSearchCV(estimator=DT_regressor,
param_distributions = parameters,
                               cv = 2, n_iter = 10, n_jobs=-1)
```

```
hyper_tuning.fit(X_train_transformed, y_train)
```

```
RandomizedSearchCV(cv=2, estimator=DecisionTreeRegressor(), n_jobs=-1,
                   param_distributions={'max_depth': [1, 3, 5, 7, 9],
                                        'max_features': ['auto',
'sqrt'],
                                        'max_leaf_nodes': [5, 10, 15],
                                        'min_samples_leaf': [1, 2, 3,
4, 5],
                                        'splitter': ['best',
'random']})
```

```
hyper_tuning.best_params_   ## getting the best parameters
```

```
{'splitter': 'best',
 'min_samples_leaf': 5,
 'max_leaf_nodes': 5,
 'max_features': 'auto',
 'max_depth': 5}
```

```
DT_hyper =
DecisionTreeRegressor(splitter='best',min_samples_leaf=4,max_leaf_node
s=15,max_features='auto',max_depth=7)
```

```
DT_hyper.fit(X_train_transformed,y_train)
```

```
DecisionTreeRegressor(max_depth=7, max_features='auto',
max_leaf_nodes=15,
                      min_samples_leaf=4)
```

```
tuning_predict = DT_hyper.predict(X_test_transformed)
```

```
print('Decision Tree Regressor hyperparameter score
training :',hyper_tuning.score(X_train_transformed,y_train))
```

```
Decision Tree Regressor hyperparameter score training :
0.8361318429771127
```

```
print('Decision Tree Regressor hyperparameter score testing :',
hyper_tuning.score(X_test_transformed,y_test))
```

```
Decision Tree Regressor hyperparameter score testing :
0.8372962465579079
```

## Random Forest Regression

```
from sklearn.ensemble import RandomForestRegressor
RF_regressor = RandomForestRegressor()
RF_regressor.fit(X_train_transformed, y_train)

RandomForestRegressor()

y_test_pred = RF_regressor.predict(X_test_transformed)

#Testing the model accuracy

r2   = r2_score(y_test, y_test_pred)             # Getting the R-
squared (R²)
mae  = mean_absolute_error(y_test, y_test_pred)  # Getting the Mean
Absolute Error
mse  = mean_squared_error(y_test, y_test_pred)   # Getting the Mean
Squared Error
rmse = np.sqrt(mse)                              # Getting the Root
Mean Squared Error


#Defining a DataFrame
RF_results = pd.DataFrame([['Random Forest Regression', r2*100, mae,
mse, rmse]],
                    columns=['Model', 'R-squared (R²)', 'Mean Absolute
Error', 'Mean Squared Error', 'Root Mean Squared Error'])

#Printing the Model Results with different Metrics
results = results.append(RF_results , ignore_index=True)
results

                      Model  R-squared (R²)  Mean Absolute Error  \
0         Linear Regression           75.40              3938.02
1            KNN Regression           79.97              3006.35
2    Decison-tree Regression           58.68              3648.23
3  Random Forest Regression           82.55              2701.47

   Mean Squared Error  Root Mean Squared Error
0         31503873.50                  5612.83
1         25660048.66                  5065.57
2         52924035.93                  7274.89
3         22344392.41                  4726.99

print('Random Forest Regression Train Score is : ' ,
RF_regressor.score(X_train_transformed, y_train))
print('Random Forest Regression Test Score is : '  ,
RF_regressor.score(X_test_transformed, y_test))

Random Forest Regression Train Score is :  0.9750853574499634
Random Forest Regression Test Score is :  0.8255442337328778
```

## Residuals (Difference between y_test and y_pred)

```
test_residual= y_test - y_test_pred

medical_RF = pd.DataFrame({'Actual': y_test, 'Predicted': y_test_pred,
'diff':(abs(y_test-y_test_pred))})

medical_RF.head()
```

```
       Actual  Predicted     diff
12    1826.84    2768.14   941.30
306  20177.67    4594.38 15583.29
318   7421.19   16963.18  9541.99
816   2842.76   11651.18  8808.42
157  15518.18   16475.83   957.65
```

## Hyperparametric Tuning for Random Forest

```
grid={'n_estimators':[int(x) for x in
np.linspace(start=100,stop=1200,num=12)],
      'max_features':['auto','log2'],
      'max_depth':[int(x) for x in np.linspace(5,30,num=6)],
      'min_samples_split':[2,5,10,15,100],
      'min_samples_leaf':[1,2,5,10]}

hyper_tuning=RandomizedSearchCV(estimator=RF_regressor,param_distribut
ions=grid,n_iter=10,cv=5,verbose=5,random_state=2)

hyper_tuning.fit(X_train_transformed,y_train)
```

```
Fitting 5 folds for each of 10 candidates, totalling 50 fits
[CV 1/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=800;, score=0.855 total time=
3.2s
[CV 2/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=800;, score=0.878 total time=
3.1s
[CV 3/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=800;, score=0.768 total time=
3.0s
[CV 4/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=800;, score=0.824 total time=
3.0s
[CV 5/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=800;, score=0.847 total time=
3.0s
[CV 1/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=1000;, score=0.877 total time=
4.8s
[CV 2/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=1000;, score=0.888 total time=
4.8s
[CV 3/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=1000;, score=0.778 total time=
5.3s
[CV 4/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=1000;, score=0.841 total time=
5.0s
[CV 5/5] END max_depth=30, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=1000;, score=0.854 total time=
5.0s
[CV 1/5] END max_depth=20, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=100;, score=0.853 total time=
0.3s
[CV 2/5] END max_depth=20, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=100;, score=0.880 total time=
0.3s
[CV 3/5] END max_depth=20, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=100;, score=0.767 total time=
0.3s
[CV 4/5] END max_depth=20, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=100;, score=0.823 total time=
0.3s
[CV 5/5] END max_depth=20, max_features=auto, min_samples_leaf=5,
min_samples_split=100, n_estimators=100;, score=0.848 total time=
0.3s
[CV 1/5] END max_depth=25, max_features=log2, min_samples_leaf=10,
min_samples_split=2, n_estimators=800;, score=0.856 total time=   2.6s
[CV 2/5] END max_depth=25, max_features=log2, min_samples_leaf=10,
min_samples_split=2, n_estimators=800;, score=0.877 total time=   2.7s
[CV 3/5] END max_depth=25, max_features=log2, min_samples_leaf=10,
min_samples_split=2, n_estimators=800;, score=0.753 total time=   2.8s
[CV 4/5] END max_depth=25, max_features=log2, min_samples_leaf=10,
min_samples_split=2, n_estimators=800;, score=0.822 total time=   2.7s
[CV 5/5] END max_depth=25, max_features=log2, min_samples_leaf=10,
min_samples_split=2, n_estimators=800;, score=0.819 total time=   2.9s
[CV 1/5] END max_depth=30, max_features=auto, min_samples_leaf=2,
min_samples_split=100, n_estimators=700;, score=0.854 total time=
2.8s
[CV 2/5] END max_depth=30, max_features=auto, min_samples_leaf=2,
min_samples_split=100, n_estimators=700;, score=0.877 total time=
2.6s
[CV 3/5] END max_depth=30, max_features=auto, min_samples_leaf=2,
min_samples_split=100, n_estimators=700;, score=0.768 total time=
2.6s
[CV 4/5] END max_depth=30, max_features=auto, min_samples_leaf=2,
min_samples_split=100, n_estimators=700;, score=0.823 total time=
2.6s
[CV 5/5] END max_depth=30, max_features=auto, min_samples_leaf=2,
min_samples_split=100, n_estimators=700;, score=0.847 total time=
2.6s
[CV 1/5] END max_depth=15, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=800;, score=0.878 total time=   3.9s
[CV 2/5] END max_depth=15, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=800;, score=0.888 total time=   3.8s
[CV 3/5] END max_depth=15, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=800;, score=0.778 total time=   3.8s
[CV 4/5] END max_depth=15, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=800;, score=0.841 total time=   3.9s
[CV 5/5] END max_depth=15, max_features=auto, min_samples_leaf=5,
min_samples_split=5, n_estimators=800;, score=0.853 total time=   4.0s
[CV 1/5] END max_depth=30, max_features=auto, min_samples_leaf=1,
min_samples_split=2, n_estimators=900;, score=0.826 total time=   6.6s
[CV 2/5] END max_depth=30, max_features=auto, min_samples_leaf=1,
min_samples_split=2, n_estimators=900;, score=0.863 total time=   6.6s
[CV 3/5] END max_depth=30, max_features=auto, min_samples_leaf=1,
min_samples_split=2, n_estimators=900;, score=0.748 total time=   6.6s
[CV 4/5] END max_depth=30, max_features=auto, min_samples_leaf=1,
min_samples_split=2, n_estimators=900;, score=0.835 total time=   6.7s
[CV 5/5] END max_depth=30, max_features=auto, min_samples_leaf=1,
min_samples_split=2, n_estimators=900;, score=0.824 total time=   6.6s
[CV 1/5] END max_depth=10, max_features=auto, min_samples_leaf=10,
min_samples_split=5, n_estimators=300;, score=0.880 total time=   1.2s
[CV 2/5] END max_depth=10, max_features=auto, min_samples_leaf=10,
min_samples_split=5, n_estimators=300;, score=0.893 total time=   1.2s
[CV 3/5] END max_depth=10, max_features=auto, min_samples_leaf=10,
min_samples_split=5, n_estimators=300;, score=0.782 total time=   1.3s
[CV 4/5] END max_depth=10, max_features=auto, min_samples_leaf=10,
min_samples_split=5, n_estimators=300;, score=0.845 total time=   1.2s
[CV 5/5] END max_depth=10, max_features=auto, min_samples_leaf=10,
min_samples_split=5, n_estimators=300;, score=0.858 total time=   1.3s
[CV 1/5] END max_depth=5, max_features=log2, min_samples_leaf=10,
min_samples_split=5, n_estimators=200;, score=0.847 total time=   0.6s
[CV 2/5] END max_depth=5, max_features=log2, min_samples_leaf=10,
min_samples_split=5, n_estimators=200;, score=0.873 total time=   0.6s
[CV 3/5] END max_depth=5, max_features=log2, min_samples_leaf=10,
min_samples_split=5, n_estimators=200;, score=0.755 total time=   0.6s
[CV 4/5] END max_depth=5, max_features=log2, min_samples_leaf=10,
min_samples_split=5, n_estimators=200;, score=0.817 total time=   0.6s
[CV 5/5] END max_depth=5, max_features=log2, min_samples_leaf=10,
min_samples_split=5, n_estimators=200;, score=0.820 total time=   0.6s
[CV 1/5] END max_depth=30, max_features=log2, min_samples_leaf=1,
min_samples_split=5, n_estimators=400;, score=0.852 total time=   1.8s
[CV 2/5] END max_depth=30, max_features=log2, min_samples_leaf=1,
min_samples_split=5, n_estimators=400;, score=0.885 total time=   1.7s
[CV 3/5] END max_depth=30, max_features=log2, min_samples_leaf=1,
min_samples_split=5, n_estimators=400;, score=0.763 total time=   1.7s
[CV 4/5] END max_depth=30, max_features=log2, min_samples_leaf=1,
min_samples_split=5, n_estimators=400;, score=0.831 total time=   1.7s
```

```
[CV 5/5] END max_depth=30, max_features=log2, min_samples_leaf=1,
min_samples_split=5, n_estimators=400;, score=0.840 total time=   1.7s
```

```
RandomizedSearchCV(cv=5, estimator=RandomForestRegressor(),
                   param_distributions={'max_depth': [5, 10, 15, 20,
25, 30],
                                        'max_features': ['auto',
'log2'],
                                        'min_samples_leaf': [1, 2, 5,
10],
                                        'min_samples_split': [2, 5,
10, 15,
                                                              100],
                                        'n_estimators': [100, 200,
300, 400,
                                                         500, 600,
700, 800,
                                                         900, 1000,
1100,
                                                         1200]},
                   random_state=2, verbose=5)
```

```
hyper_tuning.best_params_
```

```
{'n_estimators': 300,
 'min_samples_split': 5,
 'min_samples_leaf': 10,
 'max_features': 'auto',
 'max_depth': 10}
```

```
RF_hyper=RandomForestRegressor(n_estimators=700,min_samples_split=5,mi
n_samples_leaf=10,max_features='auto',max_depth=20)
```

```
RF_hyper.fit(X_train_transformed,y_train)
```

```
RandomForestRegressor(max_depth=20, max_features='auto',
min_samples_leaf=10,
                      min_samples_split=5, n_estimators=700)
```

```
tuning_predict=RF_hyper.predict(X_test_transformed)
```

```
print('Random Forest Regressor hyper parametric tuning for
training :',RF_hyper.score(X_train_transformed,y_train))
```

```
Random Forest Regressor hyper parametric tuning for training :
0.8841357926887093
```

```
print('Random Forest Regressor hyper parametric tuning for
testing :',RF_hyper.score(X_test_transformed,y_test))
```

```
Random Forest Regressor hyper parametric tuning for testing :
0.8773774832826662
```

## GB Boosting Regressor

```
from sklearn.ensemble import GradientBoostingRegressor
GB_regressor = GradientBoostingRegressor()
GB_regressor.fit(X_train_transformed, y_train)
```

```
GradientBoostingRegressor()
```

```
y_test_pred = GB_regressor.predict(X_test_transformed)

#Testing the model accuracy

r2   = r2_score(y_test, y_test_pred)              # Getting the R-
squared (R²)
mae  = mean_absolute_error(y_test, y_test_pred)  # Getting the Mean
Absolute Error
mse  = mean_squared_error(y_test, y_test_pred)   # Getting the Mean
Squared Error
rmse = np.sqrt(mse)                              # Getting the Root
Mean Squared Error


#Defining a DataFrame
GB_results = pd.DataFrame([['GBDT Regression', r2*100, mae, mse,
rmse]],
                    columns=['Model', 'R-squared (R²)', 'Mean Absolute
Error', 'Mean Squared Error', 'Root Mean Squared Error'])

#Printing the Model Results with different Metrics
results = results.append(GB_results , ignore_index=True)
results
```

```
                      Model  R-squared (R²)  Mean Absolute Error  \
0         Linear Regression           75.40              3938.02
1            KNN Regression           79.97              3006.35
2     Decison-tree Regression         58.68              3648.23
3   Random Forest Regression          82.55              2701.47
4           GBDT Regression           87.66              2310.81

   Mean Squared Error  Root Mean Squared Error
0         31503873.50                  5612.83
1         25660048.66                  5065.57
2         52924035.93                  7274.89
3         22344392.41                  4726.99
4         15805696.85                  3975.64
```

```
print('GBDT Regression Train Score is : ' ,
GB_regressor.score(X_train_transformed, y_train))
print('GBDT Regression Test Score is : ' ,
GB_regressor.score(X_test_transformed, y_test))
```

```
GBDT Regression Train Score is :  0.8993791860213253
GBDT Regression Test Score is :  0.8765956618967508
```

## Residuals (Difference between y_test and y_pred)

```
test_residual= y_test - y_test_pred

medical_GB = pd.DataFrame({'Actual': y_test, 'Predicted': y_test_pred,
'diff':(abs(y_test-y_test_pred))})

medical_GB.head()
```

```
       Actual  Predicted      diff
12    1826.84    4224.89   2398.05
306  20177.67    6809.64  13368.03
318   7421.19    9797.54   2376.35
816   2842.76    5786.27   2943.51
157  15518.18   15694.14    175.96
```

```
results[["Model","R-squared (R²)"]]
```

```
                       Model  R-squared (R²)
0          Linear Regression           75.40
1             KNN Regression           79.97
2    Decison-tree Regression           58.68
3   Random Forest Regression           82.55
4            GBDT Regression           87.66
```

## | Conclusion

In conclusion, this machine learning project successfully developed a predictive model for medical cost estimation based on the provided dataset.

The GBDT regression model showed strong performance in predicting medical costs, taking into account various features such as age, BMI, smoking status, and more.

This model can be utilized to assist in estimating medical costs for individuals and provide insights for healthcare providers and insurance companies.