```
In [1]: import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import numpy as np
sns.set_theme(color_codes=True)
In [2]: df = pd.read_csv('insurance.csv')
df.head()
```

Out[2]:

	age	sex	bmi	children	smoker	region	charges
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	ma l e	22.705	0	no	northwest	21984.47061
4	32	male	28.880	0	no	northwest	3866.85520

Data Preprocessing Part 1

```
In [3]: #Cheeck Object data types unique value
    df.select_dtypes(include='object').nunique()

Out[3]: sex     2
    smoker     2
    region     4
    dtype: int64
```

Exploratory Data Analysis

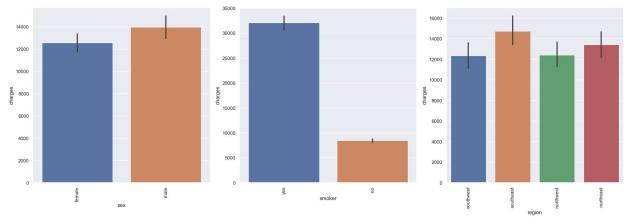
```
In [5]: # list of categorical variables to plot
    cat_vars = ['sex', 'smoker', 'region']

# create figure with subplots
fig, axs = plt.subplots(nrows=1, ncols=3, figsize=(20, 7))
axs = axs.flatten()

# create barplot for each categorical variable
for i, var in enumerate(cat_vars):
    sns.barplot(x=var, y='charges', data=df, ax=axs[i])
    axs[i].set_xticklabels(axs[i].get_xticklabels(), rotation=90)

# adjust spacing between subplots
fig.tight_layout()

# show plot
plt.show()
```



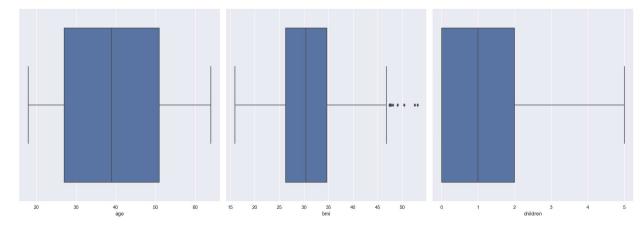
```
In [8]: # list of numerical variables to plot
    num_vars = ['age', 'bmi', 'children']

# create figure with subplots
fig, axs = plt.subplots(nrows=1, ncols=3, figsize=(20, 7))
axs = axs.flatten()

# create violinplot for each numerical variable
for i, var in enumerate(num_vars):
    sns.boxplot(x=var, data=df, ax=axs[i])

# adjust spacing between subplots
fig.tight_layout()

plt.show()
```



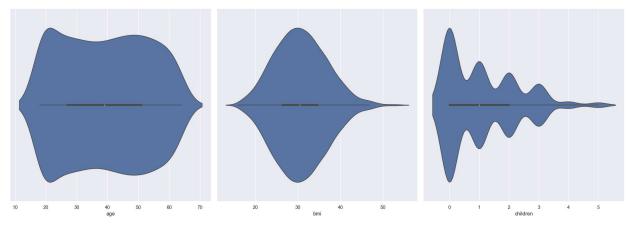
```
In [9]: # list of numerical variables to plot
    num_vars = ['age', 'bmi', 'children']

# create figure with subplots
fig, axs = plt.subplots(nrows=1, ncols=3, figsize=(20, 7))
axs = axs.flatten()

# create violinplot for each numerical variable
for i, var in enumerate(num_vars):
    sns.violinplot(x=var, data=df, ax=axs[i])

# adjust spacing between subplots
fig.tight_layout()

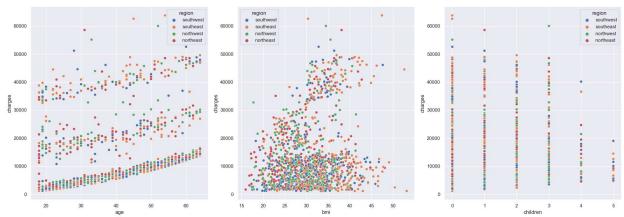
plt.show()
```



```
In [10]: num_vars = ['age', 'bmi', 'children']
    fig, axs = plt.subplots(nrows=1, ncols=3, figsize=(20, 7))
    axs = axs.flatten()

for i, var in enumerate(num_vars):
        sns.scatterplot(x=var, y='charges', hue='region', data=df, ax=axs[i])

fig.tight_layout()
    plt.show()
```



```
In [11]: num_vars = ['age', 'bmi', 'children']
        fig, axs = plt.subplots(nrows=1, ncols=3, figsize=(20, 7))
        axs = axs.flatten()
        for i, var in enumerate(num vars):
            sns.scatterplot(x=var, y='charges', hue='smoker', data=df, ax=axs[i])
        fig.tight_layout()
        plt.show()
             In [12]: | num_vars = ['age', 'bmi', 'children']
        fig, axs = plt.subplots(nrows=1, ncols=3, figsize=(20, 7))
        axs = axs.flatten()
        for i, var in enumerate(num_vars):
            sns.scatterplot(x=var, y='charges', hue='sex', data=df, ax=axs[i])
        fig.tight_layout()
        plt.show()
```

Data Preprocessing Part 2

```
In [13]: df.head()
```

Out[13]:

In [14]: df.shape

Out[15]: Series([], dtype: float64)

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

```
Out[14]: (1338, 7)

In [15]: #Check missing value
    check_missing = df.isnull().sum() * 100 / df.shape[0]
        check_missing[check_missing > 0].sort_values(ascending=False)
```

Label Encoding each Object datatypes

```
In [16]:
         # Loop over each column in the DataFrame where dtype is 'object'
         for col in df.select_dtypes(include=['object']).columns:
             # Print the column name and the unique values
             print(f"{col}: {df[col].unique()}")
         sex: ['female' 'male']
         smoker: ['yes' 'no']
         region: ['southwest' 'southeast' 'northwest' 'northeast']
In [17]: | from sklearn import preprocessing
         # Loop over each column in the DataFrame where dtype is 'object'
         for col in df.select dtypes(include=['object']).columns:
             # Initialize a LabelEncoder object
             label_encoder = preprocessing.LabelEncoder()
             # Fit the encoder to the unique values in the column
             label encoder.fit(df[col].unique())
             # Transform the column using the encoder
             df[col] = label encoder.transform(df[col])
             # Print the column name and the unique encoded values
             print(f"{col}: {df[col].unique()}")
         sex: [0 1]
```

smoker: [1 0] region: [3 2 1 0]

```
In [18]: df.dtypes
Out[18]: age
                        int64
                        int32
         sex
         bmi
                      float64
         children
                        int64
         smoker
                        int32
         region
                        int32
         charges
                      float64
         dtype: object
```

Remove Outliers using Z-Score

```
In [19]: | from scipy import stats
         # define a function to remove outliers using z-score for only selected numerical colu
         def remove outliers(df, cols, threshold=3):
             # loop over each selected column
             for col in cols:
                 # calculate z-score for each data point in selected column
                 z = np.abs(stats.zscore(df[col]))
                 # remove rows with z-score greater than threshold in selected column
                 df = df[(z < threshold) | (df[col].isnull())]</pre>
             return df
         selected_cols = ['bmi']
         df_clean = remove_outliers(df, selected_cols)
         df clean.shape
Out[20]: (1334, 7)
In [21]: #dataframe before the outlier removed
         df.shape
Out[21]: (1338, 7)
```

Correlation Heatmap

```
In [22]: #Correlation Heatmap
plt.figure(figsize=(20, 16))
sns.heatmap(df_clean.corr(), fmt='.2g', annot=True)
```

Out[22]: <AxesSubplot:>



Train Test Split

```
In [23]: X = df_clean.drop('charges', axis=1)
y = df_clean['charges']
In [24]: #test size 20% and train size 80%
```

```
In [24]: #test size 20% and train size 80%
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
X_train, X_test, y_train, y_test = train_test_split(X,y, test_size=0.2,random_state=0)
```

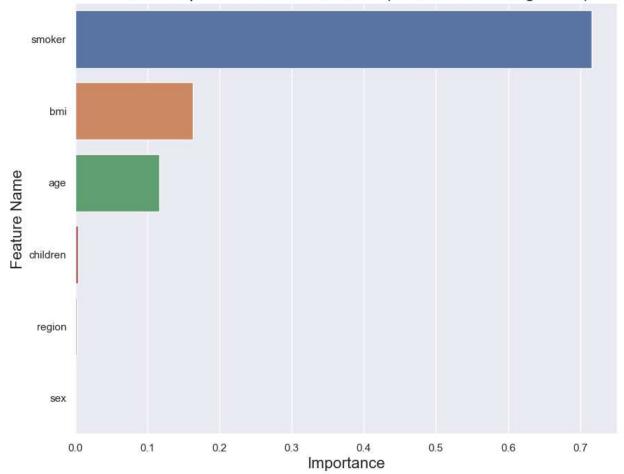
Decision Tree Regressor

```
In [25]: from sklearn.tree import DecisionTreeRegressor
         from sklearn.model selection import GridSearchCV
         from sklearn.datasets import load boston
         # Create a DecisionTreeRegressor object
         dtree = DecisionTreeRegressor()
         # Define the hyperparameters to tune and their values
         param_grid = {
             'max depth': [2, 4, 6, 8],
             'min_samples_split': [2, 4, 6, 8],
             'min_samples_leaf': [1, 2, 3, 4],
             'max_features': ['auto', 'sqrt', 'log2']
         }
         # Create a GridSearchCV object
         grid_search = GridSearchCV(dtree, param_grid, cv=5, scoring='neg_mean_squared_error')
         # Fit the GridSearchCV object to the data
         grid search.fit(X train, y train)
         # Print the best hyperparameters
         print(grid search.best params )
         {'max_depth': 4, 'max_features': 'auto', 'min_samples_leaf': 4, 'min_samples_split':
         2}
In [26]: | from sklearn.tree import DecisionTreeRegressor
         dtree = DecisionTreeRegressor(random state=0, max depth=4, max features='auto', min s
         dtree.fit(X_train, y_train)
Out[26]: DecisionTreeRegressor(max_depth=4, max_features='auto', min_samples_leaf=4,
                                random state=0)
In [27]: from sklearn import metrics
         from sklearn.metrics import mean absolute percentage error
         import math
         y pred = dtree.predict(X test)
         mae = metrics.mean_absolute_error(y_test, y_pred)
         mape = mean_absolute_percentage_error(y_test, y_pred)
         mse = metrics.mean squared error(y test, y pred)
         r2 = metrics.r2_score(y_test, y_pred)
         rmse = math.sqrt(mse)
         print('MAE is {}'.format(mae))
         print('MAPE is {}'.format(mape))
         print('MSE is {}'.format(mse))
         print('R2 score is {}'.format(r2))
         print('RMSE score is {}'.format(rmse))
         MAE is 2627.77861129252
         MAPE is 0.31327836581317675
         MSE is 21611660.168950517
         R2 score is 0.8510144440017449
         RMSE score is 4648.834280650421
```

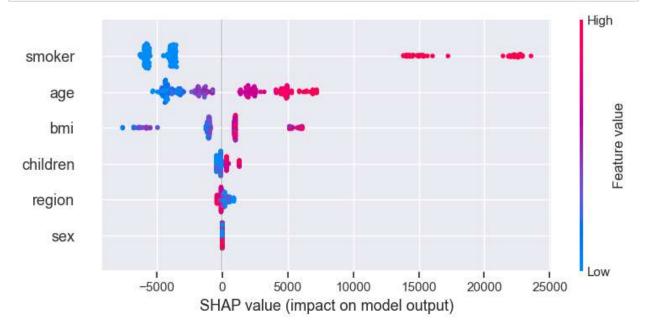
```
In [28]: imp_df = pd.DataFrame({
        "Feature Name": X_train.columns,
        "Importance": dtree.feature_importances_
})
fi = imp_df.sort_values(by="Importance", ascending=False)

fi2 = fi.head(10)
plt.figure(figsize=(10,8))
sns.barplot(data=fi2, x='Importance', y='Feature Name')
plt.title('Feature Importance Each Attributes (Decision Tree Regressor)', fontsize=18
plt.xlabel ('Importance', fontsize=16)
plt.ylabel ('Feature Name', fontsize=16)
plt.show()
```

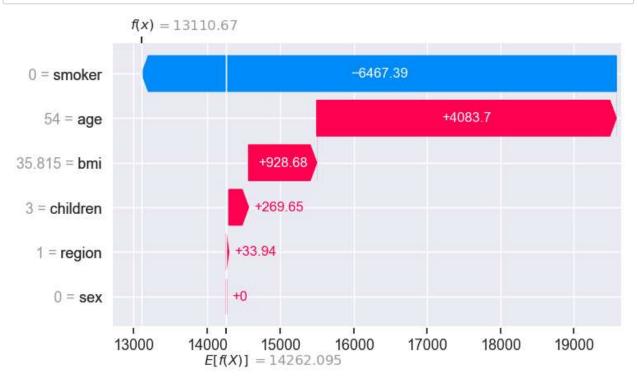
Feature Importance Each Attributes (Decision Tree Regressor)



```
In [29]: import shap
    explainer = shap.TreeExplainer(dtree)
    shap_values = explainer.shap_values(X_test)
    shap.summary_plot(shap_values, X_test)
```



```
In [30]: explainer = shap.Explainer(dtree, X_test)
shap_values = explainer(X_test)
shap.plots.waterfall(shap_values[0])
```



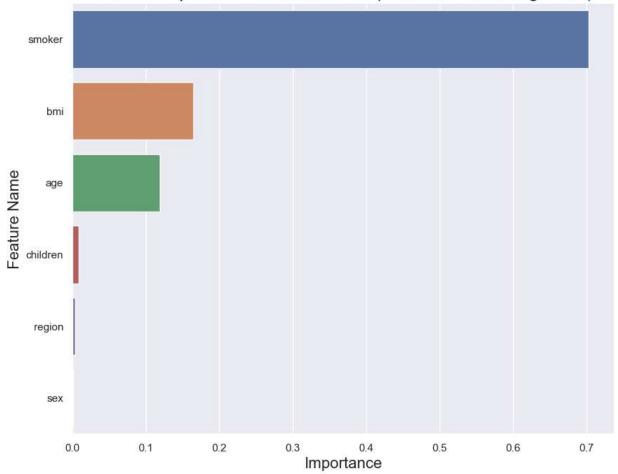
Random Forest Regressor

```
In [31]: from sklearn.ensemble import RandomForestRegressor
         from sklearn.model selection import GridSearchCV
         # Create a Random Forest Regressor object
         rf = RandomForestRegressor()
         # Define the hyperparameter grid
         param grid = {
             'max depth': [3, 5, 7, 9],
             'min_samples_split': [2, 5, 10],
             'min samples leaf': [1, 2, 4],
             'max_features': ['auto', 'sqrt']
         }
         # Create a GridSearchCV object
         grid search = GridSearchCV(rf, param grid, cv=5, scoring='r2')
         # Fit the GridSearchCV object to the training data
         grid search.fit(X train, y train)
         # Print the best hyperparameters
         print("Best hyperparameters: ", grid_search.best_params_)
         Best hyperparameters: {'max depth': 5, 'max features': 'auto', 'min samples leaf':
         4, 'min_samples_split': 10}
In [32]: from sklearn.ensemble import RandomForestRegressor
         rf = RandomForestRegressor(random_state=0, max_depth=5, min_samples_split=10, min_sam
                                     max features='auto')
         rf.fit(X train, y train)
Out[32]: RandomForestRegressor(max_depth=5, min_samples_leaf=4, min_samples_split=10,
                                random state=0)
In [33]: from sklearn import metrics
         from sklearn.metrics import mean absolute percentage error
         import math
         y_pred = rf.predict(X_test)
         mae = metrics.mean absolute error(y test, y pred)
         mape = mean absolute percentage error(y test, y pred)
         mse = metrics.mean_squared_error(y_test, y_pred)
         r2 = metrics.r2 score(y test, y pred)
         rmse = math.sqrt(mse)
         print('MAE is {}'.format(mae))
         print('MAPE is {}'.format(mape))
         print('MSE is {}'.format(mse))
         print('R2 score is {}'.format(r2))
         print('RMSE score is {}'.format(rmse))
         MAE is 2439.7944683926576
         MAPE is 0.280797784076888
         MSE is 19747580.91254748
         R2 score is 0.8638649553585273
         RMSE score is 4443.8250317207
```

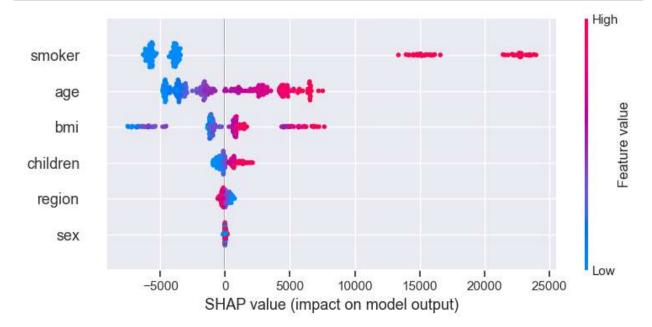
```
In [35]: imp_df = pd.DataFrame({
        "Feature Name": X_train.columns,
        "Importance": rf.feature_importances_
})
fi = imp_df.sort_values(by="Importance", ascending=False)

fi2 = fi.head(10)
plt.figure(figsize=(10,8))
sns.barplot(data=fi2, x='Importance', y='Feature Name')
plt.title('Feature Importance Each Attributes (Random Forest Regressor)', fontsize=18
plt.xlabel ('Importance', fontsize=16)
plt.ylabel ('Feature Name', fontsize=16)
plt.show()
```

Feature Importance Each Attributes (Random Forest Regressor)



```
In [36]: import shap
    explainer = shap.TreeExplainer(rf)
    shap_values = explainer.shap_values(X_test)
    shap.summary_plot(shap_values, X_test)
```



In [37]: explainer = shap.Explainer(rf, X_test, check_additivity=False)
shap_values = explainer(X_test, check_additivity=False)
shap.plots.waterfall(shap_values[0])



AdaBoost Regressor

```
from sklearn.ensemble import AdaBoostRegressor
         from sklearn.model selection import GridSearchCV
         # Define AdaBoostRegressor model
         abr = AdaBoostRegressor()
         # Define hyperparameters and possible values
         params = {'n estimators': [50, 100, 150],
                    'learning rate': [0.01, 0.1, 1, 10]}
         # Perform GridSearchCV with 5-fold cross validation
         grid_search = GridSearchCV(abr, param_grid=params, cv=5, scoring='neg_mean_squared_er
         grid_search.fit(X_train, y_train)
         # Print best hyperparameters and corresponding score
         print("Best hyperparameters: ", grid_search.best_params_)
         Best hyperparameters: {'learning_rate': 0.01, 'n_estimators': 50}
In [40]: | from sklearn.ensemble import RandomForestRegressor
         abr = AdaBoostRegressor(random_state=0, learning_rate=0.01, n_estimators=50)
         abr.fit(X_train, y_train)
Out[40]: AdaBoostRegressor(learning rate=0.01, random state=0)
In [41]: from sklearn import metrics
         from sklearn.metrics import mean absolute percentage error
         import math
         y_pred = abr.predict(X_test)
         mae = metrics.mean absolute error(y test, y pred)
         mape = mean absolute percentage error(y test, y pred)
         mse = metrics.mean squared error(y test, y pred)
         r2 = metrics.r2_score(y_test, y_pred)
         rmse = math.sqrt(mse)
         print('MAE is {}'.format(mae))
         print('MAPE is {}'.format(mape))
         print('MSE is {}'.format(mse))
         print('R2 score is {}'.format(r2))
         print('RMSE score is {}'.format(rmse))
         MAE is 2864.7990524044253
         MAPE is 0.38899081549024944
         MSE is 21532890.049069017
         R2 score is 0.8515574661488103
         RMSE score is 4640.354517606281
```

```
In [42]: imp_df = pd.DataFrame({
    "Feature Name": X_train.columns,
    "Importance": abr.feature_importances_
})
fi = imp_df.sort_values(by="Importance", ascending=False)

fi2 = fi.head(10)
plt.figure(figsize=(10,8))
sns.barplot(data=fi2, x='Importance', y='Feature Name')
plt.title('Feature Importance Each Attributes (AdaBoost Regressor)', fontsize=18)
plt.xlabel ('Importance', fontsize=16)
plt.ylabel ('Feature Name', fontsize=16)
plt.show()
```

Feature Importance Each Attributes (AdaBoost Regressor)

