Machine Learning - Black and Indigenous Program!

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Never stop learning!

Assignment 3: Regression Models

- **Deadline**: Oct 28, 16:59pm
- **Submission**: D2L (Content > Week 3 > Assignment 3)
- **Collaboration policy**: After attempting the problems on an individual basis, you may discuss and work together on the assignment with up to two classmates. However, **you must write your own code and write up your own solutions individually and explicitly name any collaborators** at the top of the homework.

For this assignment, we will be exploring a medical cost dataset with various demographic and health information on patients. We are going to tackle a main idea in supervised learning: linear regression

The goal is to predict **medical costs** (based on insurance claims) using a linear regression model.

```
# Import relevant Python packages
import matplotlib.pyplot as plt       # visualization
import numpy as np                    # matrices and high-level math functions
import pandas as pd                   # data manipulation
import seaborn as sns                 # visualization (based on matplotlib)

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

from scipy import stats               # scientific computing
# sklearn is a popular machine learning library
from sklearn import metrics
from sklearn.linear_model import LinearRegression
```

```
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
```

Part 1: Import Dataset

```
# Load the dataset into a pandas dataframe
url = 'https://raw.githubusercontent.com/salexyun/Michener-AI-for-Clinician-Champions/main/me
df = pd.read_csv(url)
```

```
# Look at the first 5 rows in the dataset
df.head()
```

	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	male	22.705	0	no	northwest	21984.47061
4	32	male	28.880	0	no	northwest	3866.85520

We have just read a comma-separated values (csv) file into a pandas data structure named `df`. This allows us to input the case study data into this programming environment.

Part 2: Exploratory Data Analysis (EDA)

Let's explore the dataset by looking at its dimension (number of rows and columns), the data types of each feature, and whether there are any missing datapoints in the dataset. These are typical ways to gain an initial understanding of a dataset using simple Python functions.

```
# Print out the number of rows and columns in the dataset
print("Dimensionality of the DataFrame:", df.shape)
```

```
Dimensionality of the DataFrame: (1338, 7)
```

```
# Print out summary statistics for each variable in the dataset
df.describe()
```

	age	bmi	children	charges
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

```
# Print out the data type of each feature in the dataset
print("Data type of each feature:")
df.dtypes
```

```
Data type of each feature:
age           int64
sex          object
bmi         float64
children      int64
smoker       object
region       object
charges     float64
dtype: object
```

```
# Determine if there are any missing datapoints or duplicate rows in the dataset
print("\nAre there any missing datapoints in the dataset?", df.isnull().values.any())
print("Number of duplicated rows:", df.duplicated().sum())
```

```
Are there any missing datapoints in the dataset? False
Number of duplicated rows: 1
```

There are 1338 individual datapoints with 7 columns or features in the dataset:

- **age:** age of the primary beneficiary
  - ratio (continuous variable)
- **sex:** sex of the beneficiary (male or female)
  - nominal (categorical variable)
- **bmi:** body mass index; a value derived from the mass and height of the beneficiary
  - interval (continuous variable)
- **children:** number of children covered by the insurance

- ratio (discrete variable)

- **smoker:** whether the beneficiary smokes or not (yes or no)
  - nominal (categorical variable)
- **region:** residential area of the beneficiary in the U.S.
  - nominal (categorical variable)
- **charges:** individual medical costs billed by the insurance
  - ratio (continuous variable)

int64 refers to integer numbers; **float64** refers to floating point numbers; and **object** refers to texts or alphanumeric values.

Luckily, there are no missing datapoints in the dataset. Missing data can be problematic when carrying out data analysis. To combat this, we can either drop the entire row or use data imputation strategies where the missing value is replaced by a substituted value.

There is one duplicated row and will be removed accordingly.

```
# Remove the duplicate row from the dataset
df.drop_duplicates(keep='first', inplace=True)


# Confirm the final number of rows and columns in the dataset after data cleaning
print("df.shape =", df.shape)
print("Number of rows =", df.shape[0])
print("Number of columns =", df.shape[1])
```

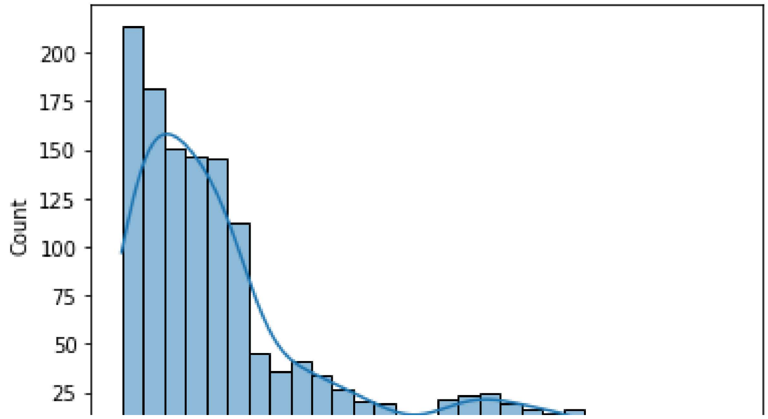
```
df.shape = (1337, 7)
Number of rows = 1337
Number of columns = 7
```

Data visualization

In addition to the descriptive statistics, visualizing the distribution of the data can provide additional information on the data itself and can guide us in how to carry out the analysis appropriately.

```
# Plot a histogram representing the distribution of the "charges" variable
sns.histplot(df['charges'], kde=True)
print(stats.shapiro(df['charges']));
```

```
ShapiroResult(statistic=0.8147611021995544, pvalue=1.1960358168550093e-36)
```



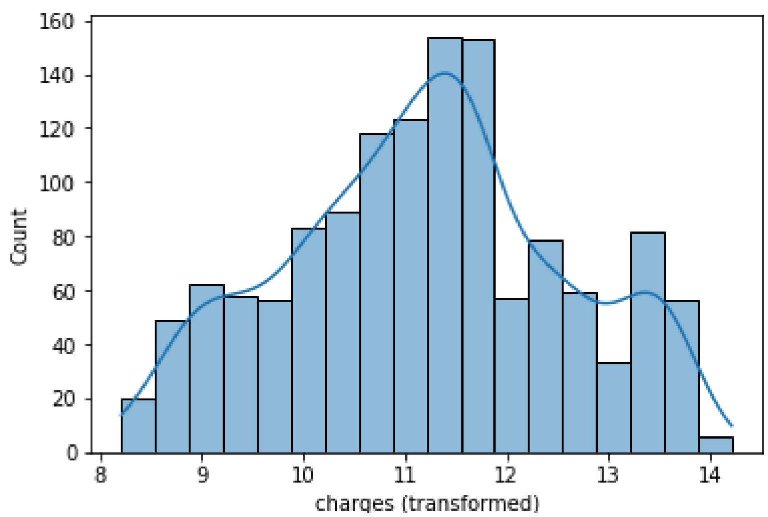
The distribution appears to be non-Gaussian and positively skewed (or right skewed). We can formally test the normality with the Shapiro–Wilk test and can confirm that the distribution is indeed not normal.

Note: normality is a condition for regression models.

While it is not always necessary to transform data, it often helps with interpretability and to meet certain assumptions for statistical inference. In our case, we will be using the Box-Cox transformation.

```
# Transform the target variable to a normal distribution
charges_transformed = stats.boxcox(df['charges'])[0]
sns.histplot(charges_transformed, kde=True);
plt.xlabel('charges (transformed)')
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f30d5ee8150>Text(0.5, 0, 'charges (transformed)')
```



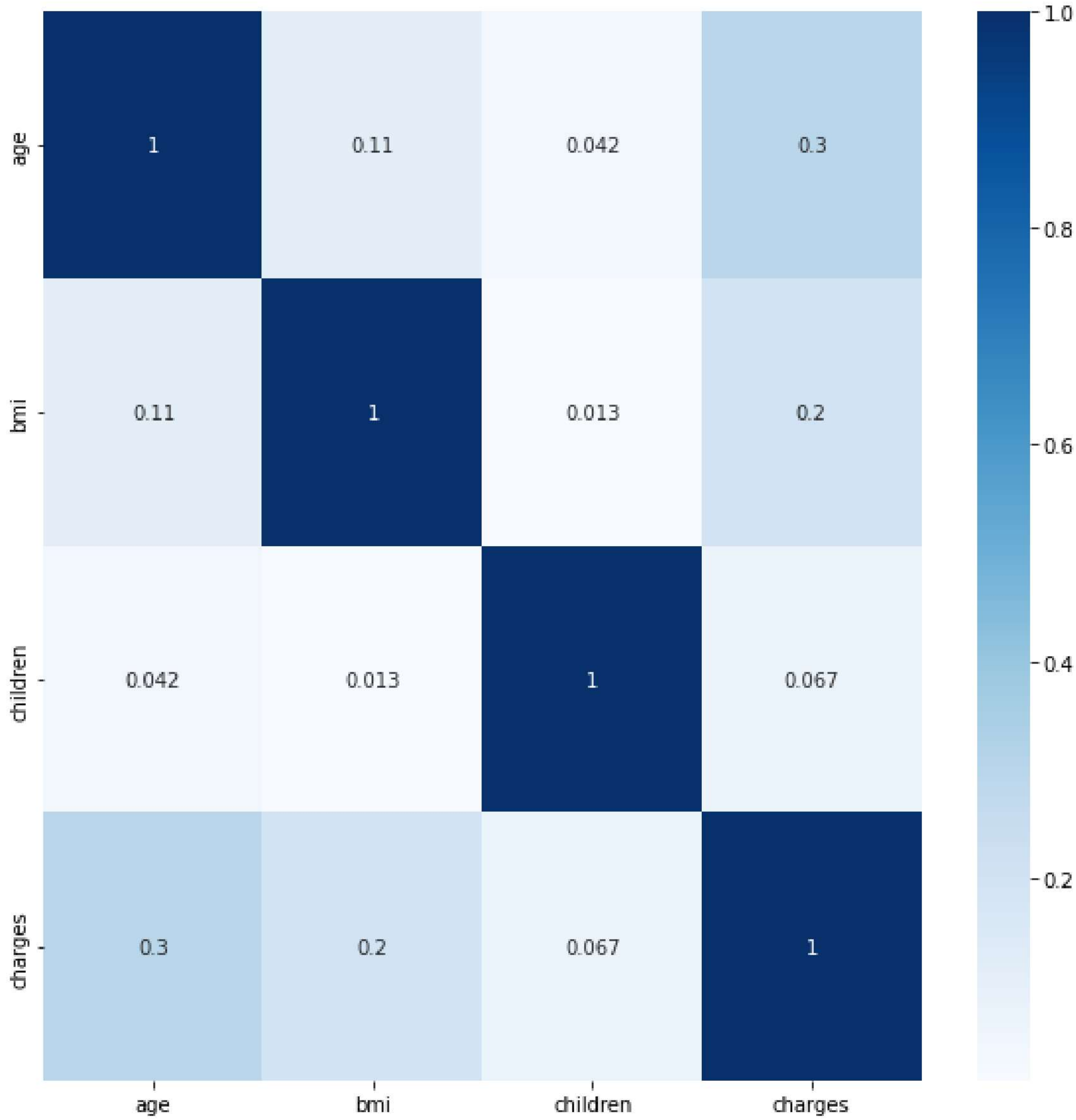

```
print("Returning two items:", stats.boxcox(df['charges']))
print("Returning the first item:", stats.boxcox(df['charges'])[0])
```

```
Returning two items: (array([12.12063392,  8.80402643, 10.1415491 , ...,  8.72519041,
        9.01435202, 12.9641992 ]), 0.043516942579678274)
```

```
Returning the first item: [12.12063392  8.80402643 10.1415491  ...  8.72519041  9.01435
 12.9641992 ]
```

One of the major assumptions of linear regression is that there should be little to no multicollinearity; that is, independent variables should be relatively independent from one another.

```
# Use a heatmap to check for collinearity between variables
# A higher (darker) value represents higher correlation between two variables
# A lower (lighter) value represents lower correlation between two variables
plt.figure(figsize=(10,10))
sns.heatmap(df.corr(), cmap='Blues', annot=True);
```

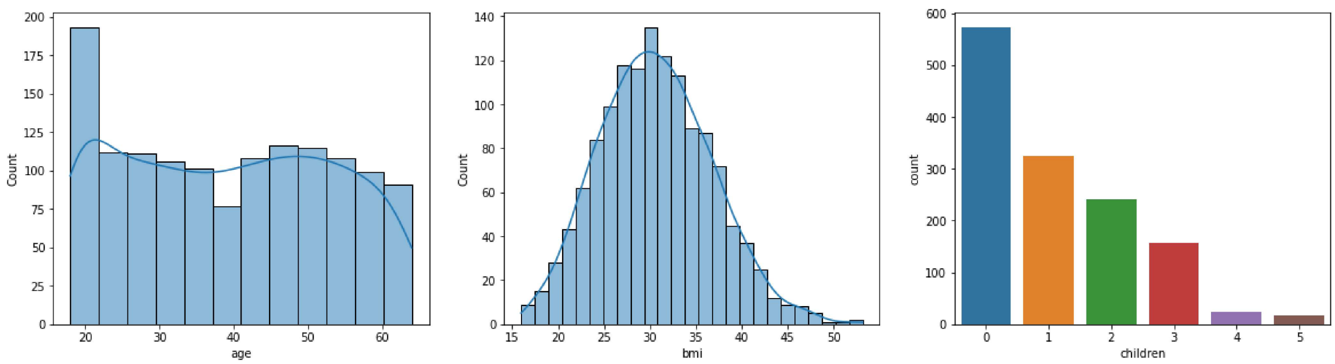


Correlation coefficient values below 0.3 are considered to be weak; 0.3-0.7 are moderate; >0.7 are strong. In this case, all correlations are 0.3 or below, so we can conclude that the variables are independent from one another.

Note: independence of variables is a condition for regression.

We can now move on to visualizing the independent variables (these are the features of your dataset).

```
# Plot the distribution of age, BMI, and number of children
fig, (ax0, ax1, ax2) = plt.subplots(1, 3, figsize=(20,5))
sns.histplot(x=df['age'], kde=True, ax=ax0);
sns.histplot(x=df['bmi'], kde=True, ax=ax1);
sns.countplot(x=df['children'], ax=ax2);
```



Using prior knowledge, we may be able to come up with a few hypotheses. In particular, older individuals and/or individuals with higher BMI would be likely to have more ailments, and thus may incur higher medical costs.

Note: correlation is different from causation. We are not establishing causal relationships between variables.

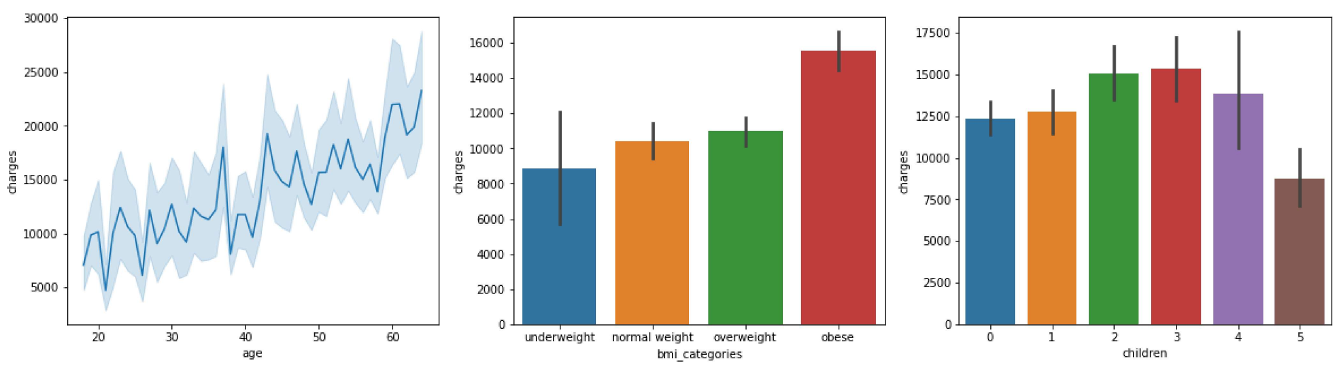
While BMI is a continuous variable, it is often described as a (ordinal) categorical variable with the following categories: (1) underweight; (2) normal weight; (3) overweight; and (4) obese. As such, we can create a new feature accordingly.

```
# Create a new feature for BMI based on categories (underweight, normal weight, overweight, o
conditions = [(df['bmi'] < 18.5),
              (df['bmi'] >= 18.5) & (df['bmi'] < 25),
              (df['bmi'] >= 25) & (df['bmi'] < 30),
              (df['bmi'] >= 30)]
labels = ['underweight', 'normal weight', 'overweight', 'obese']
df['bmi_categories'] = np.select(conditions, labels)
df.head()
```

	age	sex	bmi	children	smoker	region	charges	bmi_categories
0	19	female	27.900	0	yes	southwest	16884.92400	overweight
1	18	male	33.770	1	no	southeast	1725.55230	obese
2	28	male	33.000	3	no	southeast	4449.46200	obese
3	33	male	22.705	0	no	northwest	21984.47061	normal weight

Now let's explore the relationship between the independent variables (age, bmi, children) and the target variable (charges).

```
# Plot the relationship between the independent variables (age, bmi_categories, children)
# and the dependent/target variable (charges)
fig, (ax0, ax1, ax2) = plt.subplots(1, 3, figsize=(20,5))
sns.lineplot(x='age', y='charges', data=df, ax=ax0);
sns.barplot(x='bmi_categories', y='charges', data=df,
            order=['underweight', 'normal weight', 'overweight', 'obese'], ax=ax1);
sns.barplot(x='children', y='charges', data=df, ax=ax2);
```



As we suspected, medical cost tends to increase as a function of age or bmi. On the other hand, it is difficult to draw any conclusion regarding the medical costs based on the number of children/dependents that the beneficiary has. Let us examine rest of the independent variables.

Problem 2.1

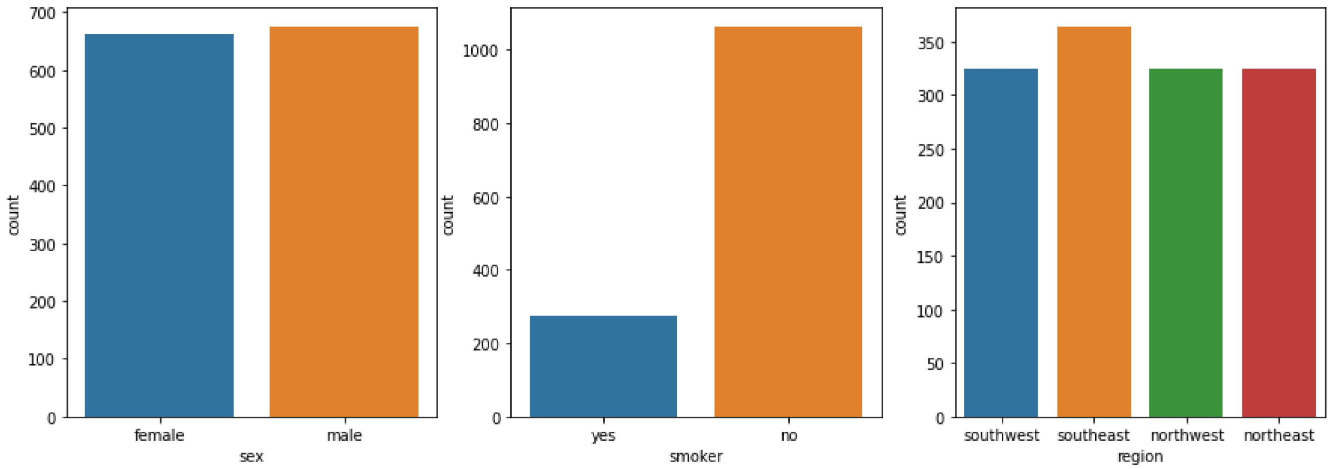
Plot the distribution of the remaining three independent variables: sex, smoker, region.

```
#***************YOUR CODE HERE (Problem 2.1) ***************#
# Hint:
# Use sns.countplot for all three of the variables since they are all categorical
```

```
# Look at the graphs above for an example of the syntax
fig, (ax0, ax1, ax2) = plt.subplots(1, 3, figsize=(15,5))
sns.countplot(x= "sex", data = df, ax=ax0)
sns.countplot(x = "smoker", data = df, ax =ax1)
sns.countplot(x= "region", data = df, ax = ax2)

#**************************************************************#
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f30ca02e5d0>
<matplotlib.axes._subplots.AxesSubplot at 0x7f30c9fdafd0>
<matplotlib.axes._subplots.AxesSubplot at 0x7f30c9f995d0>
```



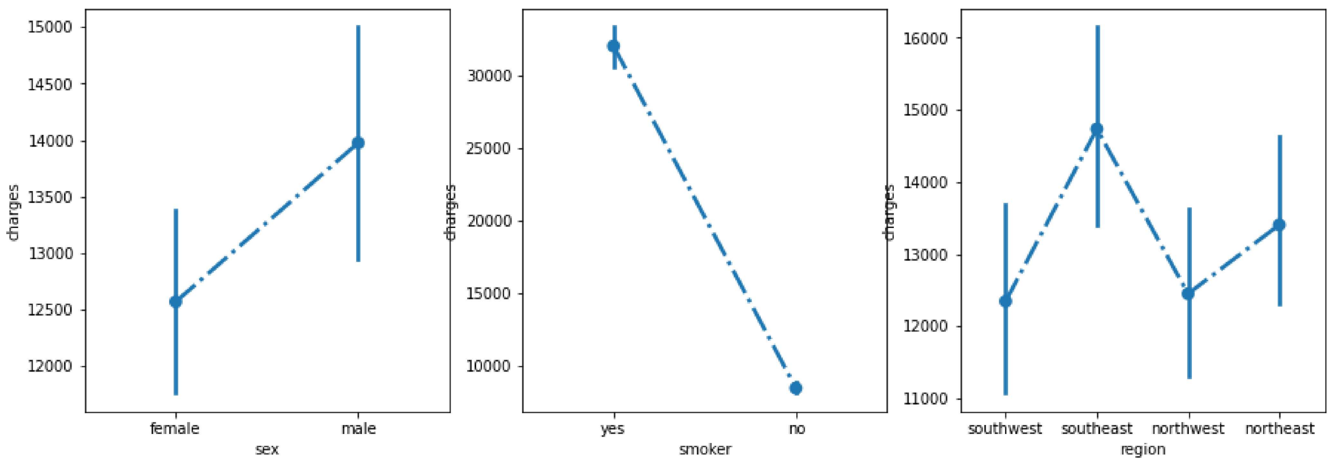
Problem 2.2

Plot the relationship between the independent variables (sex, smoker, region) and the dependent/target variable (charges).

```
#***************YOUR CODE HERE (Problem 2.2) ****************#
# Hints:
# Since there are only a few categories for all 3 of the variables,
# let's use sns.pointplot for all three of the variables
# Syntax of sns.pointplot is similar to sns.lineplot

fig, (ax0, ax1, ax2) = plt.subplots(1, 3, figsize=(15,5))
sns.pointplot(x ="sex", y ="charges", ax=ax0, data = df, linestyles='-.')
sns.pointplot(x ="smoker", y ="charges",ax=ax1, data = df, linestyles='-.')
sns.pointplot(x ="region", y ="charges", ax=ax2, data = df, linestyles='-.')
#**************************************************************#
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f30c93bd990>
<matplotlib.axes._subplots.AxesSubplot at 0x7f30c9385610>
<matplotlib.axes._subplots.AxesSubplot at 0x7f30c9337a90>
```



Initial thoughts on above plots:

- It appears that there may be sex differences in the medical costs; in particular, male, on average, spend more on medical procedures.
- Not surprisingly, medical costs are likely to be higher for smokers, compared to non-smokers.
- Interestingly, where one lives seems to have an effect on the medical costs. Most likely due to the differences in the state law, healthcare policies, and lifestyle of individuals living in different regions within the U.S.

Part 3: Preprocessing

Given that we wish to use a regression model and some of the features are non-numeric, we must transform them via a process called feature encoding. Feature encoding means to convert a categorical feature (non-numeric) into a numeric one.

There are several encoding strategies and can vary depending on the nature of the feature (i.e., nominal vs. ordinal). In our case, we will be using a simple label encoder that turns the target labels to values between `0` and `n_labelclasses - 1`.

```
# Transform categorical variables to numerical values and create a new variable
# to store each of the encoded values
encoder = LabelEncoder()
df['sex_encoded'] = encoder.fit_transform(df['sex'])
df['smoker_encoded'] = encoder.fit_transform(df['smoker'])
df['region_encoded'] = encoder.fit_transform(df['region'])
df['charges_transformed'] = stats.boxcox(df['charges'])[0]
df.head()
```

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

```
# Let's look at the number of columns we have now after data preprocessing
df.columns
```

```
Index(['age', 'sex', 'bmi', 'children', 'smoker', 'region', 'charges',
       'bmi_categories', 'sex_encoded', 'smoker_encoded', 'region_encoded',
       'charges_transformed'],
      dtype='object')
```

Instead of the original 7 columns, we now have 12 columns. Since some of these new variables that were created are simply numerical representations of the original variables, we will drop the duplicated features before training the model and store in X (features) and y (target).

```
# Define X (features) and y (target) and remove duplicate features that will not be used in t
X = df.drop(['sex', 'smoker', 'region', 'charges', 'bmi_categories', 'charges_transformed'],
y = df['charges_transformed']
X.head()
```

	age	bmi	children	sex_encoded	smoker_encoded	region_encoded
0	19	27.900	0	0	1	3
1	18	33.770	1	1	0	2
2	28	33.000	3	1	0	2
3	33	22.705	0	1	0	1
4	32	28.880	0	1	0	1

Part 4: Modelling

We have more or less completed the heavy lifting already. Contrary to popular belief, most of data science and AI (machine learning) is about exploring data and feature engineering (i.e., cleaning up data). That said, we are ready to define the model, train the model, make predictions, and evaluate the performance of our model.

Linear regression

https://scikit-learn.org/stable/modules/generated/sklearn.linear_model.LinearRegression.html

In this section, we will build a Linear Regression model to predict the amount of charges (medical costs) based on an individual's age, BMI, number of children, sex, whether they are a smoker, and what region they live in.

Build the model

We will first split the dataset into different datasets: (1) training set; and (2) test set. When we develop a model, we train the model using the samples in the training set. Once the model has learned, we evaluate the performance of our model with the samples in the test set. By testing on unseen data, we minimize the bias of our model and can accurately estimate the generalizability and predictive power of our model. Here, we will split the dataset into 90% training set and 10% test set. Other typical splits includes 70-30 split, 80-20 split, etc.

```
#***************YOUR CODE HERE (Problem 4.1) ***************#
# Split the dataset into X_train, X_test, y_train, and y_test
# Retain 10% of the data for testing, and use a random_state value of "0"
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.10, random_state = 0)

# Instantiate a linear regression model
linear_model = LinearRegression()

# Fit the model using the training data
linear_model.fit(X_train,y_train)

#**************************************************************#

# Print out the intercept and coefficients for the linear regression model
print(linear_model.intercept_)
print(linear_model.coef_)
```

```
LinearRegression()8.21342440623542
[ 0.04956316  0.01845858  0.14020894 -0.09599541  2.32086199 -0.07412003]
```

Make predictions

We will now make predictions on data (test set) that was not part of the training.

```
#****************YOUR CODE HERE (Problem 4.2) ****************#
# For each record in the test set, make a prediction for the y value using the linear_model
# The predicted values are stored in the y_pred array
y_pred = linear_model.predict(X_test)

#**************************************************************#
```

Model evaluation

Common metrics that are used to evaluate the performance of a linear regression model include Mean Squared Error (MSE), Mean Absolute Error (MAE) and the coefficient of determination (R^2).

Mean Squared Error $(MSE) = \frac{1}{n}\sum_{i=1}^{n}(y_i - \hat{y}_i)^2$

Mean Absolute Error $(MAE) = \frac{1}{n}\sum_{i=1}^{n}|y_i - \hat{y}_i|$

Both MSE and MAE represent the difference between the actual values and predicted values. Lower value indicates a better fit.

$R^2 = 1 - \frac{RSS}{TSS}$, where

$RSS = \sum_i(y_i - \hat{y})^2 =$ sum of squares of residuals

$TSS = \sum_i(y_i - \bar{y})^2 =$ total sum of squares

The coefficient of determination (R^2) is a measure of how well the model fits the dependent variable. The value ranges from 0 to 1; higher value indicating a better fit. R Squared may also be expressed as a percentage.

Problem 4.1

Derive the values for MSE, MAE and R^2 using Python's math library, based on the equations shown below.

Helpful hints:

- y_test: The actual values of y in the test set
- y_pred: The predicted values of y ("y-hat") in the test set
- n: The number of records in the test set

Python tips:

- To square a value: x**2
- To take the sum of a set of values: sum(x)
- To take the mean of a value: x.mean()
- To take the absolute value: abs(x)
- To get the number of items in an array: len(x)

Remember to use proper brackets ( ) to ensure proper order of operations!

```
# Metrics derived using Python math library

#***************YOUR CODE HERE (Problem 4.3) ***************#
# Hints:
# Use the hints provided above

MSE = metrics.mean_squared_error(y_test, y_pred)
MAE = metrics.mean_absolute_error(y_test, y_pred)
RSS = np.sqrt(metrics.mean_squared_error(y_test, y_pred))
TSS = MAE + MSE



R_squared = metrics.r2_score(y_test, y_pred)


#**********************************************************#

print("Mean squared error (MSE) =", MSE)
print("Mean absolute error (MAE) =", MAE)
print("R^2 =", R_squared)
```

```
Mean squared error (MSE) = 0.3544682461419291
Mean absolute error (MAE) = 0.39858557168153946
R^2 = 0.8284407853175861
```

Compare your results with the calculated values below using the metrics package in Python. They should be the same.

```
# The metrics package in Python can derive the model evaluation metrics
print("Mean squared error (MSE) =", metrics.mean_squared_error(y_test, y_pred))
print("Mean absolute error (MAE) =", metrics.mean_absolute_error(y_test, y_pred))
print("R^2 =", metrics.r2_score(y_test, y_pred))
```

```
Mean squared error (MSE) = 0.3544682461419291
Mean absolute error (MAE) = 0.39858557168153946
R^2 = 0.8284407853175861
```

A R^2 value of 83% indicates that our model can explain 83% of the variance in the data, so it performs quite well!

What does this mean? The results of this model show that by taking specific attributes of an individual such as their age, BMI, number of children, sex, whether they are a smoker or non-smoker, and region where they live, we can predict the approximate amount of medical costs (based on insurance claims) the individual is likely to incur.

Congratulations, you are done! 👏🙌🎉