Linear Regression Analysis Tutorial - Multiple Linear Regression

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What is Mutiple Linear Regression?

Multiple linear regression is a statistical machine learning model that aims to establish a relationship between a dependent variable and two or more independent variables. It is an extension of simple linear regression, which can only handle one independent variable.

The formula for multiple linear regression can be written as:

y = b0 + b1x1 + b2x2 + ... + bnxn + ε

where:

- **y** is the dependent variable or the target variable
- **x1, x2, ..., xn** are the independent variables or the features
- **b0, b1, b2, ..., bn** are the regression coefficients that represent the impact of each independent variable on the dependent variable
- **ε** is the error term or the random error that accounts for the variability in the dependent variable that cannot be explained by the independent variables.

The goal of multiple linear regression is to estimate the regression coefficients that best describe the relationship between the independent variables and the dependent variable, and use this model to make predictions or understand the impact of each independent variable on the dependent variable.

The California Housing Dataset for Multiple Linear Regression

The California Housing Dataset contains information on the median income, housing age, and other features for census tracts in California. The dataset was originally published by Pace, R. Kelley and Ronald Barry in their 1997 paper "Sparse Spatial Autoregressions" and is available in the sklearn.datasets module.

The dataset consists of 20,640 instances, each representing a census tract in California. There are eight features in the dataset, including:

- **MedInc:** Median income in the census tract.
- **HouseAge:** Median age of houses in the census tract.
- **AveRooms:** Average number of rooms per dwelling in the census tract.
- **AveBedrms:** Average number of bedrooms per dwelling in the census tract.
- **Population:** Total number of people living in the census tract.
- **AveOccup:** Average number of people per household in the census tract.
- **Latitude:** Latitude of the center of the census tract.
- **Longitude:** Longitude of the center of the census tract.

Step 1: Import the necessary libraries

In [1]:
```
import pandas as pd
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt
from sklearn.datasets import fetch_california_housing
from sklearn.linear_model import LinearRegression
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_squared_error, r2_score
from sklearn.model_selection import GridSearchCV
import warnings
warnings.filterwarnings('ignore')
```

Step 2: Load the dataset

In [2]:
```
# Load the California Housing Dataset from seaborn

california = fetch_california_housing()

# Convert the data to a pandas dataframe
california_df = pd.DataFrame(data=california.data, columns=california.feature_name

# Add the target variable to the dataframe
california_df['MedHouseVal'] = california.target

# Print the first 5 rows of the dataframe
california_df.head()
```

Out[2]:

	MedInc	HouseAge	AveRooms	AveBedrms	Population	AveOccup	Latitude	Longitude	MedI
0	8.3252	41.0	6.984127	1.023810	322.0	2.555556	37.88	-122.23	
1	8.3014	21.0	6.238137	0.971880	2401.0	2.109842	37.86	-122.22	
2	7.2574	52.0	8.288136	1.073446	496.0	2.802260	37.85	-122.24	
3	5.6431	52.0	5.817352	1.073059	558.0	2.547945	37.85	-122.25	
4	3.8462	52.0	6.281853	1.081081	565.0	2.181467	37.85	-122.25	

Step 2: Do Data Preprocessing along with Data Exploratory Analysis

Step 2(a): Check Shape of Dataframe

Checking the Shape of Dataframe tell hows how many rows and columns we have in the dataset

In [3]:
```
# Print the shape of the dataframe
print("Data shape:", california_df.shape)
```

```
Data shape: (20640, 9)
```

Step 2(b): Check Info of Dataframe

This is very useful to quickly get an overview of the structure and properties of a dataset, and to check for any missing or null values that may need to be addressed before performing any analysis or modeling.

In [4]:
```
california_df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 20640 entries, 0 to 20639
Data columns (total 9 columns):
 #   Column       Non-Null Count  Dtype  
---  ------       --------------  -----  
 0   MedInc       20640 non-null  float64
 1   HouseAge     20640 non-null  float64
 2   AveRooms     20640 non-null  float64
 3   AveBedrms    20640 non-null  float64
 4   Population   20640 non-null  float64
 5   AveOccup     20640 non-null  float64
 6   Latitude     20640 non-null  float64
 7   Longitude    20640 non-null  float64
 8   MedHouseVal  20640 non-null  float64
dtypes: float64(9)
memory usage: 1.4 MB
```

Step 2(c): Show Descriptive Statistics of each numerical column

Looking at descriptive statistics in machine learning is important because it gives an overview of the dataset's distribution and key characteristics. Some of the reasons why we should look at descriptive statistics include:

- **Understanding the distribution of data:** Descriptive statistics provide information about the central tendency and the spread of the data. This information is useful in determining the type of distribution and whether the data is skewed or symmetrical.
- **Identifying outliers:** Descriptive statistics help to identify any extreme values or outliers in the dataset. These outliers can have a significant impact on the analysis and should be investigated further.

From the descriptive statistics, we can observe the following:

- **Outliers:** The 'AveRooms', 'AveBedrms', 'Population', and 'AveOccup' columns have high maximum values, indicating the presence of outliers in the data. These outliers may need to be treated or removed before model selection. we will create visuals to see them more clearly
- **Distribution:** The 'MedInc', 'HouseAge', and 'MedHouseVal' columns appear to be normally distributed, as the mean and median values are close to each other, and the standard deviation is not very high. The 'Latitude' column is skewed to the left, as the mean is less than the median. The 'Longitude' column is skewed to the right, as the mean is greater than the median.

In [5]:
```
california_df.describe().T
```

Out[5]:

	count	mean	std	min	25%	50%	7!
MedInc	20640.0	3.870671	1.899822	0.499900	2.563400	3.534800	4.7432
HouseAge	20640.0	28.639486	12.585558	1.000000	18.000000	29.000000	37.0000
AveRooms	20640.0	5.429000	2.474173	0.846154	4.440716	5.229129	6.0523
AveBedrms	20640.0	1.096675	0.473911	0.333333	1.006079	1.048780	1.0995
Population	20640.0	1425.476744	1132.462122	3.000000	787.000000	1166.000000	1725.0000
AveOccup	20640.0	3.070655	10.386050	0.692308	2.429741	2.818116	3.2822
Latitude	20640.0	35.631861	2.135952	32.540000	33.930000	34.260000	37.7100
Longitude	20640.0	-119.569704	2.003532	-124.350000	-121.800000	-118.490000	-118.0100
MedHouseVal	20640.0	2.068558	1.153956	0.149990	1.196000	1.797000	2.6472

Step 2(d): Check for missing values in the Dataframe

This is important because most machine learning algorithms cannot handle missing data and will throw an error if missing values are present. Therefore, it is necessary to check for missing values and impute or remove them before fitting the data into a machine learning model. This helps to ensure that the model is trained on complete and accurate data, which leads to better performance and more reliable predictions.

Here we have no missing values so lets move on.

In [6]:
```
# Check for missing values
print("Missing values:\n", california_df.isnull().sum())
```

```
Missing values:
 MedInc          0
HouseAge        0
AveRooms        0
AveBedrms       0
Population      0
AveOccup        0
Latitude        0
Longitude       0
MedHouseVal     0
dtype: int64
```

Step 2(e): Check for duplicate values in the Dataframe

Checking for duplicate values in machine learning is important because it can affect the accuracy of your model. Duplicate values can skew your data and lead to overfitting, where your model is too closely fit to the training data and does not generalize well to new data.

We have no duplicate values so thats good.

In [7]:
```
california_df.duplicated().sum()
```

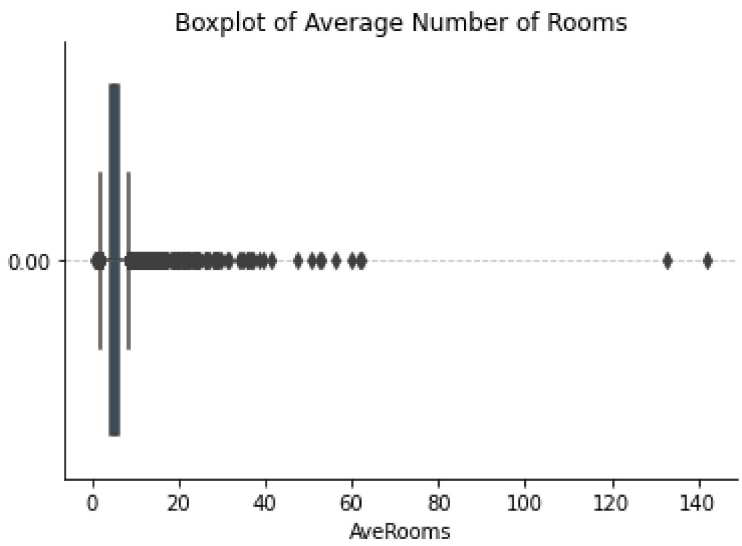
Out[7]:
```
0
```

Step 2(f)(i): Check for Outliers in the Dataframe

We should check for outliers as they can have a negative impact on machine learning algorithms as they can skew the results of the analysis. Outliers can significantly alter the mean, standard deviation, and other statistical measures, which can misrepresent the true characteristics of the data. Linear regression models, are sensitive to outliers and can produce inaccurate results if the outliers are not properly handled or removed. Therefore, it is important to identify and handle outliers appropriately to ensure the accuracy and reliability of the models.

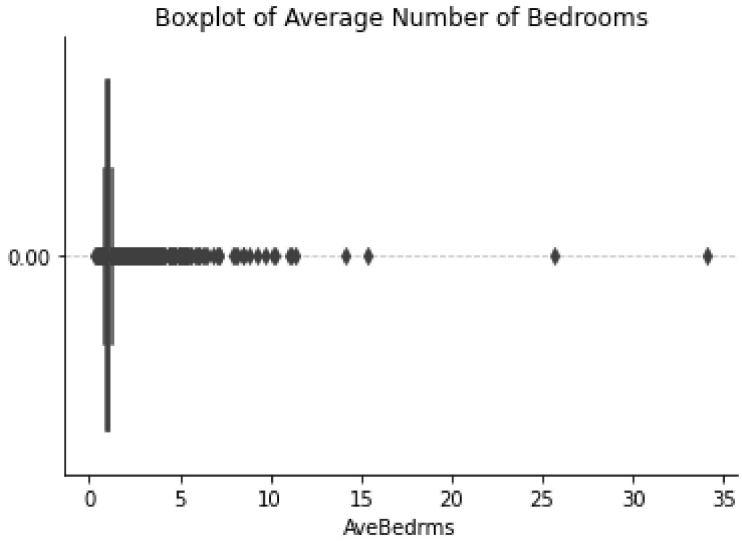
Here in the plots we can clearly see very high outliers on the right hand side. So we need to deal with them appropriately

In [8]:
```
# Create a boxplot of the 'AveRooms' column
ax = sns.boxplot(x=california_df['AveRooms'])

# Set the title and axes labels
ax.set_title('Boxplot of Average Number of Rooms')
ax.set_xlabel('AveRooms')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```



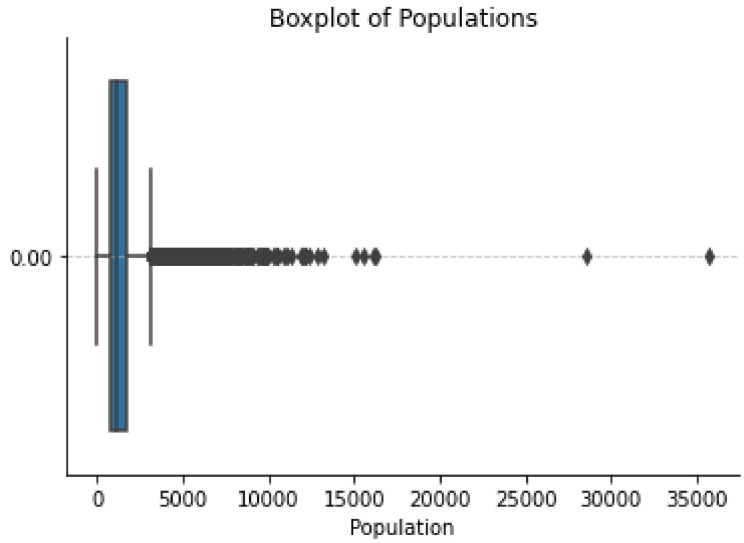
In [9]:
```
# Create a boxplot of the 'AveBedrms' column
ax = sns.boxplot(x=california_df['AveBedrms'])

# Set the title and axes labels
ax.set_title('Boxplot of Average Number of Bedrooms')
ax.set_xlabel('AveBedrms')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])
```

```
# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```

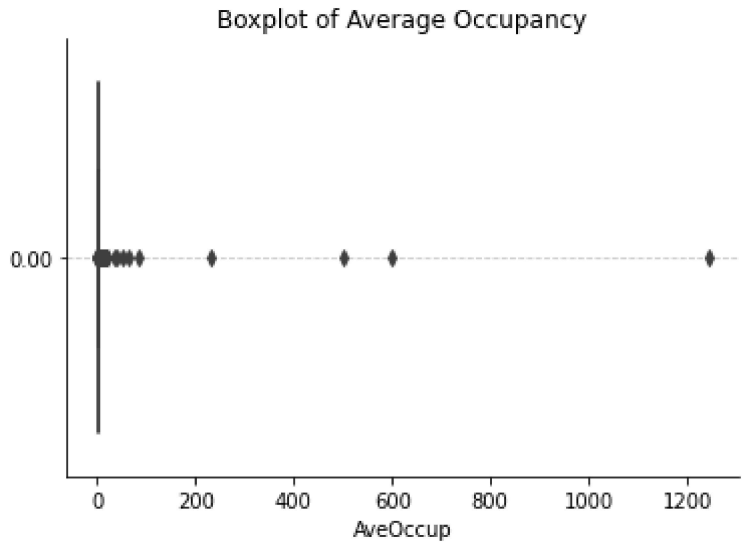


In [10]:

```
# Create a boxplot of the 'Population' column
ax = sns.boxplot(x=california_df['Population'])

# Set the title and axes labels
ax.set_title('Boxplot of Populations')
ax.set_xlabel('Population')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```

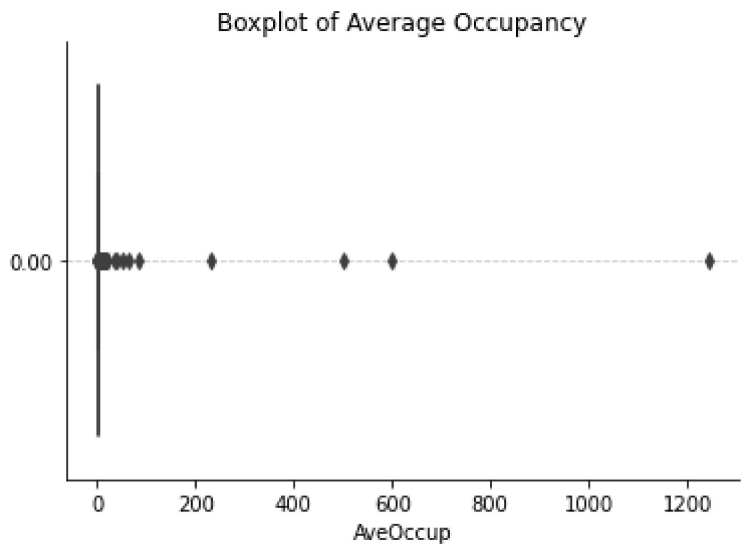


In [11]:
```
# Create a boxplot of the 'AveOccup' column
ax = sns.boxplot(x=california_df['AveOccup'])

# Set the title and axes labels
ax.set_title('Boxplot of Average Occupancy')
ax.set_xlabel('AveOccup')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```



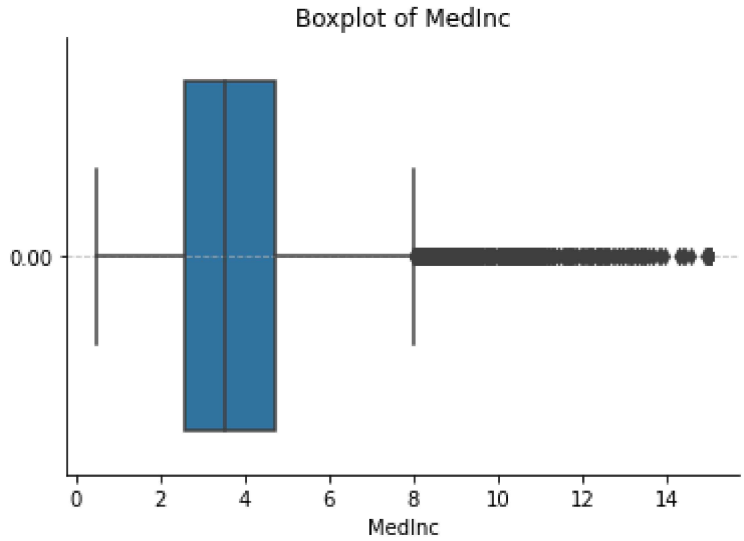
In [12]:
```
# Create a boxplot of the 'AveOccup' column
ax = sns.boxplot(x=california_df['AveOccup'])

# Set the title and axes labels
ax.set_title('Boxplot of Average Occupancy')
ax.set_xlabel('AveOccup')
ax.set_ylabel('')
```

```
# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```



In [13]:

```
# Create a boxplot of the 'MedInc' column
ax = sns.boxplot(x=california_df['MedInc'])

# Set the title and axes labels
ax.set_title('Boxplot of MedInc')
ax.set_xlabel('MedInc')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```



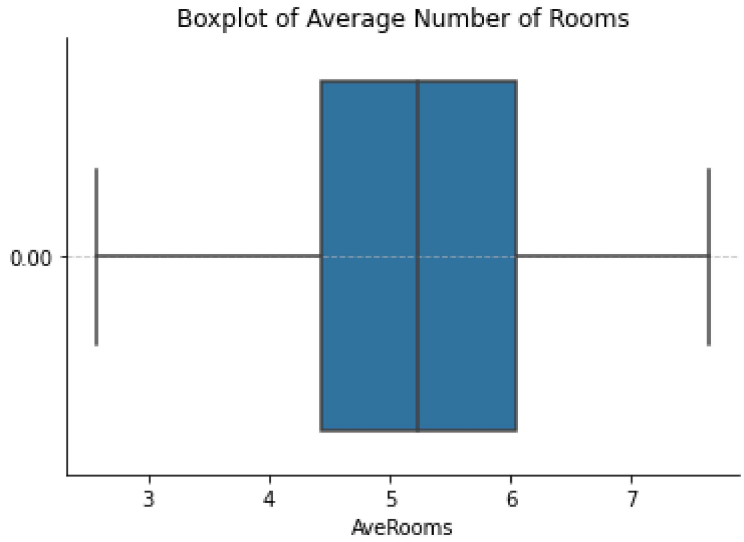
Step 2(f)(ii): Deal with Outliers in the Dataframe using Winsorization:

This method involves replacing extreme values with the nearest values that are within a certain percentile range. For example, we replace values above the 95th percentile with the value at the 95th percentile and values below the 1st percentile with the value at the 1st percentile. From the visuals we can clearly see that the data is way more normally distributed now

In [14]:
```
# Define the percentile limits for winsorization
pct_lower = 0.01
pct_upper = 0.95

# Apply winsorization to the five columns
california_df['AveRooms'] = np.clip(california_df['AveRooms'],
                                    california_df['AveRooms'].quantile(pct_lower),
                                    california_df['AveRooms'].quantile(pct_upper))
california_df['AveBedrms'] = np.clip(california_df['AveBedrms'],
                                     california_df['AveBedrms'].quantile(pct_lower
                                     california_df['AveBedrms'].quantile(pct_upper
california_df['Population'] = np.clip(california_df['Population'],
                                      california_df['Population'].quantile(pct_low
                                      california_df['Population'].quantile(pct_upp
california_df['AveOccup'] = np.clip(california_df['AveOccup'],
                                    california_df['AveOccup'].quantile(pct_lower),
                                    california_df['AveOccup'].quantile(pct_upper))
california_df['MedInc'] = np.clip(california_df['MedInc'],
                                    california_df['MedInc'].quantile(pct_lower),
                                    california_df['MedInc'].quantile(pct_upper))
```

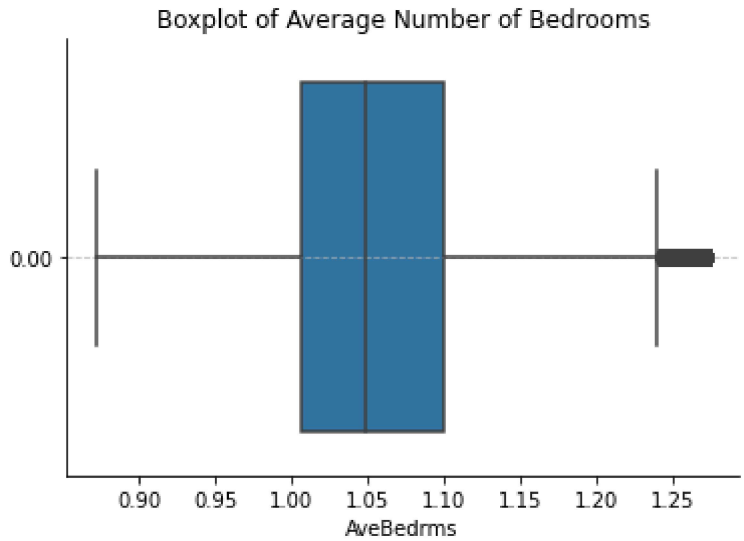
In [15]:
```
# Create a boxplot of the 'AveRooms' column
ax = sns.boxplot(x=california_df['AveRooms'])

# Set the title and axes labels
ax.set_title('Boxplot of Average Number of Rooms')
ax.set_xlabel('AveRooms')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
```

```
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```



In [16]:

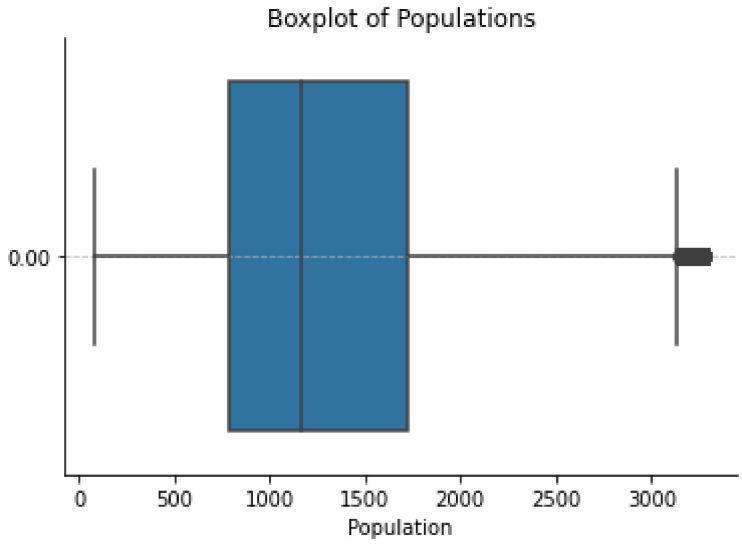
```
# Create a boxplot of the 'AveBedrms' column
ax = sns.boxplot(x=california_df['AveBedrms'])

# Set the title and axes labels
ax.set_title('Boxplot of Average Number of Bedrooms')
ax.set_xlabel('AveBedrms')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```



In [17]:

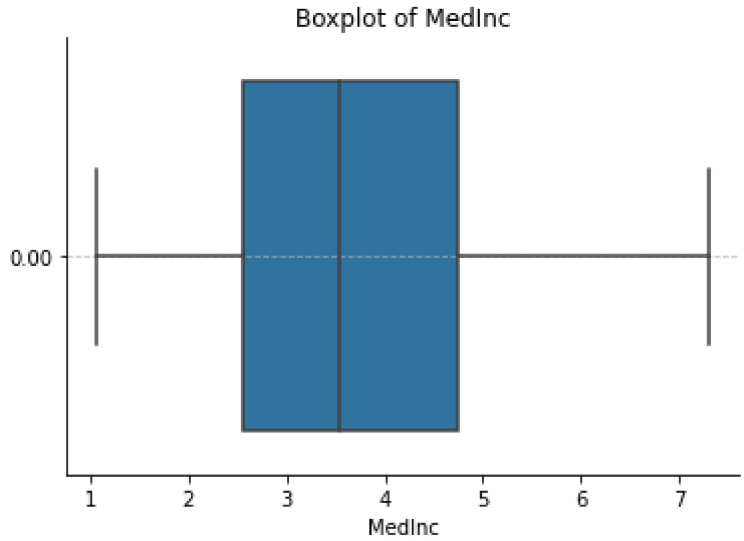
```
# Create a boxplot of the 'Population' column
ax = sns.boxplot(x=california_df['Population'])
```

```
# Set the title and axes labels
ax.set_title('Boxplot of Populations')
ax.set_xlabel('Population')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```



In [18]:

```
# Create a boxplot of the 'MedInc' column
ax = sns.boxplot(x=california_df['MedInc'])

# Set the title and axes labels
ax.set_title('Boxplot of MedInc')
ax.set_xlabel('MedInc')
ax.set_ylabel('')

# Customize the y-axis tick labels to display values in millions
yticks = ax.get_yticks() / 1000000
ax.set_yticklabels(['{:.2f}'.format(ytick) for ytick in yticks])

# Add grid lines and remove top and right spines
ax.grid(axis='y', linestyle='--', alpha=0.7)
ax.spines['top'].set_visible(False)
ax.spines['right'].set_visible(False)

# Show the plot
plt.show()
```



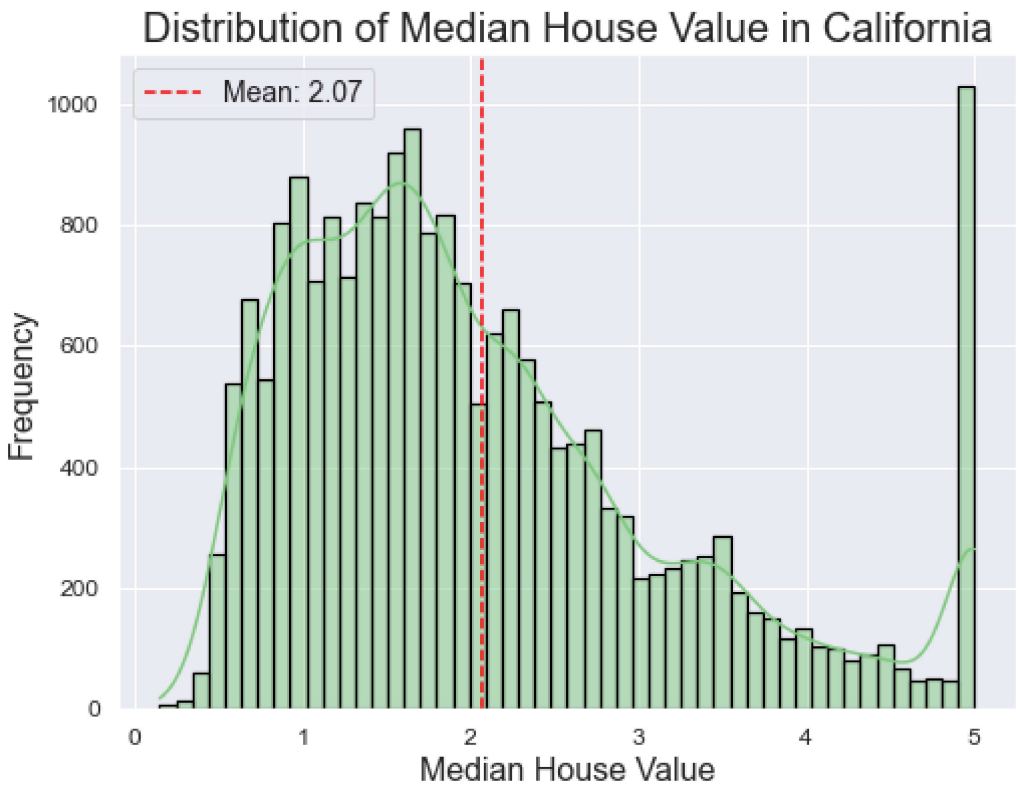
Step 2(g): Check for Skewness using a Histogram

Skewed data can result in biased estimates of model parameters and reduce the accuracy of predictions. Therefore, it is important to assess the distribution of features and target variables to identify any potential issues and take appropriate measures to address them.

Here almost all the features and target look normally distributed. There is some Skewness In MedHouseVal but not enough to do Transformation on it.

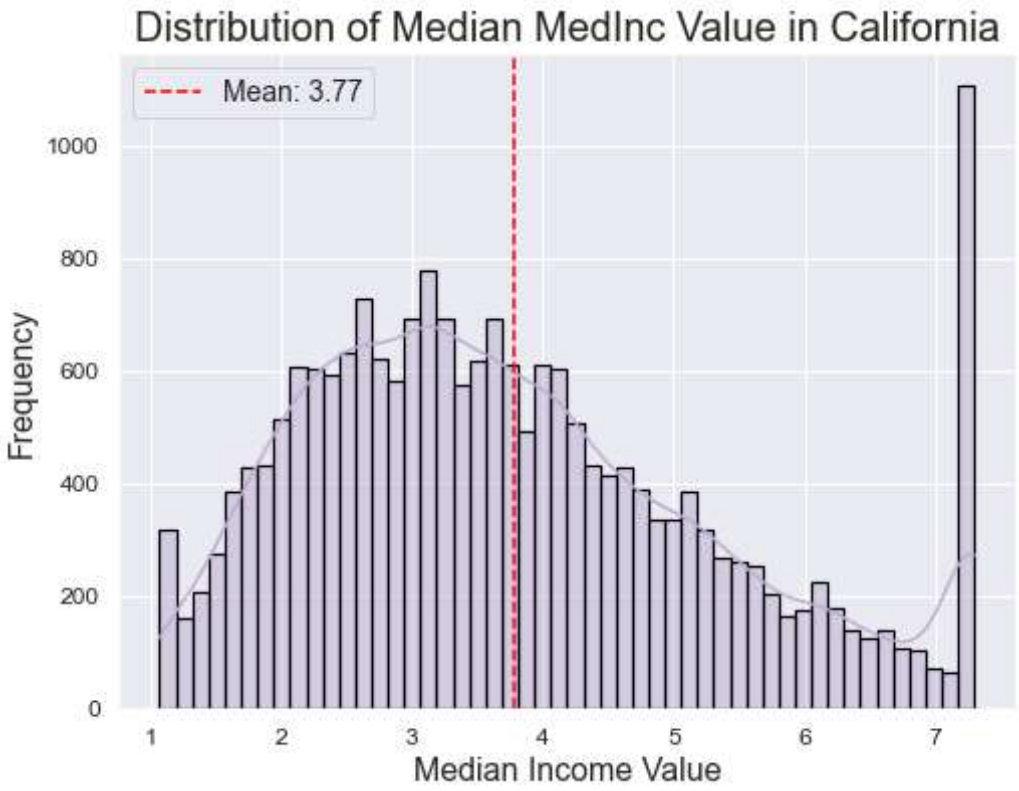
Note: For learning purposes I have shown how to do MedHouseVal transformation for skewness in my previous tutorial of Simple Linear Regression. Feel free to check that out!

In [19]:
```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='MedHouseVal', kde=True, bins=50, color='#7fc97

# Set x and y axis labels and title
plt.xlabel('Median House Value', fontsize=16)
plt.ylabel('Frequency', fontsize=16)
plt.title('Distribution of Median House Value in California', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for mean
mean = california_df['MedHouseVal'].mean()
plt.axvline(mean, color='red', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



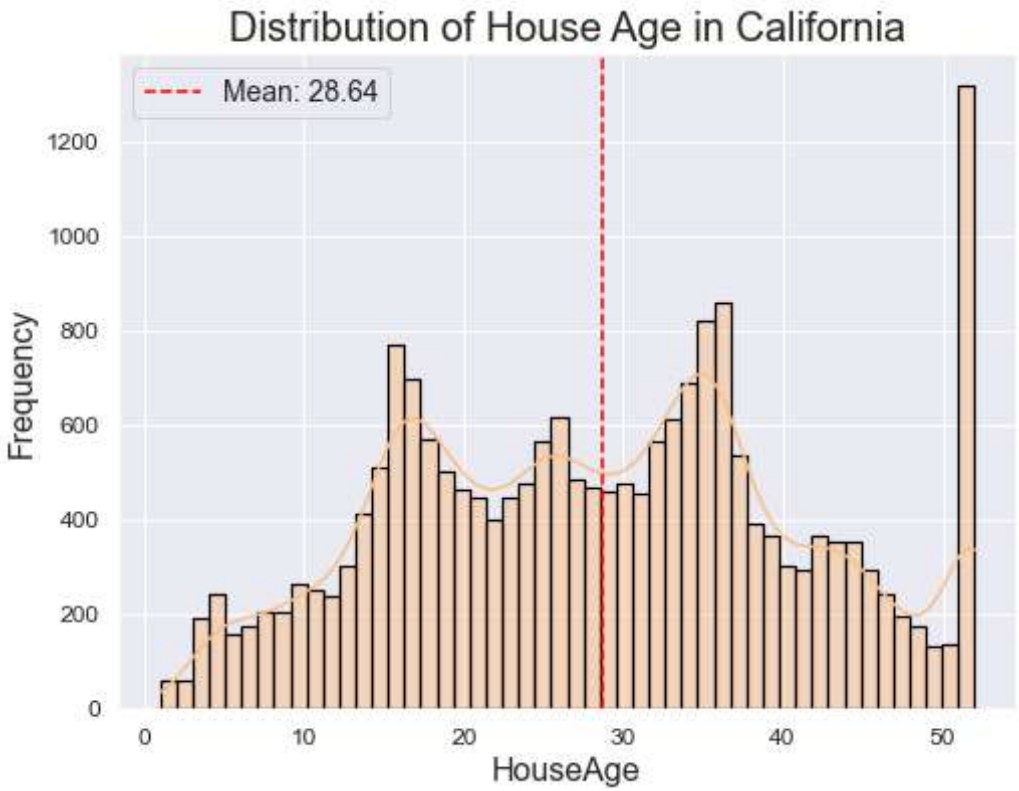
In [20]:

```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='MedInc', kde=True, bins=50, color='#beaed4', e

# Set x and y axis labels and title
plt.xlabel('Median Income Value', fontsize=16)
plt.ylabel('Frequency', fontsize=16)
plt.title('Distribution of Median MedInc Value in California', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for MedInc
mean = california_df['MedInc'].mean()
plt.axvline(mean, color='red', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



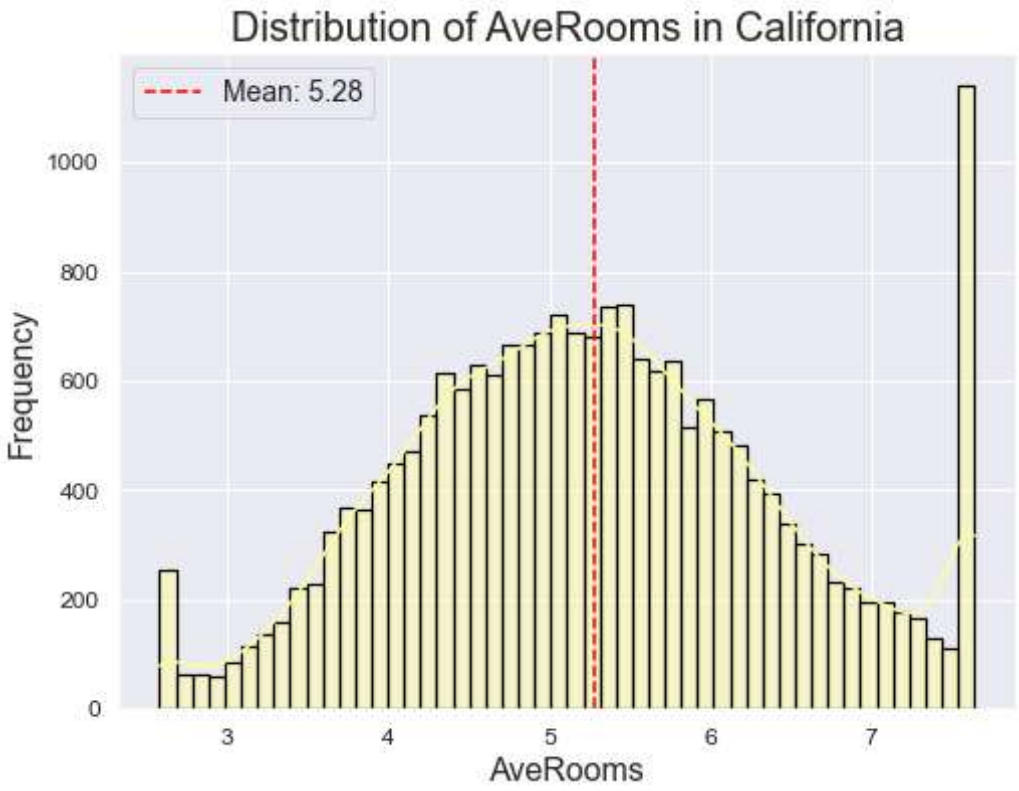
In [21]:

```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='HouseAge', kde=True, bins=50, color='#fdc086',

# Set x and y axis labels and title
plt.xlabel('HouseAge', fontsize=16)
plt.ylabel('Frequency', fontsize=16)
plt.title('Distribution of House Age in California', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for mean
mean = california_df['HouseAge'].mean()
plt.axvline(mean, color='red', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



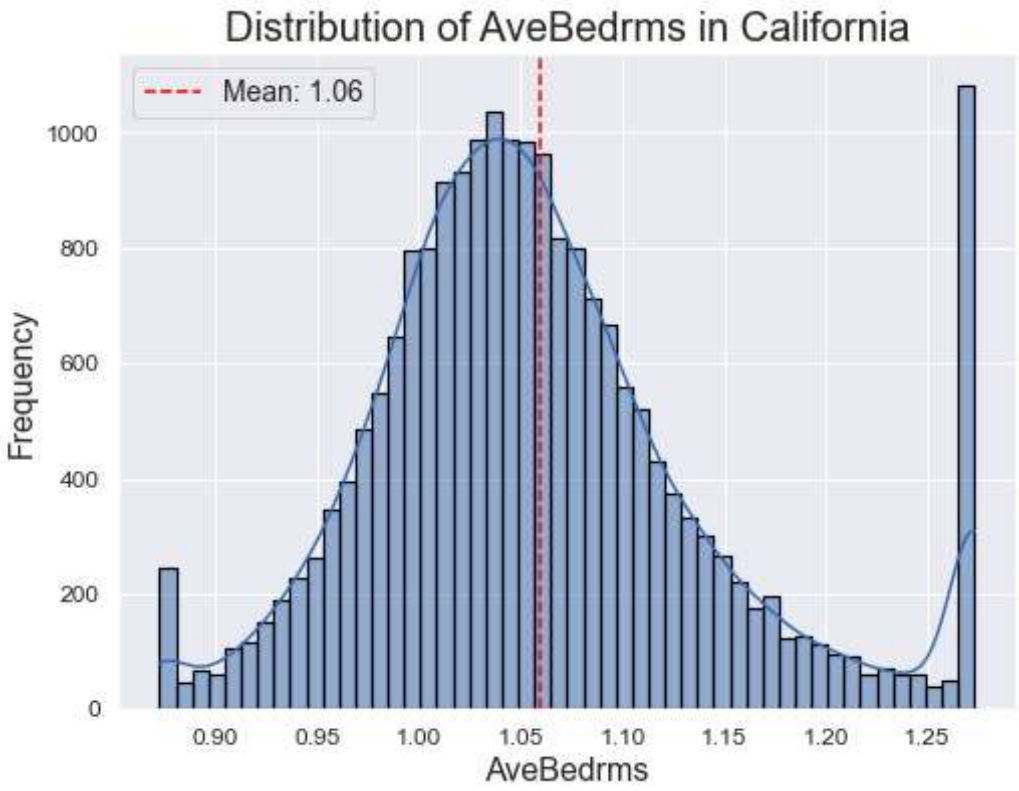
In [22]:

```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='AveRooms', kde=True, bins=50, color='#ffff99',

# Set x and y axis labels and title
plt.xlabel('AveRooms', fontsize=16)
plt.ylabel('Frequency', fontsize=16)
plt.title('Distribution of AveRooms in California', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for mean
mean = california_df['AveRooms'].mean()
plt.axvline(mean, color='red', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



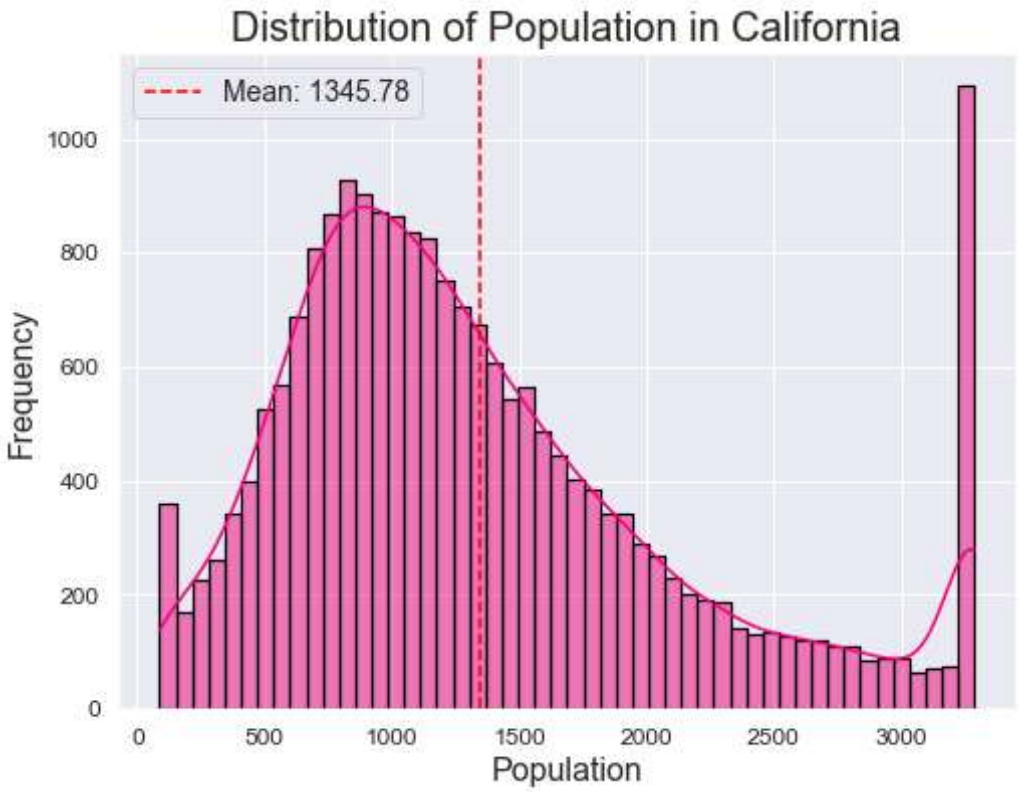
In [23]:

```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='AveBedrms', kde=True, bins=50, color='#386cb0'

# Set x and y axis labels and title
plt.xlabel('AveBedrms', fontsize=16)
plt.ylabel('Frequency', fontsize=16)
plt.title('Distribution of AveBedrms in California', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for mean
mean = california_df['AveBedrms'].mean()
plt.axvline(mean, color='red', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



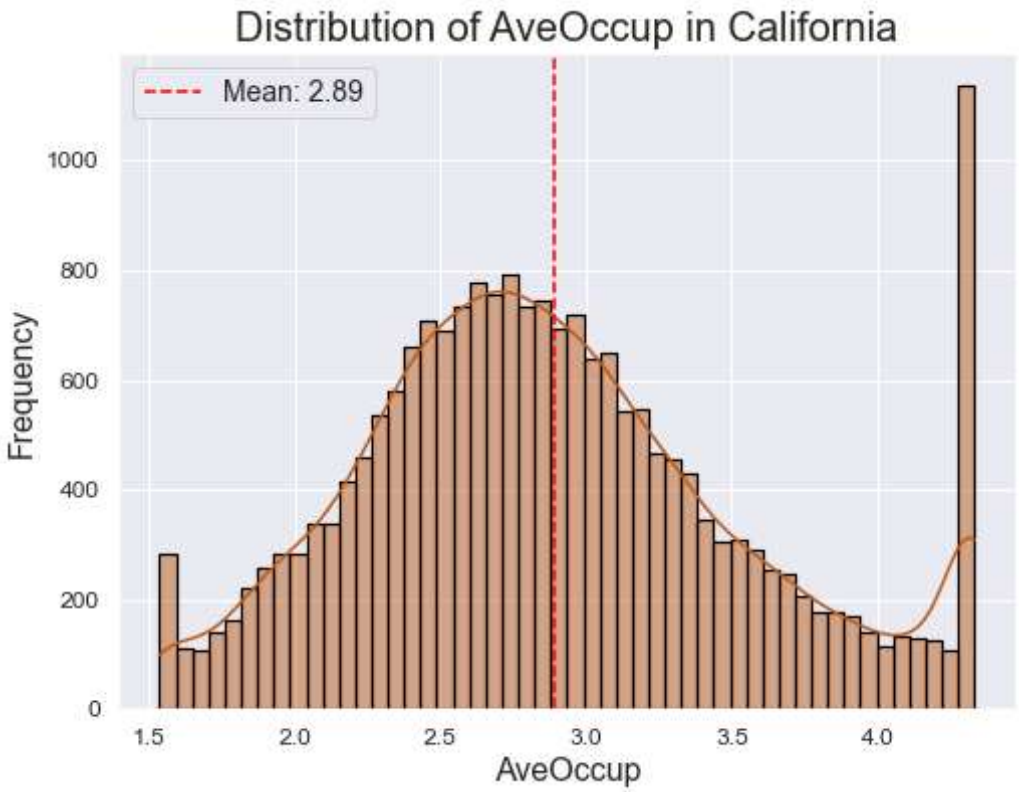
In [24]:

```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='Population', kde=True, bins=50, color='#f0027f

# Set x and y axis labels and title
plt.xlabel('Population', fontsize=16)
plt.ylabel('Frequency', fontsize=16)
plt.title('Distribution of Population in California', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for mean
mean = california_df['Population'].mean()
plt.axvline(mean, color='red', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



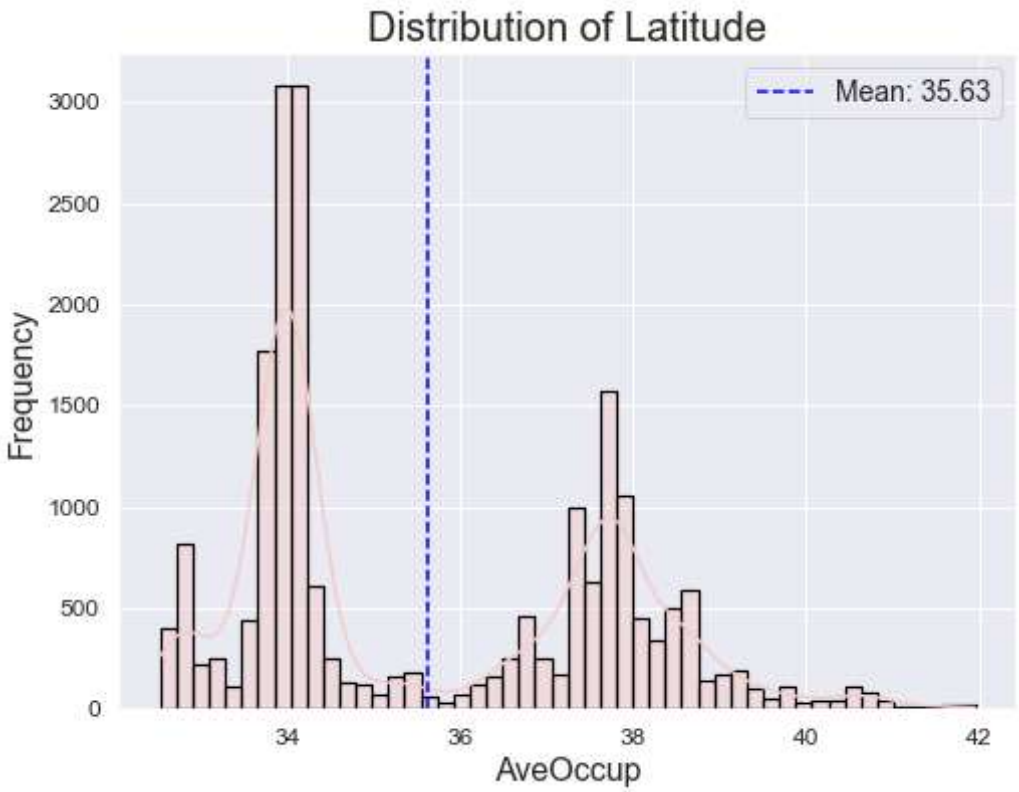
In [25]:

```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='AveOccup', kde=True, bins=50, color='#bf5b17',

# Set x and y axis labels and title
plt.xlabel('AveOccup', fontsize=16)
plt.ylabel('Frequency', fontsize=16)
plt.title('Distribution of AveOccup in California', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for mean
mean = california_df['AveOccup'].mean()
plt.axvline(mean, color='red', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



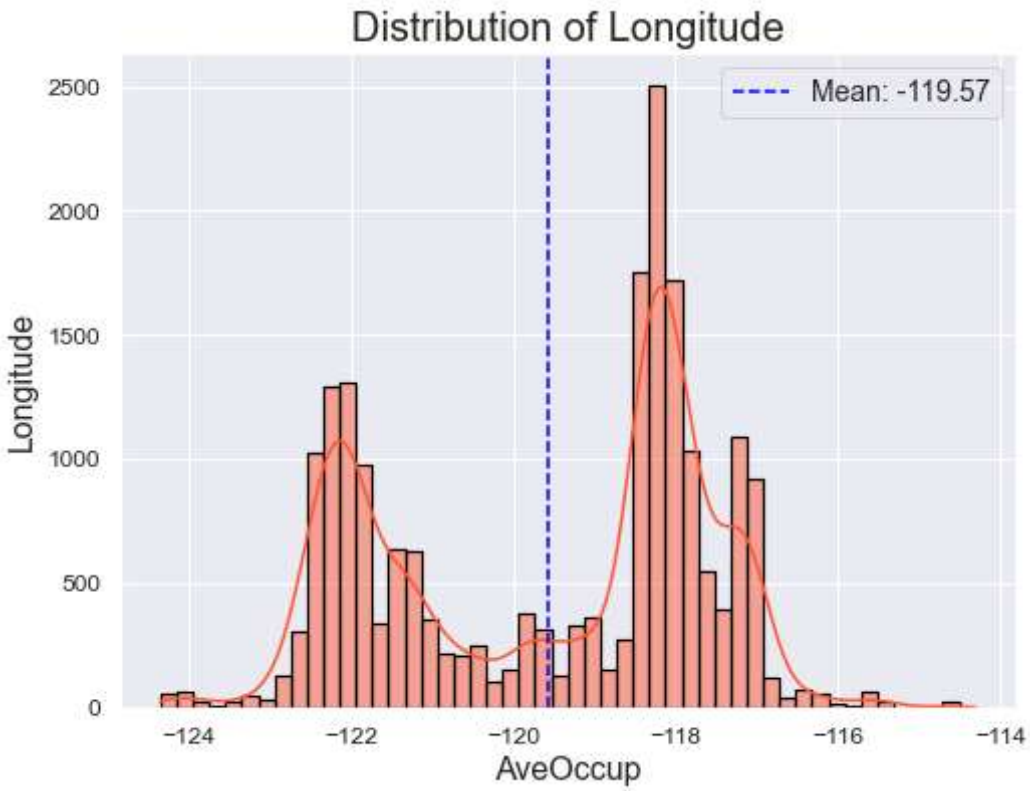
In [26]:

```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='Latitude', kde=True, bins=50, color='#F4CCCC',

# Set x and y axis labels and title
plt.xlabel('AveOccup', fontsize=16)
plt.ylabel('Frequency', fontsize=16)
plt.title('Distribution of Latitude', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for mean
mean = california_df['Latitude'].mean()
plt.axvline(mean, color='blue', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



In [27]:

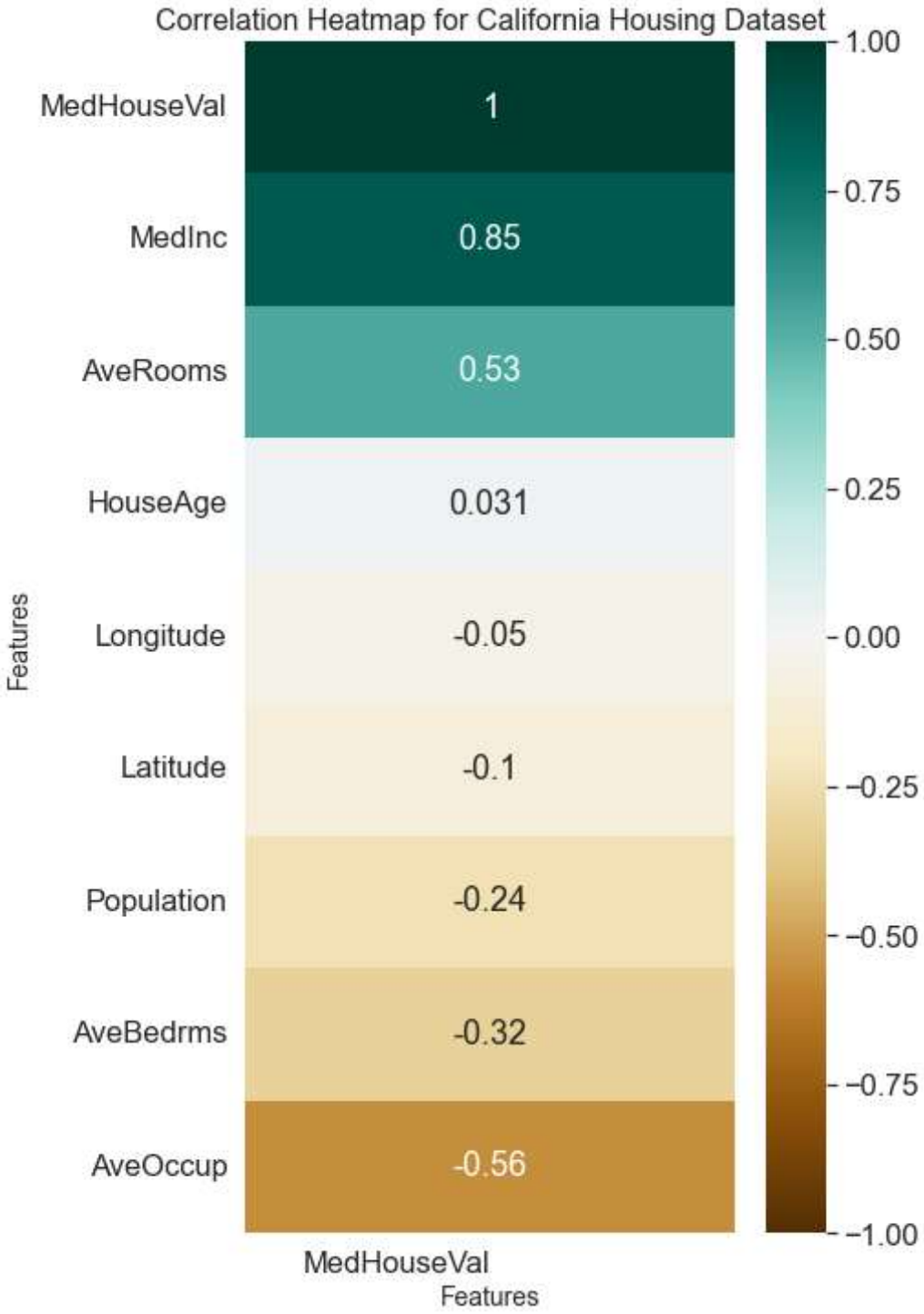
```
# Set figure size and font scale
plt.figure(figsize=(8, 6))
sns.set(font_scale=1.5)

# Create histogram
sns.histplot(data=california_df, x='Longitude', kde=True, bins=50, color='#FF5733'

# Set x and y axis labels and title
plt.xlabel('AveOccup', fontsize=16)
plt.ylabel('Longitude', fontsize=16)
plt.title('Distribution of Longitude', fontsize=20)

# Customize x and y axis tick marks and labels
plt.xticks(fontsize=12)
plt.yticks(fontsize=12)

# Add vertical line for mean
mean = california_df['Longitude'].mean()
plt.axvline(mean, color='blue', linestyle='--', label=f'Mean: {mean:.2f}')
plt.legend(fontsize=14)

# Show the plot
plt.show()
```



Step 2(d): Create a Vertical Correlation Heatmap

The correlation matrix shows the correlation coefficients between every pair of variables in the dataset. A correlation coefficient ranges from -1 to 1 and measures the strength and direction of the linear relationship between two variables. A coefficient of -1 indicates a perfect negative correlation, a coefficient of 0 indicates no correlation, and a coefficient of 1 indicates a perfect positive correlation.

In [28]:
```
# Calculate the correlation matrix
corr_matrix = california_df.corr()

# Set up the matplotlib figure
fig, ax = plt.subplots(figsize=(6, 12))

# Create the heatmap
#sns.heatmap(corr_matrix, cmap='BrBG', annot=True, fmt='.2f', linewidths=.5, ax=ax,
sns.heatmap(corr_matrix.corr()[['MedHouseVal']].sort_values(by='MedHouseVal', ascen

# Set the title and axis labels
ax.set_title('Correlation Heatmap for California Housing Dataset', fontsize=16)
ax.set_xlabel('Features', fontsize=14)
ax.set_ylabel('Features', fontsize=14)

# Rotate the x-axis labels for readability
plt.xticks(rotation=0, ha='right')

# Show the plot
plt.show()
```



Step 3: Define Dependant and Independant Variable

In [29]:
```
X = california_df.drop(['MedHouseVal'],axis=1)
y = california_df['MedHouseVal']
```

Step 3: Do Train-Test Split in the ratio 70-30

In [30]:
```
# Split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.3, random_st
```

Step 4: Perform Simple Linear Regression

In [31]:
```
# Create an instance of the LinearRegression class
```

```
lr = LinearRegression()
```

In [32]:
```
# Create a grid of possible intercept values to try
intercept_grid = {'fit_intercept': [True, False], 'normalize': [True, False], 'copy
```

In [33]:
```
# Use cross-validation to find the best intercept value
grid_search = GridSearchCV(lr, intercept_grid, cv=5)
grid_search.fit(X_train, y_train)
```

Out[33]:
```
GridSearchCV(cv=5, estimator=LinearRegression(),
             param_grid={'copy_X': [True, False],
                         'fit_intercept': [True, False],
                         'normalize': [True, False]})
```

In [34]:
```
# Fit the linear regression model with the best intercept value
lr = grid_search.best_estimator_
lr.fit(X_train, y_train)
```

Out[34]:
```
LinearRegression(normalize=False)
```

In [35]:
```
# Predict the median house value using the test data
y_pred = lr.predict(X_test)
```

Step 4: Evalute the Performance of the Model

The mean squared error (MSE) measures how close the predicted values are to the actual values, with lower values indicating better performance. In this case, the MSE is 0.46, which is relatively high. Showing that there is room for improvement

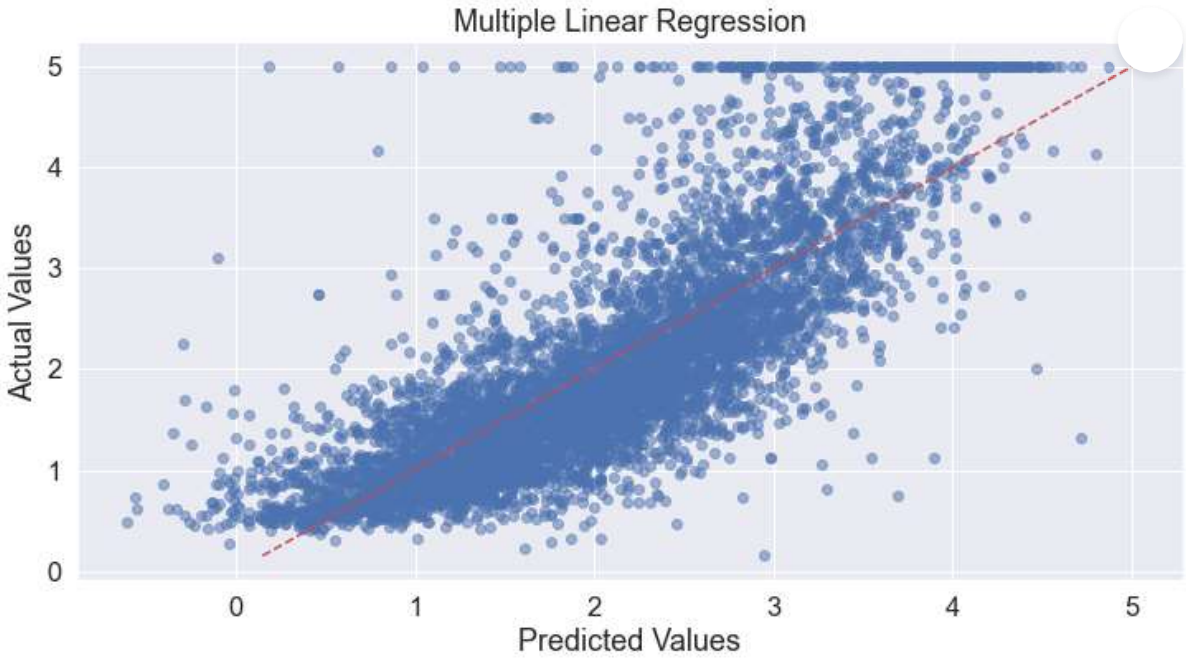
The R-squared score measures how well the regression model fits the actual data, with values closer to 1 indicating a better fit. The R-squared score here is 0.65 (Better than SLR), which means that approximately 65% of the variation in median house value can be explained by all predictor variables. This indicates that the model has some better predictive power, but there is still room for Improvement.

In [36]:
```
# Evaluate the model using mean squared error and R-squared score
mse = mean_squared_error(y_test, y_pred)
r2 = r2_score(y_test, y_pred)

# Print the mean squared error and R-squared score
print("Mean Squared Error:", mse)
print("R-squared Score:", r2)
```

```
Mean Squared Error: 0.4627426910774296
R-squared Score: 0.6529178520320509
```

Step 4(a): Visualize the Regression

In [37]:
```
# Create scatter plot of predicted vs. actual values
plt.figure(figsize=(12, 6))
plt.scatter(y_pred, y_test, alpha=0.5)
plt.plot([y.min(), y.max()], [y.min(), y.max()], 'r--')
plt.xlabel('Predicted Values')
plt.ylabel('Actual Values')
plt.title('Multiple Linear Regression')
plt.show()
```



Conclusion

In this Multiple linear regression tutorial, we explored how to use linear regression to model the relationship between more than 1 variable with the target feature, specifically the median house value in California. We started by loading and cleaning the dataset, and then visualizing the relationship between the variables.

Next, we split the data into training and testing sets and used linear regression to fit a model to the training data. We then used the model to make predictions on the test data and evaluated the model's performance using mean squared error and R-squared score.

To further optimize our model, we used hyperparameter tuning with GridSearchCV to find the best intercept value. Finally, we fit the linear regression model with the best intercept value, made predictions on the test data, and evaluated the model's performance using mean squared error and R-squared score.

Overall, multiple linear regression is a powerful tool for modeling the relationship with more than one variable and making predictions. However, it is important to properly clean and preprocess the data, and to evaluate the model's performance using appropriate metrics.