

# ExploratoryDataAnalysisCaliforniaHousing

November 7, 2022

Exploratory Data Analysis for the California Housing census

Author: Jose Pena

Github: JoseJuan98

---

## 0.1 Aims

The aims of this exercise are an opportunity to produce a quality exploratory analysis that is ready to highlight my analytical skills and once completed and insights are drawn, its features can then be used for a future machine learning modeling exercise.

## 1 Setup

For this Exploratory Data Analisis project the following libraries will be used:

- `pandas` for managing the data.
- `numpy` for mathematical operations.
- `seaborn` for visualizing the data.
- `matplotlib` for visualizing the data.
- `sklearn` for machine learning related functions.
- `scipy` for statistical computations.

### 1.1 Imports

```
[1]: import pandas
import numpy
import seaborn

from scipy.stats import boxcox, ttest_ind
from matplotlib import pyplot
from pandas.plotting import scatter_matrix

from sklearn.impute import SimpleImputer
from sklearn.preprocessing import OneHotEncoder, MinMaxScaler, StandardScaler

# utils.py
```

```
from utils import fetch_housing_data, HOUSING_URL, HOUSING_PATH, plot_scatters,\n    \\\n    plot_univariate_boxplots, remove_outliers_iqr
```

Setting up some options:

```
[2]: # Display and store plot within the notebook\n%matplotlib inline\n\n# Show all columns when displaying dataframe\npandas.options.display.max_columns = None
```

Load data, if it wasn't downloaded before it will fetch it from the URL specified, otherwise will load it from a local '.csv' file.

```
[3]: data = fetch_housing_data(url=HOUSING_URL,\n                             path=HOUSING_PATH)
```

## 2 Plan of Exploration

---

1. Description of data set and summary of attributes
2. Data Cleaning and Feature Engineering
  1. Normalizing the distribution of the target variable
  2. Handling duplicated values
  3. Handling missing values
  4. Handling the outliers
  5. Encoding categorical variables
  6. Scaling numerical variables
3. Exploratory Data Analysis (EDA)
  1. Histogram of variables
  2. Geographical visualization
  3. Variables Correlation
4. Hypothesis Testing
  1. Hypothesis one
    1. Define hypothesis
    2. Define a sample statistic
    3. Testing hypothesis by significance tests
    4. Evaluate and interpret results
  2. Hypothesis two
    1. Define hypothesis
    2. Define a sample statistic
    3. Testing hypothesis by significance tests
    4. Evaluate and interpret results
  3. Hypothesis three
    1. Define hypothesis
    2. Define a sample statistic

3. Testing hypothesis by significance tests
  4. Evaluate and interpret results
  5. Next steps and Conclusions
    1. Next steps
    2. Conclusions
      1. Findings
      2. Data quality
- 

### 3 1. Description of data set and summary of attributes

This California Housing dataset is available from [Luís Torgo's page](#) (University of Porto).

This dataset appeared in a 1997 paper titled Sparse Spatial Autoregressions by Pace, R. Kelley and Ronald Barry, published in the Statistics and Probability Letters journal. They built it using the 1990 California census data. It contains one row per census block group. A block group is the smallest geographical unit for which the U.S. Census Bureau publishes sample data (a block group typically has a population of 600 to 3,000 people).

The target variable or dependent variable for this analysis will be the `median_house_value`, which describes median price of the houses per block group.

#### Shape of the dataset

```
[4]: data.shape
```

```
[4]: (20640, 10)
```

#### List of columns

```
[5]: data.columns.to_list()
```

```
[5]: ['longitude',
      'latitude',
      'housing_median_age',
      'total_rooms',
      'total_bedrooms',
      'population',
      'households',
      'median_income',
      'median_house_value',
      'ocean_proximity']
```

#### First 5 rows of the dataset

```
[6]: data.head()
```

```
[6]:   longitude  latitude  housing_median_age  total_rooms  total_bedrooms \
0     -122.23      37.88              41.0        880.0         129.0
1     -122.22      37.86              21.0       7099.0        1106.0
```

```

2    -122.24      37.85          52.0      1467.0      190.0
3    -122.25      37.85          52.0      1274.0      235.0
4    -122.25      37.85          52.0      1627.0      280.0

```

	population	households	median_income	median_house_value	ocean_proximity
0	322.0	126.0	8.3252	452600.0	NEAR BAY
1	2401.0	1138.0	8.3014	358500.0	NEAR BAY
2	496.0	177.0	7.2574	352100.0	NEAR BAY
3	558.0	219.0	5.6431	341300.0	NEAR BAY
4	565.0	259.0	3.8462	342200.0	NEAR BAY

Non-null values count, type of feature and memory usage

```
[7]: data.info()
```

```

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 20640 entries, 0 to 20639
Data columns (total 10 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   longitude        20640 non-null   float64
 1   latitude         20640 non-null   float64
 2   housing_median_age 20640 non-null   float64
 3   total_rooms      20640 non-null   float64
 4   total_bedrooms   20433 non-null   float64
 5   population       20640 non-null   float64
 6   households       20640 non-null   float64
 7   median_income    20640 non-null   float64
 8   median_house_value 20640 non-null   float64
 9   ocean_proximity  20640 non-null   object  
dtypes: float64(9), object(1)
memory usage: 1.6+ MB

```

Statistical properties of the dataset

```
[8]: data.describe(include='all')
```

	longitude	latitude	housing_median_age	total_rooms	\
count	20640.000000	20640.000000	20640.000000	20640.000000	
unique	NaN	NaN	NaN	NaN	
top	NaN	NaN	NaN	NaN	
freq	NaN	NaN	NaN	NaN	
mean	-119.569704	35.631861	28.639486	2635.763081	
std	2.003532	2.135952	12.585558	2181.615252	
min	-124.350000	32.540000	1.000000	2.000000	
25%	-121.800000	33.930000	18.000000	1447.750000	
50%	-118.490000	34.260000	29.000000	2127.000000	
75%	-118.010000	37.710000	37.000000	3148.000000	
max	-114.310000	41.950000	52.000000	39320.000000	

	total_bedrooms	population	households	median_income	\
count	20433.000000	20640.000000	20640.000000	20640.000000	
unique	NaN	NaN	NaN	NaN	NaN
top	NaN	NaN	NaN	NaN	NaN
freq	NaN	NaN	NaN	NaN	NaN
mean	537.870553	1425.476744	499.539680	3.870671	
std	421.385070	1132.462122	382.329753	1.899822	
min	1.000000	3.000000	1.000000	0.499900	
25%	296.000000	787.000000	280.000000	2.563400	
50%	435.000000	1166.000000	409.000000	3.534800	
75%	647.000000	1725.000000	605.000000	4.743250	
max	6445.000000	35682.000000	6082.000000	15.000100	
	median_house_value	ocean_proximity			
count	20640.000000	20640			
unique	NaN	5			
top	NaN	<1H OCEAN			
freq	NaN	9136			
mean	206855.816909	NaN			
std	115395.615874	NaN			
min	14999.000000	NaN			
25%	119600.000000	NaN			
50%	179700.000000	NaN			
75%	264725.000000	NaN			
max	500001.000000	NaN			

## 4 2. Data Cleaning and Feature Engineering

Most of the real-world data, is raw data, meaning that it can contain repeated, missing, and irrelevant entries of information. Hence, if this data is used in any machine learning analysis, it will result in low accuracy or incorrect prediction. For this reason, data cleaning, also known as data cleansing, is an important technique that comes prior to any model building.

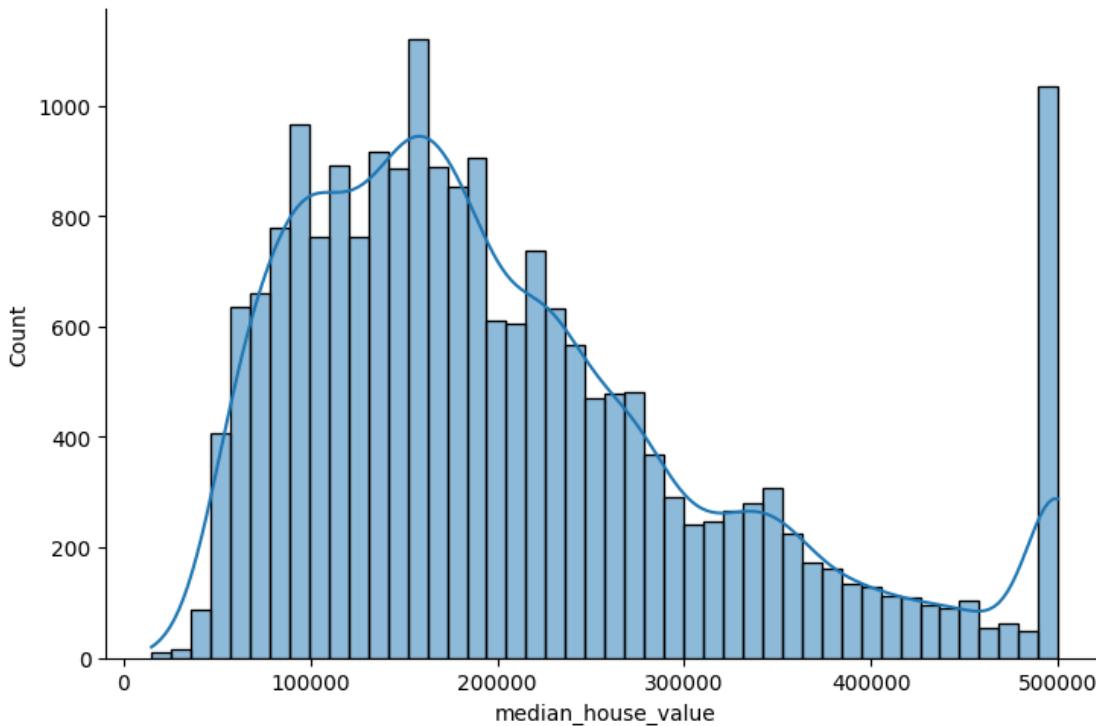
Also, a critical part of the successful Machine Learning project is coming up with a good set of features to train on. This process is called feature engineering, and it involves three steps: - Feature transformation (transforming the original features) - Feature selection (selecting the most useful features to train on) - Feature extraction (combining existing features to produce more useful ones)

### 4.1 2.1 - Normalizing the distribution of the target variable

The target variable needs to be inspected, `median_house_value`, whether is normally distributed or not, because the assumption of the normal distribution must be met in order to perform any type of regression analysis.

There are several ways to check for this assumption, first a visual method can be used, by plotting the `median_house_value` distribution using the `distplot()` function from the seaborn library.

```
[9]: seaborn.distplot(data['median_house_value'], height=5, aspect=1.5, kde=True);
```



As the plot shows, the `median_house_value` deviates from the normal distribution. It has a longer tail to the right, so we call it a positive skew. In statistics skewness is a measure of asymmetry of the distribution. In addition to skewness, there is also a kurtosis, parameter which refers to the pointedness of a peak in the distribution curve. Both skewness and kurtosis are frequently used together to characterize the distribution of data.

To quantify the skewness level of this variable the `pandas.skew()` function can be used.

```
[10]: print(f'Skewness: {data.median_house_value.skew()}'")
```

Skewness: 0.9777632739098341

The range of skewness for a fairly symmetrical bell curve distribution is between -0.5 and 0.5; moderate skewness is -0.5 to -1.0 and 0.5 to 1.0; and highly skewed distribution is < -1.0 and > 1.0. In this case, there is ~0.98, so it is considered moderate skewed data.

Now, this data can be transformed, so that it will look more normally distributed. For example, it can be used the `numpy.log()` function from the `numpy` library to perform the *log transformation*. This [documentation](#) contains more information about the `numpy log transform`.

Alternatively, there are other ways to correct the high level skewness of the data. For example, Square Root Transform (`numpy.sqrt()`) and the Box-Cox Transform (`stats.boxcox()` from the `scipy stats` library). To learn more about these two methods, please check out this [article](#).

```
[11]: log_data = pandas.DataFrame(numpy.log(data.median_house_value))
sqr_data = pandas.DataFrame(numpy.sqrt(data.median_house_value))
boxcox_data = pandas.DataFrame(boxcox(data.median_house_value)[0])
```

```
[12]: for data_t, name in zip([log_data['median_house_value'],  
    ↪sqr_data['median_house_value'],  
        boxcox_data[0]], ['Log', 'Square Root', 'Box-Cox']):  
    print(f'Skewness of {name} transform: {data_t.skew()}')
```

Skewness of Log transform: -0.1731753903249557

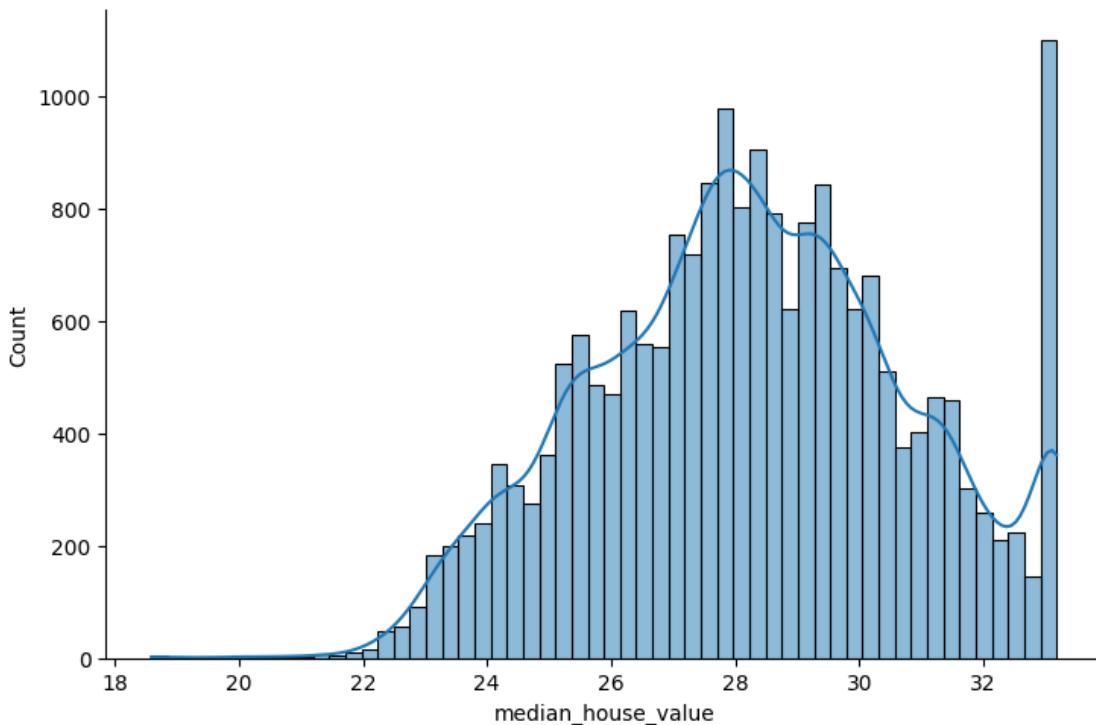
Skewness of Square Root transform: 0.43938209295248964

Skewness of Box-Cox transform: -0.012149417116265352

So as the Box-Cox transform makes the skewness the lowest, this transform method will be selected to make more normally distributed the target data.

```
[13]: data['median_house_value'] = pandas.DataFrame(boxcox(data.  
    ↪median_house_value)[0])
```

```
[14]: seaborn.displot(data.median_house_value, height=5, aspect=1.5, kde=True);
```



```
[15]: print(f'Skewness after box-cox transformation: {data.median_house_value.  
    ↪skew()}')
```

Skewness after box-cox transformation: -0.012149417116265352

As it can be seen, theBbox-cox method transformed the target variable distribution into a more symmetrical bell curve and the skewness level now is ~0.01, well within the range.

## 4.2 2.2 - Handling duplicated values

Before handling duplicated data, first it's checked if there are any duplicated rows

```
[16]: f'There are {data.duplicated().sum()} duplicated rows in this dataset'
```

```
[16]: 'There are 0 duplicated rows in this dataset'
```

In addition, to check that there are not values duplicated in the index:

```
[17]: if data.index.is_unique: print('No duplicated values in the index.')
else: print('There are duplicated values in the index.')
```

```
No duplicated values in the index.
```

## 4.3 2.3 - Handling missing values

As previously shown in the description of the data, the variable `total_bedrooms` has missing values. To be sure the entire dataset missing values can be counted as follows:

```
[18]: f'There are {data.isna().sum().sum()} missing values in the dataset'
```

```
[18]: 'There are 207 missing values in the dataset'
```

```
[19]: f'There are {data.total_bedrooms.isna().sum()} missing values in the variable
`total_bedrooms`'
```

```
[19]: 'There are 207 missing values in the variable `total_bedrooms`'
```

To know what to do with this missing values we can check the following:

```
[20]: data['total_bedrooms'].describe()
```

```
[20]: count    20433.000000
      mean     537.870553
      std     421.385070
      min     1.000000
      25%    296.000000
      50%    435.000000
      75%    647.000000
      max    6445.000000
Name: total_bedrooms, dtype: float64
```

So, to handle the missing values a class `SimpleImputer` from `sklearn` can be used. There are other alternatives like directly using `pandas.fillna()`, but later on for production ready code it will be easier to be managed by this class.

```
[21]: imputer = SimpleImputer(missing_values=pandas.NA, strategy='mean')
data.total_bedrooms = imputer.fit_transform(X=data.total_bedrooms.to_numpy()
                                             .reshape(-1, 1))
```

```
[22]: f'Total missing values after imputation: {data.total_bedrooms.isna().sum()}'
```

```
[22]: 'Total missing values after imputation: 0'
```

#### 4.4 2.4 - Handling outliers

In statistics, an outlier is an observation point that is distant from other observations. An outlier can be due to some mistakes in data collection or recording, or due to natural high variability of data points. How to treat an outlier highly depends on our data or the type of analysis to be performed. Outliers can markedly affect our models and can be a valuable source of information, providing us insights about specific behaviours.

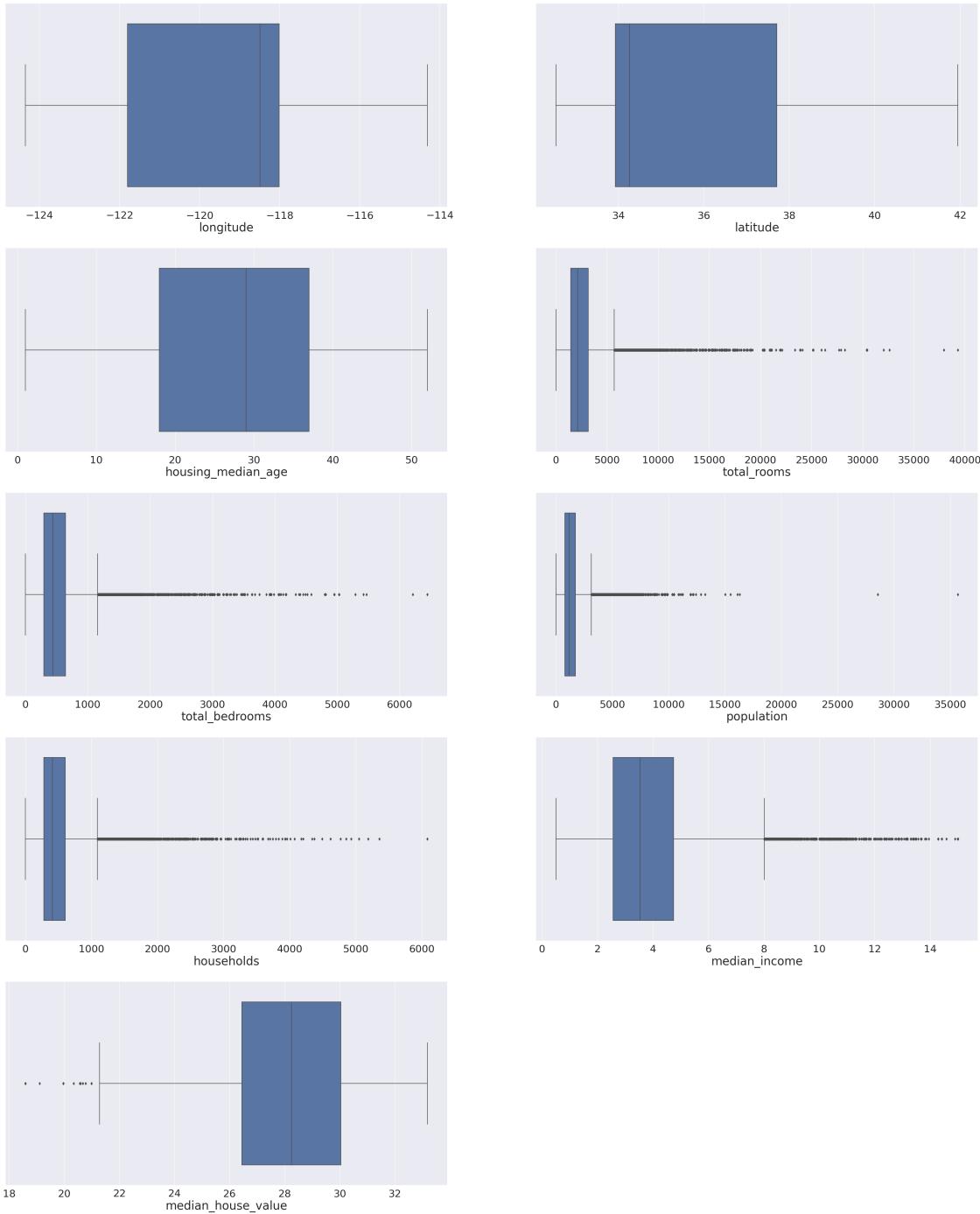
In machine learning projects, during model building, it is important to remove those outliers because the presence of those outliers can mislead the model. The presence of outliers may change the mean and standard deviation of the whole dataset which can badly affect the performance of the model. Outliers also increase the variance error and reduce the power of the statistical tests.

There are many ways to discover outliers in our data. We can do Uni-variate analysis (using one variable analysis) or Multi-variate analysis (using two or more variables). One of the simplest ways to detect an outlier is to inspect the data visually, by making box plots or scatter plots.

##### 4.4.1 Uni-variate Analysis

A box plot is a method for graphically depicting groups of numerical data through their quartiles. Box plots may also have lines extending vertically from the boxes (whiskers) indicating variability outside the upper and lower quartiles. Outliers may be plotted as individual points. To learn more about box plots please click [here](#).

```
[23]: plot_univariate_boxplots(data=data);
```

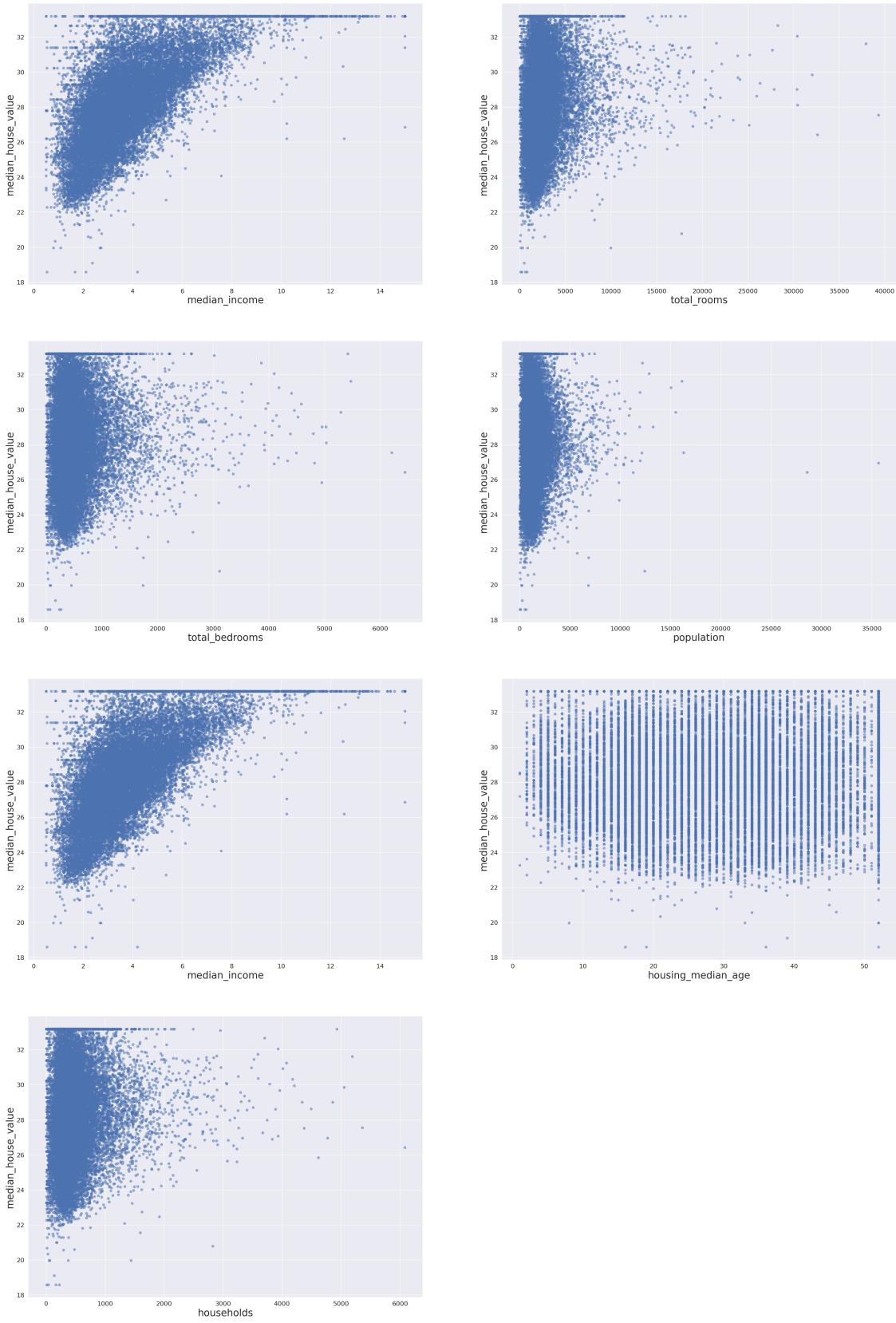


As it is shown, some plots have some points plotted outside the box plot area and that greatly deviate from the rest of the population. Whether to remove or keep them will greatly depend on the understanding of our data and the type of analysis to be performed. In this case, the points that are outside of our box plots might be the actual true data points

#### 4.4.2 Bi-variate Analysis

So to know in more detail if the variables with some of these points outside of the box plot could be outliers, it can be plotted the scatter plot of the relationship between these the variables and the target variable.

```
[24]: variables_with_outliers = ["median_income", "total_rooms", "total_bedrooms",  
    ↴"population", "median_income", "housing_median_age", "households"]  
  
plot_scatters(data=data, variables=variables_with_outliers,  
    ↴target='median_house_value')
```



#### 4.4.3 Interquartile range(IQR)

The visualization of *Uni-variate* and *Bi-variate Analysis* gave an idea on how to treat the outliers. A deep understanding of the data is always needed, but if there is lack of this understanding the treatment of outliers can rely on experimentation relying on a statistical method like the interquartile range to adjust this treatment or removal.

The interquartile range is a difference between the third quartile(Q3) and the first quartile(Q1). In this method, anything lying above  $Q3 + 1.5 * IQR$  and below  $Q1 - 1.5 * IQR$  is considered an outlier.

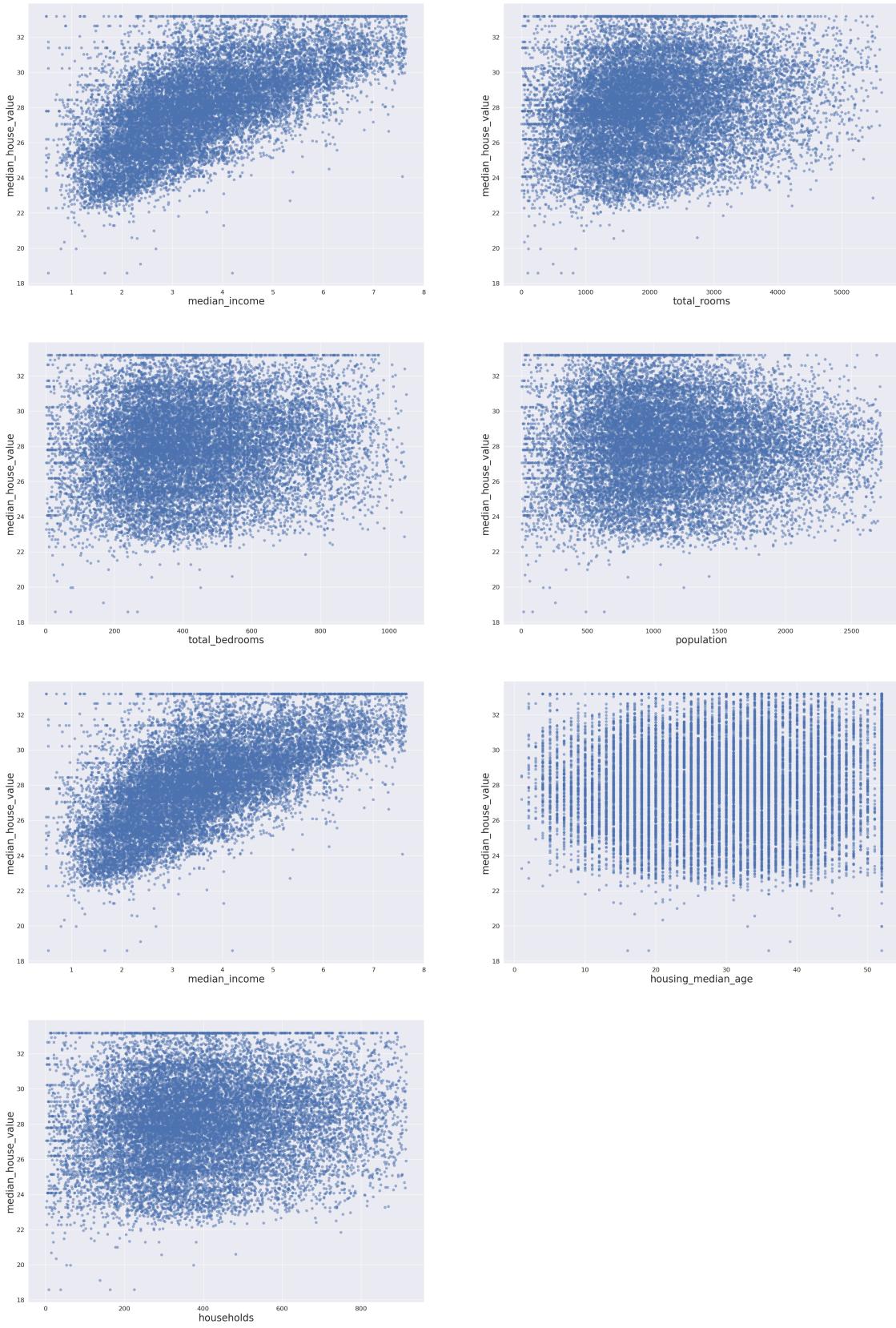
$$Q1 - 1.5 * IQR < data < Q3 + 1.5 * IQR$$

This 1.5, called *whisker width* in the boxplots, or *hereinafter scale* controls the sensitivity of the range and hence the decision rule. A bigger scale would make the outliers to be considered as data points while a smaller one would make some data points to be perceived as outliers. And if not sure, none of these cases is desirable.

```
[25]: for col in variables_with_outliers:  
    data = remove_outliers_iqr(dataframe=data, column=col, whisker_width=1.5)
```

Now after applying IQR can be seen that the points are less dispersed, hence most of the outliers were removed. If still some outliers persists, the whisker width can be tuned to capture this too.

```
[26]: plot_scatters(data=data, variables=variables_with_outliers, ▾  
    ↪target='median_house_value')
```



For interpretability reasons for the visualizations is better to make a copy before transforming the variables.

```
[27]: data_visualization = data.copy(deep=True)
```

## 4.5 2.5 - Encoding Categorical Variables

Categorical variables represent qualitative data with no apparent inherent mathematical meaning. Therefore, for any Machine Learning analysis, all the categorical data must be transformed into the numerical data types. The `unique()` method can be used to obtain all the categories of categorical columns.

```
[28]: categorical_variables = data.select_dtypes('object').columns.to_list()
for col in categorical_variables:
    print(f'Column {col} with categories: {data[col].unique()}' )
```

```
Column ocean_proximity with categories: ['NEAR BAY' '<1H OCEAN' 'INLAND' 'NEAR OCEAN' 'ISLAND']
```

### 4.5.1 One Hot Encoding

Now, to be recognized by Machine Learning algorithms, the categorical variables should be converted into numerical ones. One way to do this is through *One Hot Encoding*. To learn more about this process, please visit this [documentation](#).

The class `OneHotEncoder` from `sklearn` can be used to do this transformation.

```
[29]: cat_encoder = OneHotEncoder(sparse=False, handle_unknown='ignore')
```

Storing original index of data to later be able to concat it with the rest of variables

```
[30]: original_index = data[categorical_variables].index
```

Fitting the encoder

```
[31]: new_cat_data = cat_encoder.fit_transform(data[categorical_variables])
```

Concating the new variables with the rest

```
[32]: new_cat_columns = cat_encoder.get_feature_names_out().tolist()
new_cat_data = pandas.DataFrame(data=new_cat_data, columns=new_cat_columns)
new_cat_data.set_index(original_index, inplace=True)

data = pandas.concat([data, new_cat_data], axis=1, join='inner')
del new_cat_data, original_index

data.drop(columns=categorical_variables, inplace=True, axis=1)
```

```
[33]: data.head()
```

```
[33]:    longitude  latitude  housing_median_age  total_rooms  total_bedrooms \
2      -122.24     37.85           52.0        1467.0         190.0
3      -122.25     37.85           52.0        1274.0         235.0
4      -122.25     37.85           52.0        1627.0         280.0
5      -122.25     37.85           52.0         919.0         213.0
6      -122.25     37.84           52.0        2535.0         489.0

population  households  median_income  median_house_value \
2        496.0       177.0        7.2574        31.420574
3        558.0       219.0        5.6431        31.267608
4        565.0       259.0        3.8462        31.280515
5        413.0       193.0        4.0368        30.130543
6       1094.0       514.0        3.6591        30.627720

ocean_proximity_<1H_OCEAN  ocean_proximity_INLAND  ocean_proximity_ISLAND \
2                  0.0            0.0             0.0
3                  0.0            0.0             0.0
4                  0.0            0.0             0.0
5                  0.0            0.0             0.0
6                  0.0            0.0             0.0

ocean_proximity_NEAR_BAY  ocean_proximity_NEAR_OCEAN
2                  1.0            0.0
3                  1.0            0.0
4                  1.0            0.0
5                  1.0            0.0
6                  1.0            0.0
```

## 4.6 2.6 - Scaling Numerical Variables

### 4.6.1 Feature Scaling

One of the most important transformations to apply to the data is *Feature Scaling*. There are two common ways to get all attributes to have the same scale: **Min-max Scaling** and **Standardization**. Min-max Scaling (or normalization) is the simplest: values are shifted and rescaled, so they end up ranging from 0 to 1. This is done by subtracting the minimum value and dividing by the maximum minus minimum value. Standardization is different, first it subtracts the mean value (so standardized values always have a zero mean), and then it divides by the standard deviation, so that the resulting distribution has unit variance.

Sklearn library provides **MinMaxScaler** for normalization and **StandardScaler** for standardization needs. For more information on `sklearn MinMaxScaler` and `StandardScaler` please visit their respective documentation websites.

So, the data can be normalized, but for interpretability reasons is better to keep the target variable in the original scale, so that is easier to interpret the results.

```
[34]: norm_cols = [col for col in data.columns.tolist() if col not in new_cat_columns
   ↵+ ['median_house_value']]
```

```

norm_data = MinMaxScaler().fit_transform(data[norm_cols])

original_index = data[norm_cols].index

norm_data = pandas.DataFrame(data=norm_data, columns=norm_cols)
norm_data.set_index(original_index, inplace=True)

data[norm_cols] = norm_data[norm_cols]

```

[35]: data.head()

```

[35]:    longitude  latitude  housing_median_age  total_rooms  total_bedrooms \
2    0.213996  0.564293           1.0      0.260630      0.179389
3    0.212982  0.564293           1.0      0.226294      0.222328
4    0.212982  0.564293           1.0      0.289094      0.265267
5    0.212982  0.564293           1.0      0.163138      0.201336
6    0.212982  0.563231           1.0      0.450632      0.464695

population  households  median_income  median_house_value \
2    0.180851     0.191676      0.944748      31.420574
3    0.203595     0.237678      0.719057      31.267608
4    0.206163     0.281490      0.467837      31.280515
5    0.150404     0.209200      0.494485      30.130543
6    0.400220     0.560789      0.441679      30.627720

ocean_proximity_<1H_OCEAN  ocean_proximity_INLAND  ocean_proximity_ISLAND \
2                  0.0          0.0                  0.0
3                  0.0          0.0                  0.0
4                  0.0          0.0                  0.0
5                  0.0          0.0                  0.0
6                  0.0          0.0                  0.0

ocean_proximity_NEAR_BAY  ocean_proximity_NEAR_OCEAN
2                  1.0          0.0
3                  1.0          0.0
4                  1.0          0.0
5                  1.0          0.0
6                  1.0          0.0

```

### 5 3. Exploratory Data Analysis

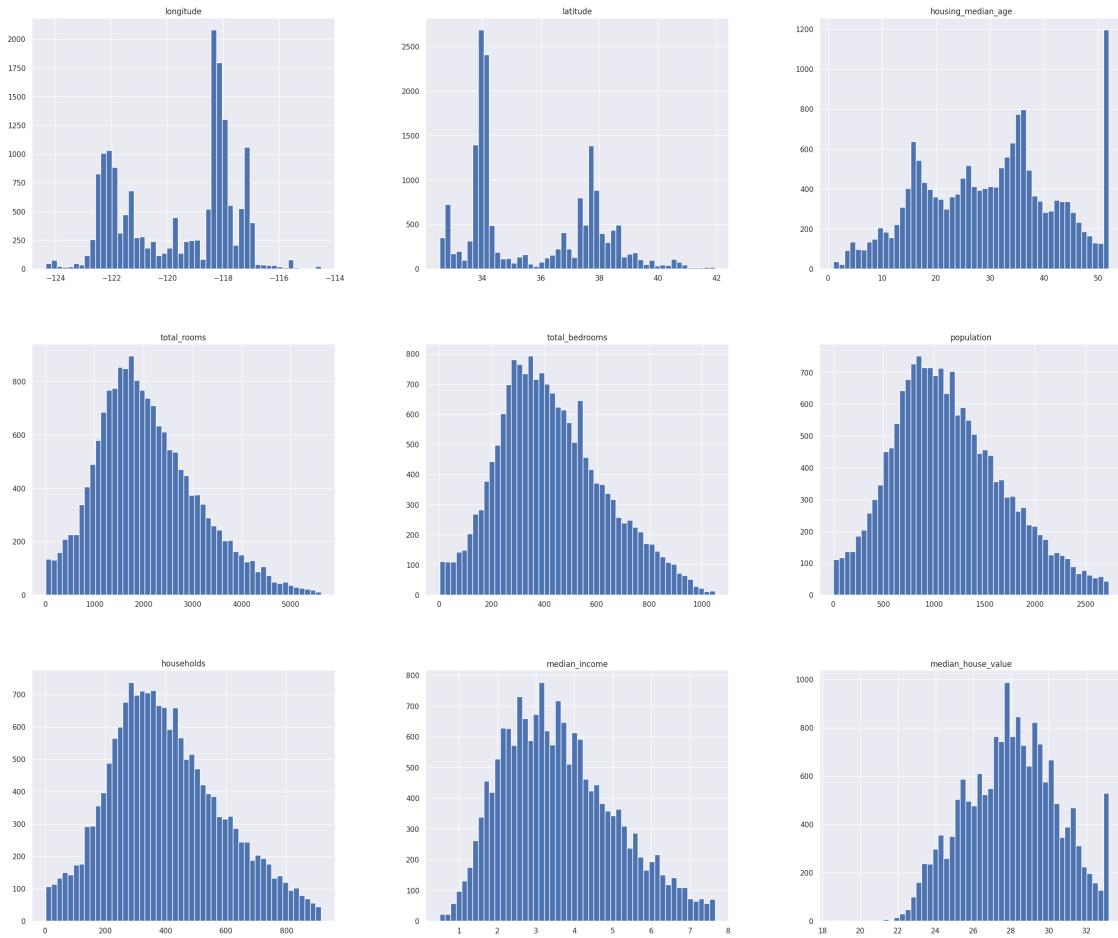
Exploratory Data Analysis (EDA) is the crucial process of using summary statistics and graphical representations to perform preliminary investigations on data to uncover patterns, detect anomalies, test hypotheses, and verify assumptions.

## 5.1 3.1 - Histograms of variables

To have a first look of the data it's useful to plot the histogram of each variable.

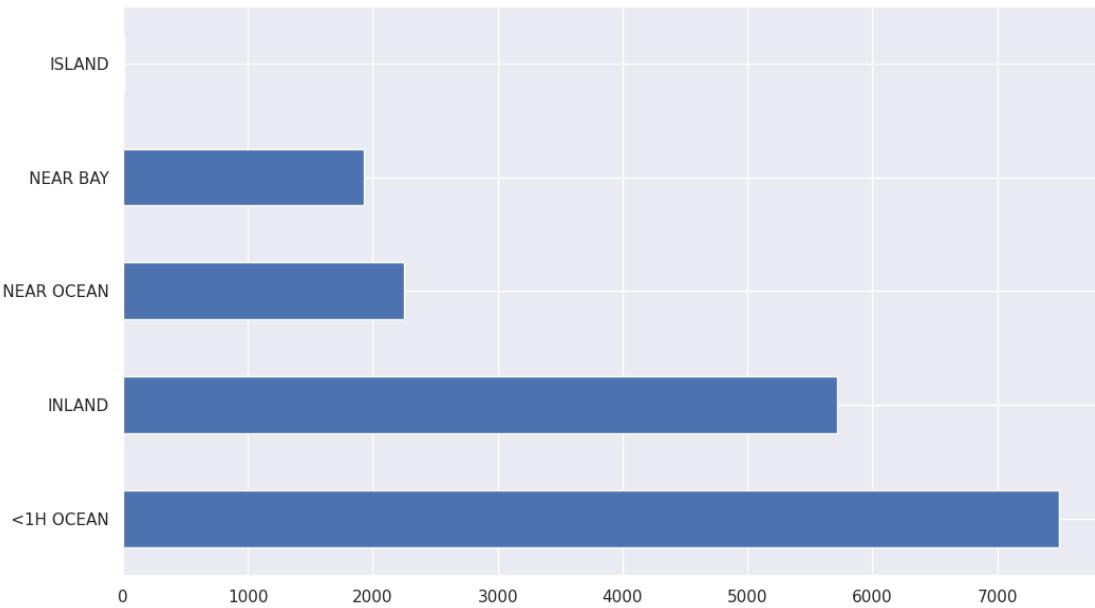
On an overview of the variables it's clear that there are some outliers in the variables `housing_median_age` and `median_house_value`. Also, some variables are skewed, like `total_rooms`, `total_bedrooms`, `population` and `households` or not following normal patterns, such as `longitude` and `latitude`.

```
[36]: data_visualization.hist(bins=50, figsize=(30,25)) # .loc[:,~data_visualization.  
˓→columns.isin(new_cat_columns)]  
pyplot.show();
```



To visualize the `ocean_proximity` variable a horizontal bar plot can be used.

```
[37]: data_visualization.ocean_proximity.value_counts().sort_values(ascending=False).  
˓→plot(kind='barh');
```

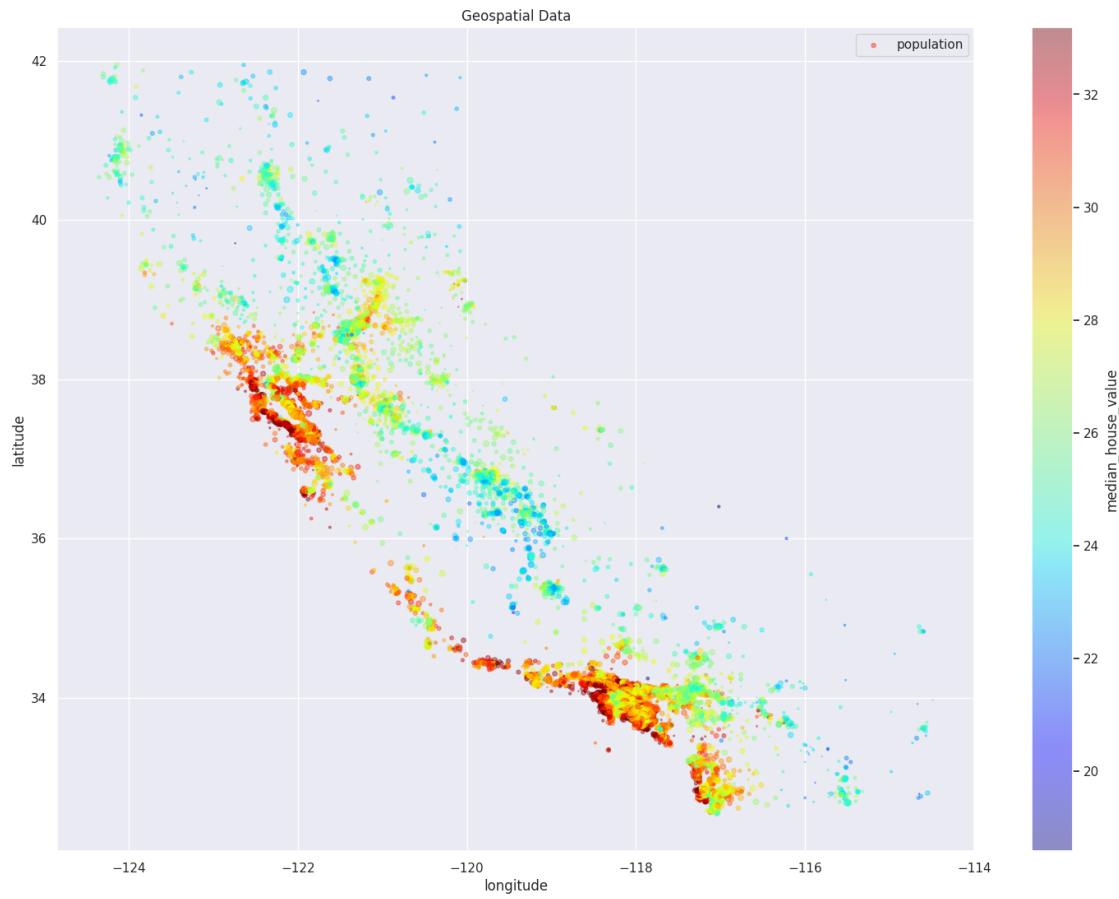


## 5.2 3.2 - Geographical Data

One interesting insight to understand some patterns of the data could be to see the dataset as geographical data, like a scatterplot.

This shows, as it was described previously, that they density of population and the price per geographical point are not normally distributed across the state and the mayor density of population and higher prices are around the major metropolis like the ones surrounding San Francisco, Los Angeles and Sacramento.

```
[38]: data_visualization.plot(kind="scatter", x="longitude", y="latitude", alpha=0.4,
    s=data_visualization["population"]/100, label="population", figsize=(18,13),
    c="median_house_value", cmap=plt.get_cmap("jet"), colorbar=True,
)
plt.title('Geospatial Data');
```



### 5.3 3.3 - Variables Correlation

To see how the variables correlates to the target variable, let's proceed by creating a correlation matrix for the continuous variables, which can show how important the attributes are for the median house value. Also, this matrix can show us if there is any codependent variable.

**Correlation of numerical values** This show the pvalue of the Pearson Correlation Coefficient between the target variable (`median_house_income`) and the rest in order of importance.

```
[39]: corr_matrix = data_visualization.corr(numeric_only=True, method='pearson').
      ↪round(4)
corr_matrix["median_house_value"].sort_values(ascending=False)[1:]
```

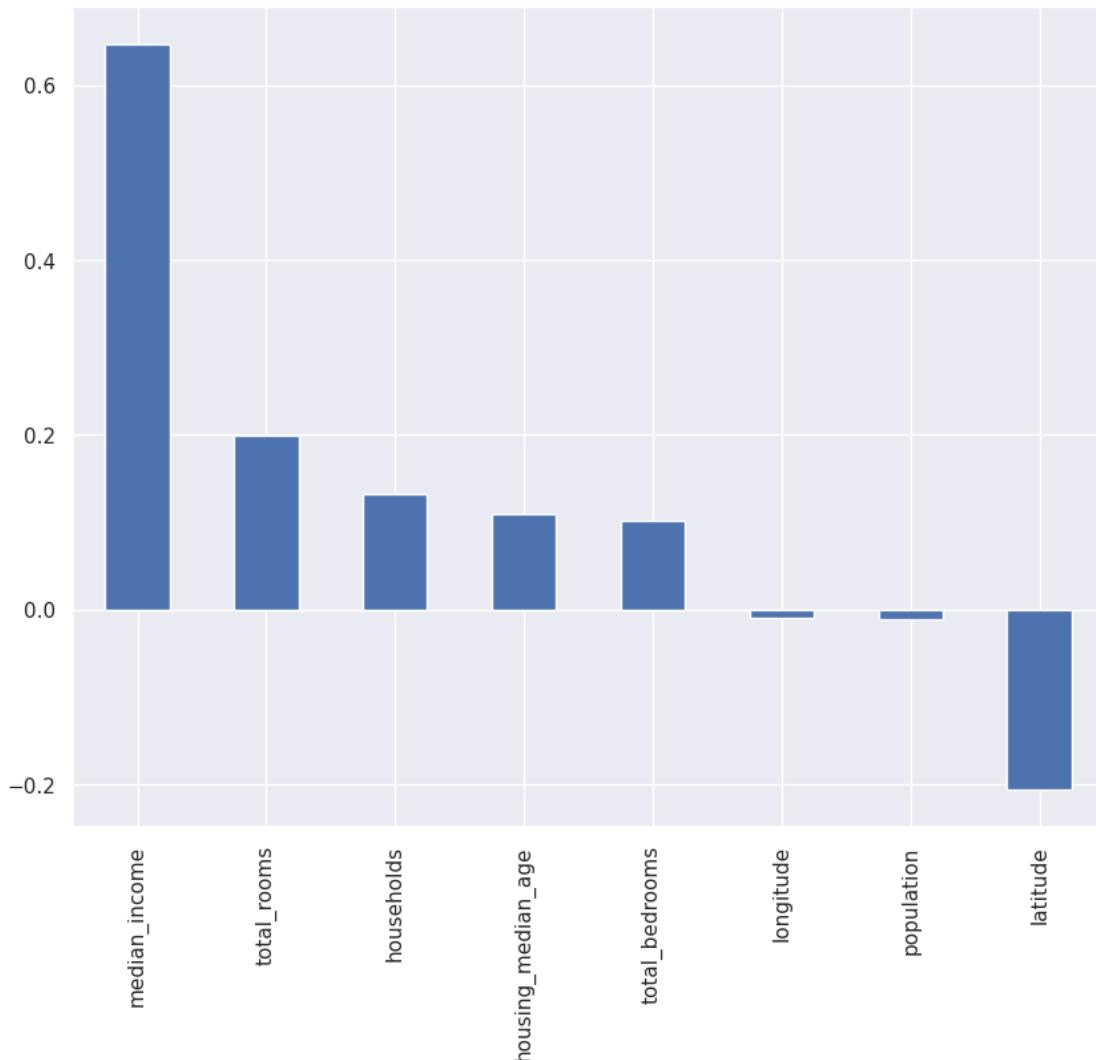
[39]:	median_income	0.6463
	total_rooms	0.1994
	households	0.1312
	housing_median_age	0.1091
	total_bedrooms	0.1014

```

longitude           -0.0102
population         -0.0108
latitude          -0.2067
Name: median_house_value, dtype: float64

```

```
[40]: corr_matrix["median_house_value"].sort_values(ascending=False)[1:].
      plot(kind='bar', figsize=(10, 8));
```

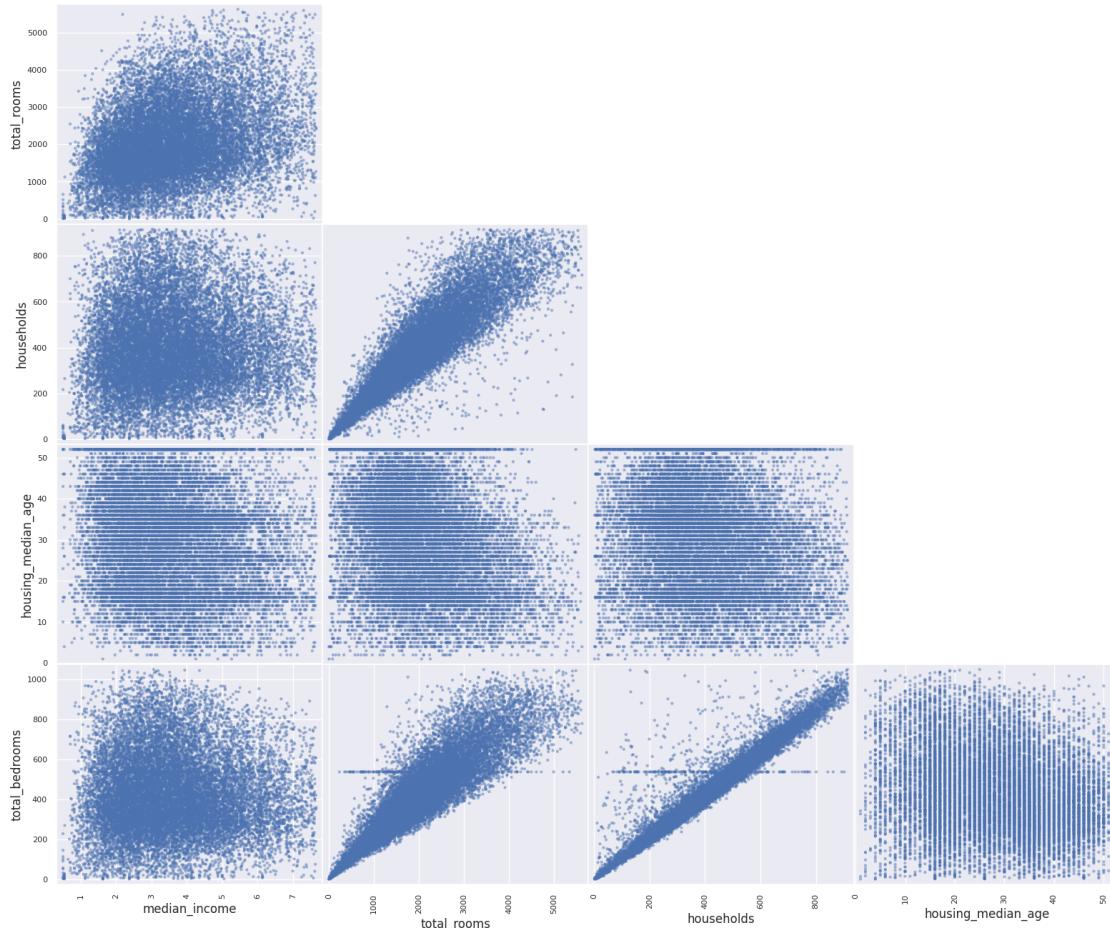


To know if they are statistically significant the variables with a pvalue greater or equal than 0.05 can be selected.

```
[41]: significant_vars = corr_matrix["median_house_value"].
      sort_values(ascending=False)[1:].loc[corr_matrix["median_house_value"]].
      sort_values(ascending=False)[1:] > 0.05].index.values.tolist()
```

**Collinearity Visual Check** To check if there are any collinearity within the independent variables it can be plotted the scatter plot of each variable with the rest of variables to check if there is any clear pattern that could show such a phenomena.

```
[42]: scatter_plots = scatter_matrix(data_visualization[significant_vars],  
    figsize=(24, 20));  
  
for i in range(len(significant_vars)):  
    for j in range(len(significant_vars)):  
        if i-1 < j:  
            scatter_plots[i,j].set_visible(False)  
  
pyplot.show()
```



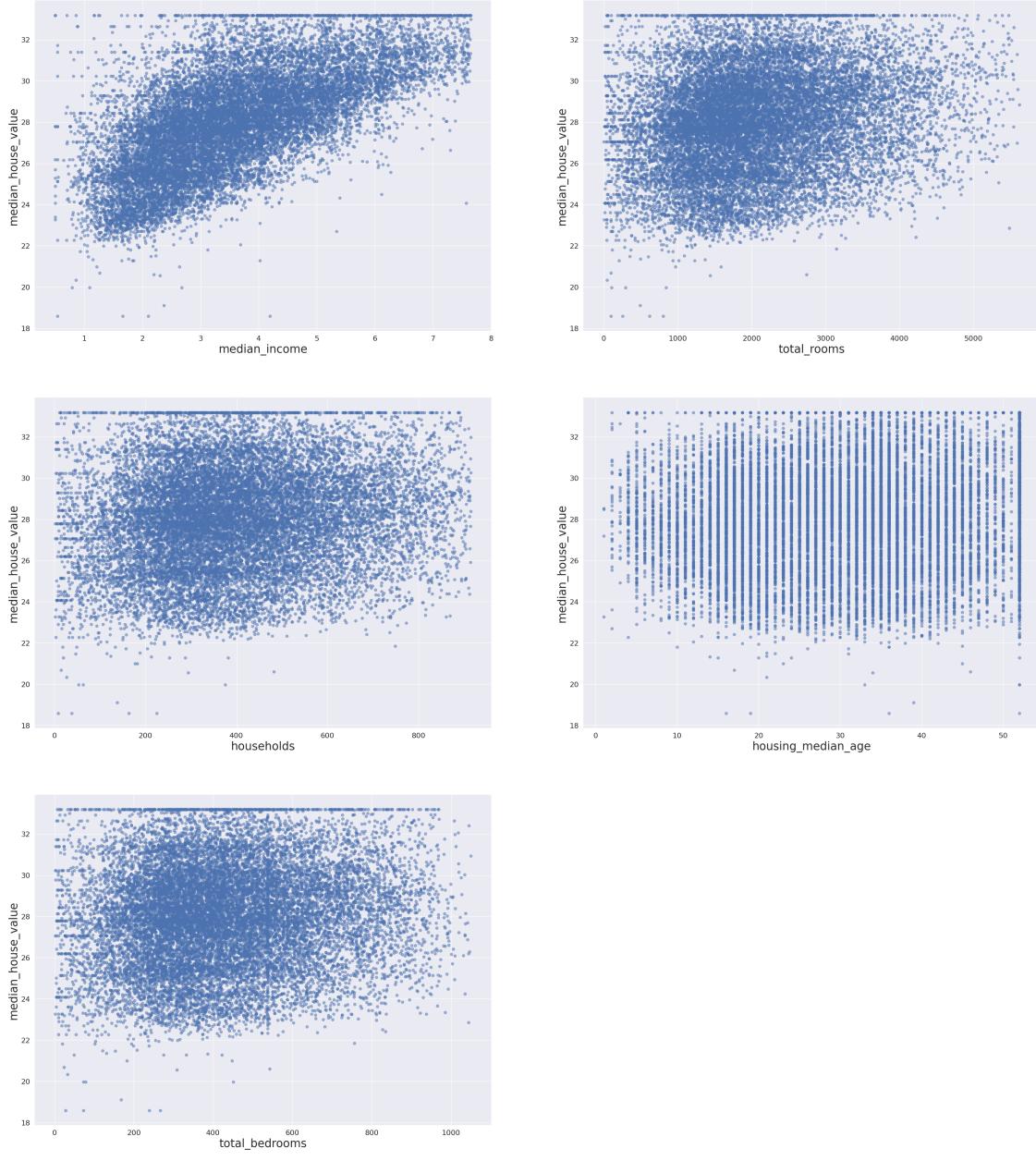
The variable `total_rooms` shows a clear collinearity with the variable `households`. This needs to be treated to produce a quality Machine Learning Modelling, but it's out of the scope of this analysis, so it will be taken into consideration for the next exercises based on this one.

**Bivariate Analysis** Another insightfull visualization is the a bivariate visual analysis of the most statistically significant variables with the target variable.

```
[43]: corr_matrix["median_house_value"].sort_values(ascending=False)[1:]
```

```
[43]: median_income          0.6463
total_rooms                 0.1994
households                  0.1312
housing_median_age          0.1091
total_bedrooms               0.1014
longitude                   -0.0102
population                  -0.0108
latitude                     -0.2067
Name: median_house_value, dtype: float64
```

```
[44]: plot_scatters(data=data_visualization, variables=significant_vars, ↴
                     target='median_house_value')
```



As `corr(method='pearson')` uses Pearson Correlation Coefficient to compute the correlation between continuous variables, so for categorical variables we will need to use other tests, such as **Chi-squared test**.

## 6 4. Hypothesis Testing

Defining hypothesis about the data will provide more insights about it.

The hypothesis is defined in two ways - null hypothesis and alternative hypothesis.

- Null hypothesis is a statistical hypothesis which assumes that the difference in observations

is due to a random factor. It is denoted by

$$H_0$$

- Alternative hypothesis is the opposite of null hypothesis. It assumes that the difference in observations is the result of a real effect. The alternate hypothesis is denoted by

$$H_1$$

After defining the hypothesis, it's needed to set the criteria for a decision, it states the level of significance for a test. It could be 5%, 1% or 0.5%. Based on the level of significance, a decision can be made whether to accept the null hypothesis and reject the alternate, and vice versa.

And then finally evaluate and interpret the result to get to a conclusion.

The `prepared_data` will be used for Hypothesis testing, which has been prepared for this and `original_data` will be used for interpretability reason, like to plot something.

```
[45]: # To not compute all the cells above and save the prepared data for later
      # data_visualization.to_csv(path_or_buf='data/housing_prepared.csv', sep=';', index=True, header=True)
```

```
[46]: import pandas
      import seaborn
      from scipy.stats import ttest_ind
```

```
[47]: prepared_data = pandas.read_csv(filepath_or_buffer='data/housing_prepared.csv', sep=';', header=0, index_col='index')

      original_data = pandas.read_csv(filepath_or_buffer='data/housing.csv', low_memory=False)
```

## 6.1 4.1 - Hypothesis One

It will be proved or disproved that houses near bay or ocean have higher prices compare with inland houses.

### 6.1.1 4.1.1 - Define a sample statistic

It's needed the sample of houses near bay and those which are not near.

```
[48]: near_bay_ocean_houses = prepared_data.loc[prepared_data['ocean_proximity'].isin(['NEAR BAY', 'NEAR OCEAN'])]
      inland_houses = prepared_data.loc[prepared_data['ocean_proximity'] == 'INLAND']
```

### 6.1.2 4.1.2 - Define hypothesis

Let's define the Null and Alternative Hypothesis:

Being,  $\mu_1$  : the mean value of near bay and ocean houses and,  $\mu_2$  : the mean value of inland houses.

$H_0 : \mu_1 \leq \mu_2$  The mean value of near ocean and bay houses is less or equal than the ones inland.  
 $H_1 : \mu_1 > \mu_2$  The mean value of near ocean or bay houses is higher than the ones inland.

The ' $>$ ' sign in the alternate hypothesis indicates the test is *right tailed*. To compare the mean values of near bay and ocean and inland populations, so **t-test** will be used. If **z-values** (calculated from a t-test) fall into the area on the right side of a distribution curve, this would cause us to reject the null hypothesis.

First the mean values of each sample can be checked, but as the target variable was normalized the values lost interpretability, so the original data can be used to just give an idea and visualize it, but for the statistical test it is needed to be done with the normalized target in order to work.

```
[49]: mean_near_oc_bay = original_data.loc[original_data['ocean_proximity'].  
    ↪isin(['NEAR BAY', 'NEAR OCEAN'])].median_house_value.mean()  
mean_inland = original_data.loc[original_data['ocean_proximity'] == 'INLAND'].  
    ↪median_house_value.mean()
```

```
[50]: f' Mean value of houses near bay or ocean: {round(mean_near_oc_bay, 4)}'
```

```
[50]: ' Mean value of houses near bay or ocean: 253959.5202'
```

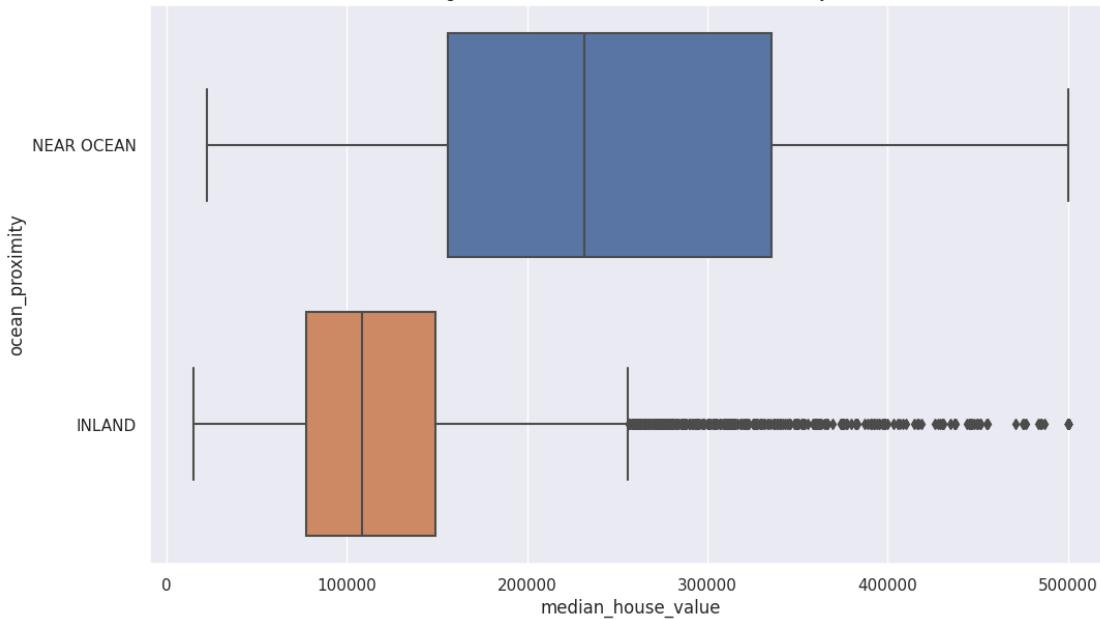
```
[51]: f' Mean value of houses inland: {round(mean_inland, 4)}'
```

```
[51]: ' Mean value of houses inland: 124805.392'
```

Both samples can be plotted by using seaborn **boxplot()** function. It is always useful to have a visual representation of the data which is being tested.

```
[52]: data2plot = original_data.copy()  
data2plot.ocean_proximity = original_data.ocean_proximity.str.replace('NEAR  
    ↪BAY', 'NEAR OCEAN')  
data2plot = data2plot.loc[data2plot.ocean_proximity.isin(['NEAR OCEAN',  
    ↪'INLAND'])]  
  
seaborn.boxplot(x=data2plot.median_house_value, y=data2plot.ocean_proximity,  
    ↪data=data2plot).set(title='Fig 1: Median House Value vs Ocean Proximity');
```

Fig 1: Median House Value vs Ocean Proximity



By checking the mean and visualizing the data is possible to make an assumption if to reject or fail to reject the null hypothesis, but to prove it rigorously let's test the hypothesis by a significance test.

### 6.1.3 4.1.3 - Testing hypothesis by significance tests

To set the criteria for a decision, for this test the level of significance will be 5%. Based on the level of significance, a decision can be made whether to accept the null hypothesis and reject the alternate, and vise versa.

To calculate the *t-value* and *p-value* of the *t-test* for both samples using the data prepared with the normalized target it can be used the method `ttest_ind()` from `scipy.stats`.

```
[53]: alpha = 0.05
t_value_1, p_value_1 = ttest_ind(a=prepared_data.loc[prepared_data.
    ↪ocean_proximity == 'NEAR OCEAN'].median_house_value,
    b=prepared_data.loc[prepared_data.ocean_proximity
    ↪== 'INLAND'].median_house_value)
p_value_onetail = p_value_1/2
print(f't-value: {t_value_1}, p-value: {p_value_1}, p-value-onetail: '
    ↪{p_value_onetail}')
```

t-value: 56.92941213083418, p-value: 0.0, p-value-onetail: 0.0

### 6.1.4 4.1.4 - Evaluate and interpret results

Next, although optional, it is useful to print ‘if/else’ statements to make our conclusions about the hypothesis.

```
[54]: msg1 = f"Conclusion: since p_value {p_value_1} is "+"{}"+ f" than alpha {alpha}"  
msg2 = "{} the null hypothesis that the mean value of near ocean and bay houses  
is {} than the ones inland."  
  
if p_value_1 < alpha:  
    print(msg1.format('less'))  
    print(msg2.format("Reject", "less or equal"))  
  
else:  
    print(msg1.format('greater'))  
    print(msg2.format("Fail to reject", "greater"))
```

Conclusion: since p\_value 0.0 is less than alpha 0.05  
 Reject the null hypothesis that the mean value of near ocean and bay houses is  
 less or equal than the ones inland.

## 6.2 4.2 - Hypothesis 2

It will be proved or disproved that houses higher populated areas have higher prices compare with the ones in low populated areas.

### 6.2.1 4.2.1 - Define a sample statistic

To define the sample to be tested it's needed the sample of houses in high populated areas and the one in low populated areas.

```
[55]: median_population = original_data.population.median()  
low_population_houses = original_data.loc[original_data.population <=  
    ↪median_population]  
high_population_houses = original_data.loc[original_data.population >  
    ↪median_population]
```

### 6.2.2 4.2.2 - Define hypothesis

Let's define the Null and Alternative Hypothesis:

Being,  $\mu_1$  : the mean value of high population area houses and,  $\mu_2$  : the mean value of low population areas

$H_0 : \mu_1 \leq \mu_2$  The mean value of houses in high populated areas is less or equal than the ones low populated areas.  $H_1 : \mu_1 > \mu_2$  The mean value of houses in high populated areas is higher than the ones in low populated areas.

The ‘>’ sign in the alternate hypothesis indicates the test is *right tailed*. To compare the mean values of low and high populated populations, so **t-test** will be used. If **z-values** (calculated from a t-test) fall into the area on the right side of a distribution curve, this would cause us to reject the null hypothesis.

As in the previous hypothesis, first the mean values of each sample can be checked, but as the target variable was normalized the values lost interpretability, so the original data can be used

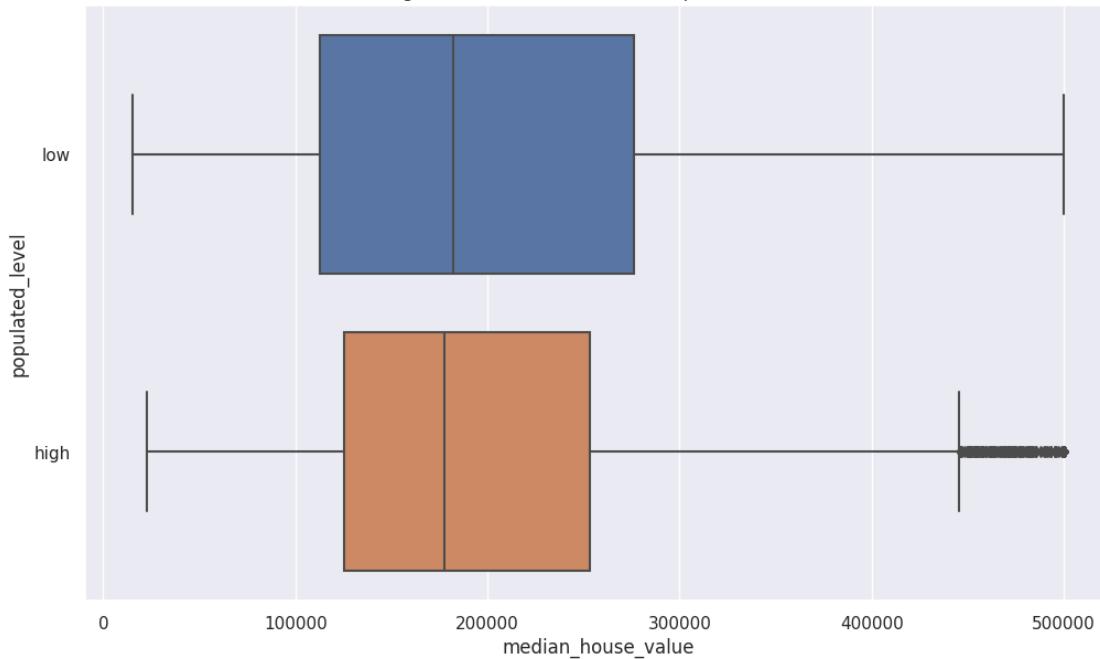
to just gave an idea and visualize it, but for the statistical test it is needed to be done with the normalized target in order to work.

```
[56]: mean_high_population = high_population_houses.median_house_value.mean()  
mean_low_population = low_population_houses.median_house_value.mean()  
  
[57]: f' Mean value of houses in high populated areas: {round(mean_high_population, 4)}'  
  
[57]: ' Mean value of houses in high populated areas: 201573.4199'  
  
[58]: f' Mean value of houses in low populated areas: {round(mean_low_population, 4)}'  
  
[58]: ' Mean value of houses in low populated areas: 212133.0978'
```

Both samples can be plotted by using seaborn `boxplot()` function. It is always useful to have a visual representation of the data which is being tested.

```
[59]: def populated_level(x):  
    if x <= median_population:  
        return 'low'  
    else:  
        return 'high'  
  
data2plot_pop = original_data.copy()  
data2plot_pop['populated_level'] = data2plot_pop.population.  
apply(populated_level)  
  
seaborn.boxplot(x=data2plot_pop.median_house_value, y=data2plot_pop.  
populated_level, data=data2plot_pop).set(title='Fig 2: Median House Value vs  
Populated Level');
```

Fig 2: Median House Value vs Populated Level



### 6.2.3 4.2.3 - Testing hypothesis by significance tests

To set the criteria for a decision, for this test the level of significance will be 5%. Based on the level of significance, a decision can be made whether to accept the null hypothesis and reject the alternate, and vice versa. To calculate the t-value and p-value of the t-test for both samples using the data prepared with the normalized target it can be used the method `ttest_ind()` from `scipy.stats`.

```
[60]: alpha_2 = 0.05
t_value_2, p_value_2 = ttest_ind(a=prepared_data.loc[prepared_data.population >
    ↪median_population].median_house_value,
                                    b=prepared_data.loc[prepared_data.population <=
    ↪median_population].median_house_value)
p_value_onetail_2 = p_value_2/2
print(f't-value: {t_value_2}, p-value: {p_value_2}, p-value-onetail: '
    ↪{p_value_onetail_2}')
```

t-value: -3.2799648287486387, p-value: 0.0010402411366680733, p-value-onetail:  
0.0005201205683340366

### 6.2.4 4.2.4 - Evaluate and interpret results

```
[61]: msg1 = f"Conclusion: since p_value {p_value_2} is "+'{}'+ f" than alpha_2"
    ↪{alpha_2}"
msg2 = "{} the null hypothesis that the mean value of houses in high populated_
    ↪areas is {} than the ones in low populated areas."
```

```

if p_value_2 < alpha_2:
    print(msg1.format('less'))
    print(msg2.format("Reject", "less or equal"))

else:
    print(msg1.format('greater'))
    print(msg2.format("Fail to reject", "greater"))

```

Conclusion: since `p_value` 0.0010402411366680733 is less than `alpha` 0.05  
 Reject the null hypothesis that the mean value of houses in high populated areas  
 is less or equal than the ones in low populated areas.

### 6.3 4.3 - Hypothesis 3

It will be proved or disproved that areas with newer median age houses with less or equal than 10 years have higher value than house with more or equal than 20 years of median age.

#### 6.3.1 4.3.1 - Define a sample statistic

To define the sample to be tested it's needed the sample of houses with less than 10 years and more than 20 years of median age.

```
[62]: newer_houses = original_data.loc[original_data.housing_median_age <= 10]
older_houses = original_data.loc[original_data.housing_median_age > 20]
```

#### 6.3.2 4.3.2 - Define hypothesis

Let's define the Null and Alternative Hypothesis:

Being,  $\mu_1$  : the mean value house are with median age lower or equal than 10 and,  $\mu_2$  : the mean value of houses with median age higher than 20.

$H_0 : \mu_1 \leq \mu_2$  The mean value of houses with meadian age lower or equal than 10 is less or equal than the ones higher than 20.  $H_1 : \mu_1 > \mu_2$  The mean value of houses with meadian age lower or equal than 10 is higher than the ones higher than 20.

The ' $>$ ' sign in the alternate hypothesis indicates the test is *right tailed*. To compare the mean values of the value of newer and older houses, **t-test** will be used. If **z-values** (calculated from a t-test) fall into the area on the right side of a distribution curve, this would cause us to reject the null hypothesis.

As in the previous hypothesis, first the mean values of each sample can be checked, but as the target variable was normalized the values lost interpretability, so the original data can be used to just gave an idea and visualize it, but for the statistical test it is needed to be done with the normalized target in order to work.

```
[63]: mean_newer_houses = newer_houses.median_house_value.mean()
mean_old_houses = older_houses.median_house_value.mean()
```

```

print(f' Mean value of houses with median age lower or equal than 10: {round(mean_newer_houses, 4)}')
print(f' Mean value of houses older than 20 years: {round(mean_older_houses, 4)}')

```

Mean value of houses with median age lower or equal than 10: 200263.2549  
 Mean value of houses older than 20 years: 212737.7854

Both samples can be plotted by using seaborn ‘boxplot()’ function. It is always useful to have a visual representation of the data which is being tested.

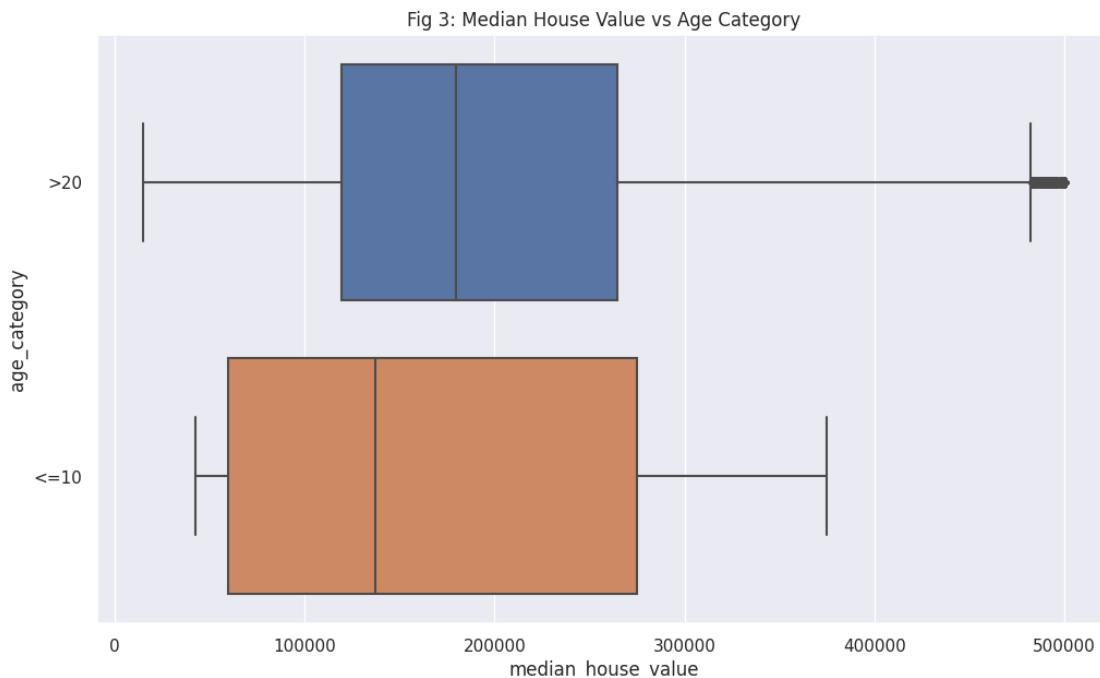
```

[64]: def age_category(x):
    if x <= 10:
        return '<=10'
    else:
        return '>20'

data2plot_pop = original_data.copy()
data2plot_pop['age_category'] = data2plot_pop.population.apply(age_category)

seaborn.boxplot(x=data2plot_pop.median_house_value, y=data2plot_pop.
    ↪age_category, data=data2plot_pop).set(title='Fig 3: Median House Value vs
    ↪Age Category');

```



### 6.3.3 4.2.3 - Testing hypothesis by significance tests

To set the criteria for a decision, for this test the level of significance will be 5%. Based on the level of significance, a decision can be made whether to accept the null hypothesis and reject the alternate, and vice versa. To calculate the t-value and p-value of the t-test for both samples using the data prepared with the normalized target it can be used the method `ttest_ind()` from `scipy.stats`.

```
[65]: alpha_3 = 0.05
t_value_3, p_value_3 = ttest_ind(a=prepared_data.loc[prepared_data.
    ↪housing_median_age <= 10].median_house_value,
                                    b=prepared_data.loc[prepared_data.
    ↪housing_median_age > 20].median_house_value)
p_value_onetail_3 = p_value_3/2
print(f't-value: {t_value_3}, p-value: {p_value_3}, p-value-onetail: '
    ↪{p_value_onetail_3}')
```

t-value: -3.674609119652722, p-value: 0.00023911926135748468, p-value-onetail:  
0.00011955963067874234

### 6.3.4 4.3.4 - Evaluate and interpret results

```
[66]: msg1 = f"Conclusion: since p_value {p_value_3} is "+'{}'+ f" than alpha"
    ↪{alpha_3}"
msg2 = "{} the null hypothesis that the mean value of houses with median house
    ↪age less or equal than 10 is {} than the ones older than 20 years."
if p_value_3 < alpha_3:
    print(msg1.format('less'))
    print(msg2.format("Reject", "less or equal"))

else:
    print(msg1.format('greater'))
    print(msg2.format("Fail to reject", "greater"))
```

Conclusion: since p\_value 0.00023911926135748468 is less than alpha 0.05  
Reject the null hypothesis that the mean value of houses with median house age  
less or equal than 10 is less or equal than the ones older than 20 years.

## 7 5. Next steps and Conclusions

### 7.1 5.1 - Next steps

This exercise can be used as the base of a future machine learning modeling exercise. Also, some points could be dived deeper like in the correlation of variables which show a clear case of collinearity of the variable `total_rooms` with `households`, new variables could be derived from these ones and teament or derivation of variables from geopraphical data.

## 7.2 5.2 - Conclusions

The purpose of exploratory analysis, therefore this exercise, is to help look at data before making any assumptions. It can help identify obvious errors, as well as better understand patterns within the data, detect outliers or anomalous events, find interesting relations among the variables.

Once this analysis is complete and insights are drawn, its features can then be used for more sophisticated data analysis or modeling, including machine learning.

The data used in this exercise had a good quality in terms of consistency and completeness.

## 7.3 Author

Author: Jose Pena

Github: JoseJuan98

## 7.4 Change Log

Date (YYYY-MM-DD)	Version	Changed By	Change Description
2022-11-07	1.0	Jose	First version