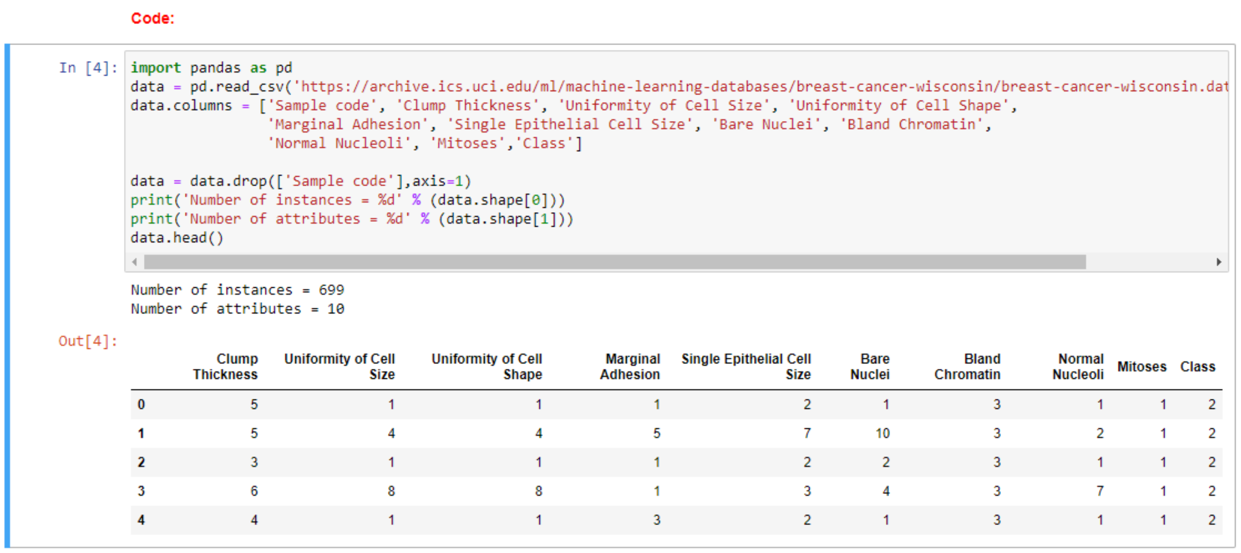
1. Data Quality Issues: We need to make sure we have good data, so we start by displaying the first 5 data points, as well as how many rows and columns we have.



Code:

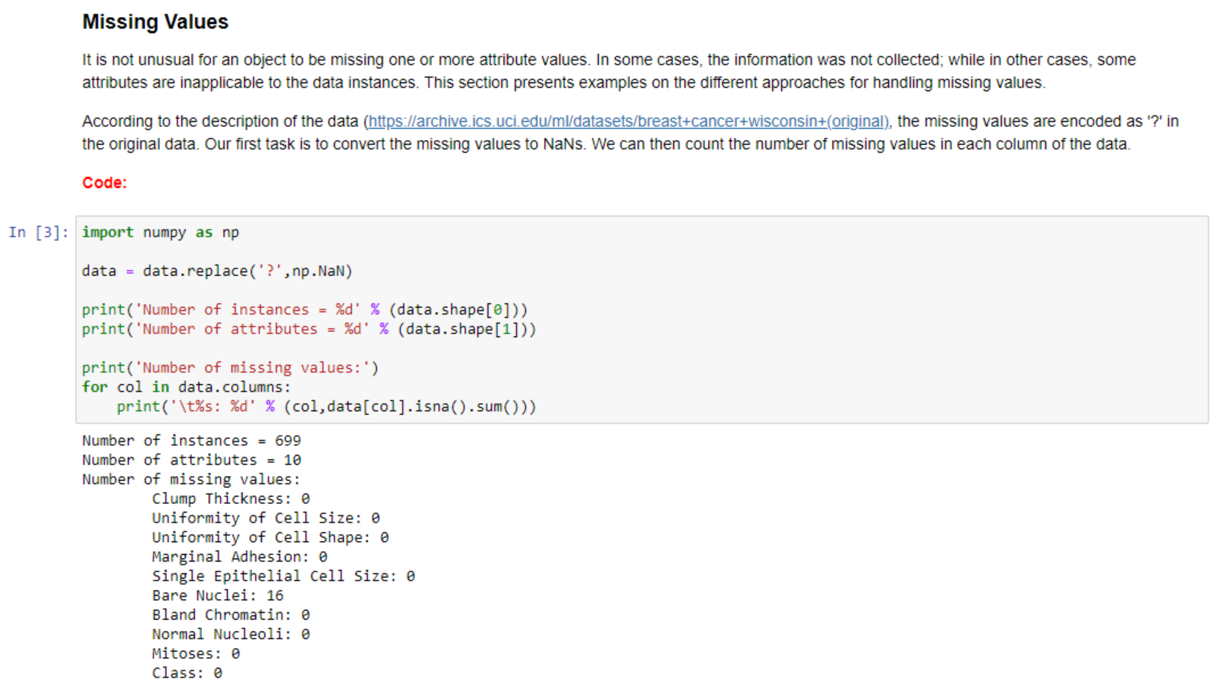
```
In [4]: import pandas as pd
        data = pd.read_csv('https://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wisconsin/breast-cancer-wisconsin.dat
        data.columns = ['Sample code', 'Clump Thickness', 'Uniformity of Cell Size', 'Uniformity of Cell Shape',
                        'Marginal Adhesion', 'Single Epithelial Cell Size', 'Bare Nuclei', 'Bland Chromatin',
                        'Normal Nucleoli', 'Mitoses','Class']

        data = data.drop(['Sample code'],axis=1)
        print('Number of instances = %d' % (data.shape[0]))
        print('Number of attributes = %d' % (data.shape[1]))
        data.head()
```

```
Number of instances = 699
Number of attributes = 10
```

Out[4]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
0	5	1	1	1	2	1	3	1	1	2
1	5	4	4	5	7	10	3	2	1	2
2	3	1	1	1	2	2	3	1	1	2
3	6	8	8	1	3	4	3	7	1	2
4	4	1	1	3	2	1	3	1	1	2

2. Missing Values: In order to properly analyze our data, set we need to determine where our missing data is. Here, the code determines how many missing values each column contains.



Missing Values

It is not unusual for an object to be missing one or more attribute values. In some cases, the information was not collected; while in other cases, some attributes are inapplicable to the data instances. This section presents examples on the different approaches for handling missing values.

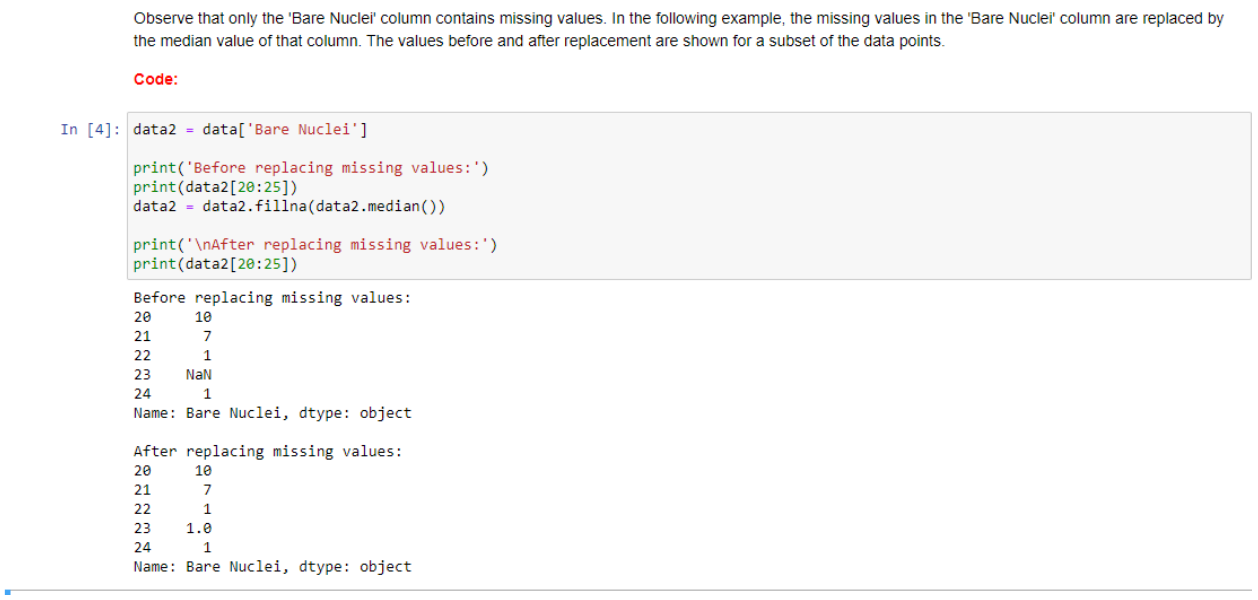
According to the description of the data (https://archive.ics.uci.edu/ml/datasets/breast+cancer+wisconsin+(original), the missing values are encoded as '?' in the original data. Our first task is to convert the missing values to NaNs. We can then count the number of missing values in each column of the data.

Code:

```
In [3]: import numpy as np

        data = data.replace('?',np.NaN)

        print('Number of instances = %d' % (data.shape[0]))
        print('Number of attributes = %d' % (data.shape[1]))

        print('Number of missing values:')
        for col in data.columns:
            print('\t%s: %d' % (col,data[col].isna().sum()))
```

```
Number of instances = 699
Number of attributes = 10
Number of missing values:
        Clump Thickness: 0
        Uniformity of Cell Size: 0
        Uniformity of Cell Shape: 0
        Marginal Adhesion: 0
        Single Epithelial Cell Size: 0
        Bare Nuclei: 16
        Bland Chromatin: 0
        Normal Nucleoli: 0
        Mitoses: 0
        Class: 0
```

3. Once the columns with missing values is determined, the missing values in those columns are replaced with the median value of that column to help prevent inaccurate data.



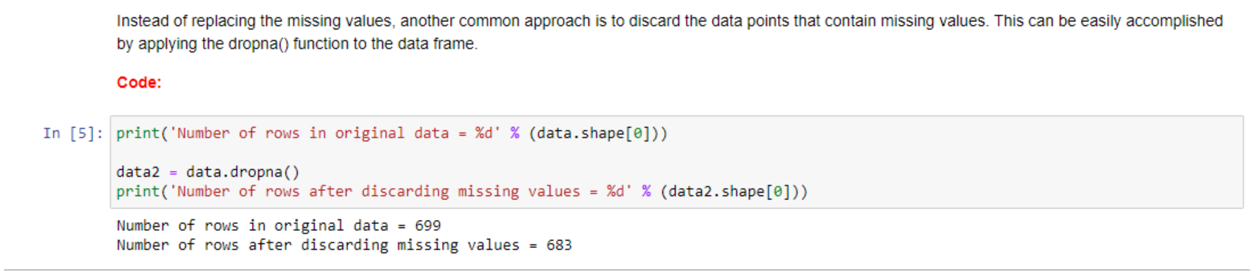
Observe that only the 'Bare Nuclei' column contains missing values. In the following example, the missing values in the 'Bare Nuclei' column are replaced by the median value of that column. The values before and after replacement are shown for a subset of the data points.

Code:

```
In [4]: data2 = data['Bare Nuclei']

        print('Before replacing missing values:')
        print(data2[20:25])
        data2 = data2.fillna(data2.median())

        print('\nAfter replacing missing values:')
        print(data2[20:25])
```

```
Before replacing missing values:
20     10
21      7
22      1
23    NaN
24      1
Name: Bare Nuclei, dtype: object

After replacing missing values:
20     10
21      7
22      1
23    1.0
24      1
Name: Bare Nuclei, dtype: object
```

4. Instead of replacing the missing values with the median of the particular column, we can also just drop the entire row.



Instead of replacing the missing values, another common approach is to discard the data points that contain missing values. This can be easily accomplished by applying the dropna() function to the data frame.

Code:

```
In [5]: print('Number of rows in original data = %d' % (data.shape[0]))

        data2 = data.dropna()
        print('Number of rows after discarding missing values = %d' % (data2.shape[0]))
```

```
Number of rows in original data = 699
Number of rows after discarding missing values = 683
```

5. Here, boxplots are generated to help find the columns that have outliers. Because one of the columns vales are stored as string, we need to convert it to numeric in order for it to show up on the boxplot.

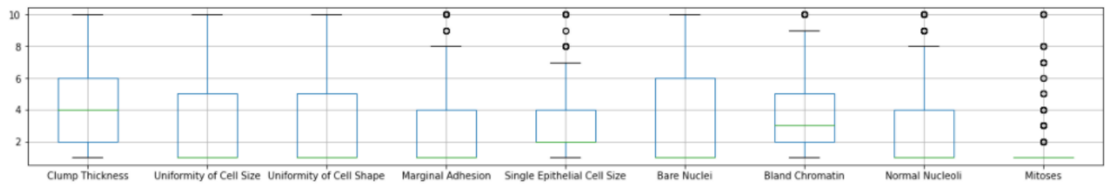
Outliers

Outliers are data instances with characteristics that are considerably different from the rest of the dataset. In the example code below, we will draw a boxplot to identify the columns in the table that contain outliers. Note that the values in all columns (except for 'Bare Nuclei') are originally stored as 'int64' whereas the values in the 'Bare Nuclei' column are stored as string objects (since the column initially contains strings such as '?' for representing missing values). Thus, we must convert the column into numeric values first before creating the boxplot. Otherwise, the column will not be displayed when drawing the boxplot.

Code:

```
In [6]: %matplotlib inline

        data2 = data.drop(['Class'],axis=1)
        data2['Bare Nuclei'] = pd.to_numeric(data2['Bare Nuclei'])
        data2.boxplot(figsize=(20,3))
```

```
Out[6]: <AxesSubplot:>
```



6. Here we compute the Z-score so we can see which values we need to discard.

The boxplots suggest that only 5 of the columns (Marginal Adhesion, Single Epithelial Cell Size, Bland Cromatin, Normal Nucleoli, and Mitoses) contain abnormally high values. To discard the outliers, we can compute the Z-score for each attribute and remove those instances containing attributes with abnormally high or low Z-score (e.g., if Z > 3 or Z <= -3).

Code:

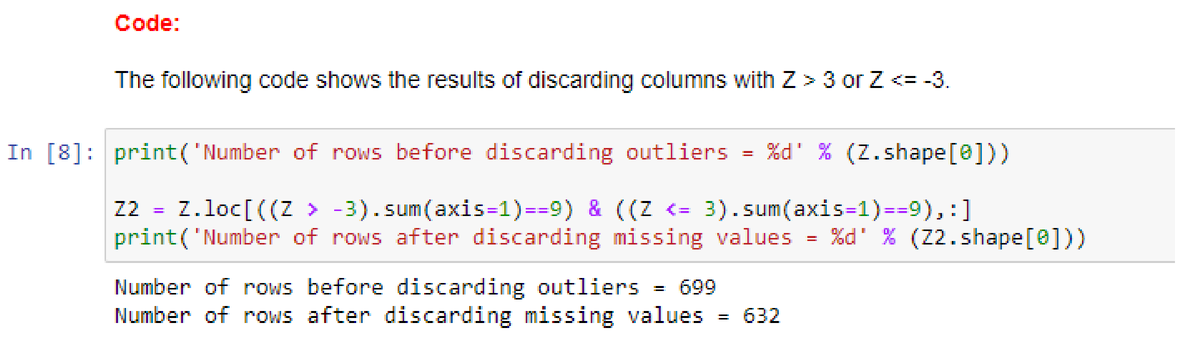
The following code shows the results of standardizing the columns of the data. Note that missing values (NaN) are not affected by the standardization process.

```
In [7]: Z = (data2-data2.mean())/data2.std()
        Z[20:25]
```

Out[7]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses
20	0.917080	-0.044070	-0.406284	2.519152	0.805662	1.771569	0.640688	0.371049	1.405526
21	1.982519	0.611354	0.603167	0.067638	1.257272	0.948266	1.460910	2.335921	-0.343666
22	-0.503505	-0.699494	-0.742767	-0.632794	-0.549168	-0.698341	-0.589645	-0.611387	-0.343666
23	1.272227	0.283642	0.603167	-0.632794	-0.549168	NaN	1.460910	0.043570	-0.343666
24	-1.213798	-0.699494	-0.742767	-0.632794	-0.549168	-0.698341	-0.179534	-0.611387	-0.343666

7. In this code snippet, the Z-score is used to discard the rows that have outliers. Discarding the outliers has made a huge difference in the number of rows in our dataframe.



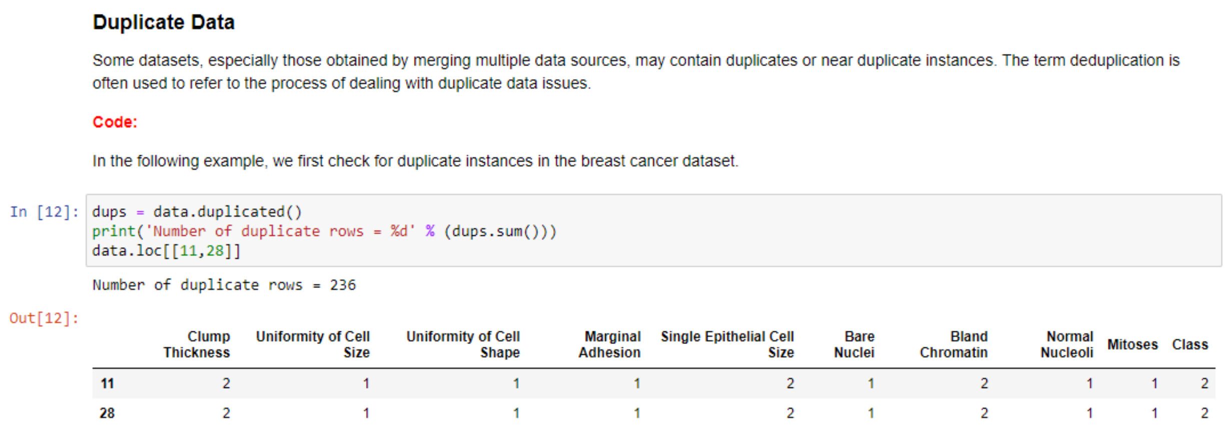
Code:

The following code shows the results of discarding columns with Z > 3 or Z <= -3.

```
In [8]: print('Number of rows before discarding outliers = %d' % (Z.shape[0]))

        Z2 = Z.loc[((Z > -3).sum(axis=1)==9) & ((Z <= 3).sum(axis=1)==9),:]
        print('Number of rows after discarding missing values = %d' % (Z2.shape[0]))
```

```
Number of rows before discarding outliers = 699
Number of rows after discarding missing values = 632
```

8. Another potential problem in dealing with data is duplicates. Here we check to see how many duplicate rows exist in our data.



Duplicate Data

Some datasets, especially those obtained by merging multiple data sources, may contain duplicates or near duplicate instances. The term deduplication is often used to refer to the process of dealing with duplicate data issues.

Code:

In the following example, we first check for duplicate instances in the breast cancer dataset.

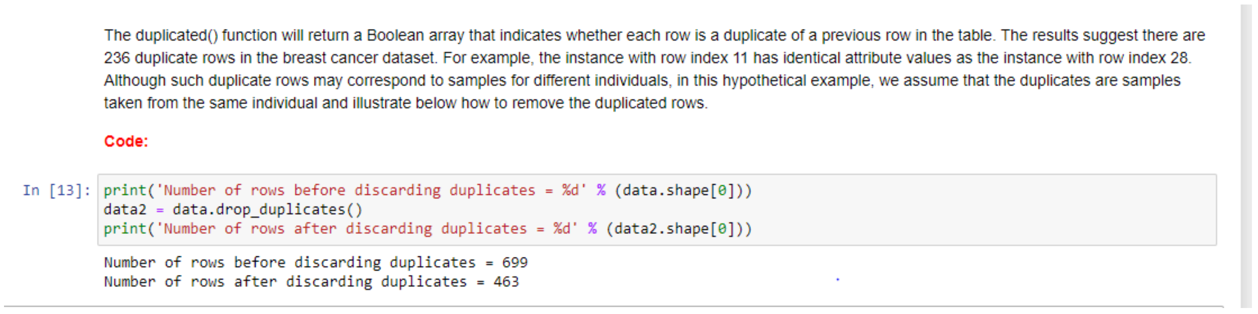
```
In [12]: dups = data.duplicated()
         print('Number of duplicate rows = %d' % (dups.sum()))
         data.loc[[11,28]]
```

```
Number of duplicate rows = 236
```

Out[12]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
11	2	1	1	1	2	1	2	1	1	2
28	2	1	1	1	2	1	2	1	1	2

9. The code below uses a function to drop the duplicate rows



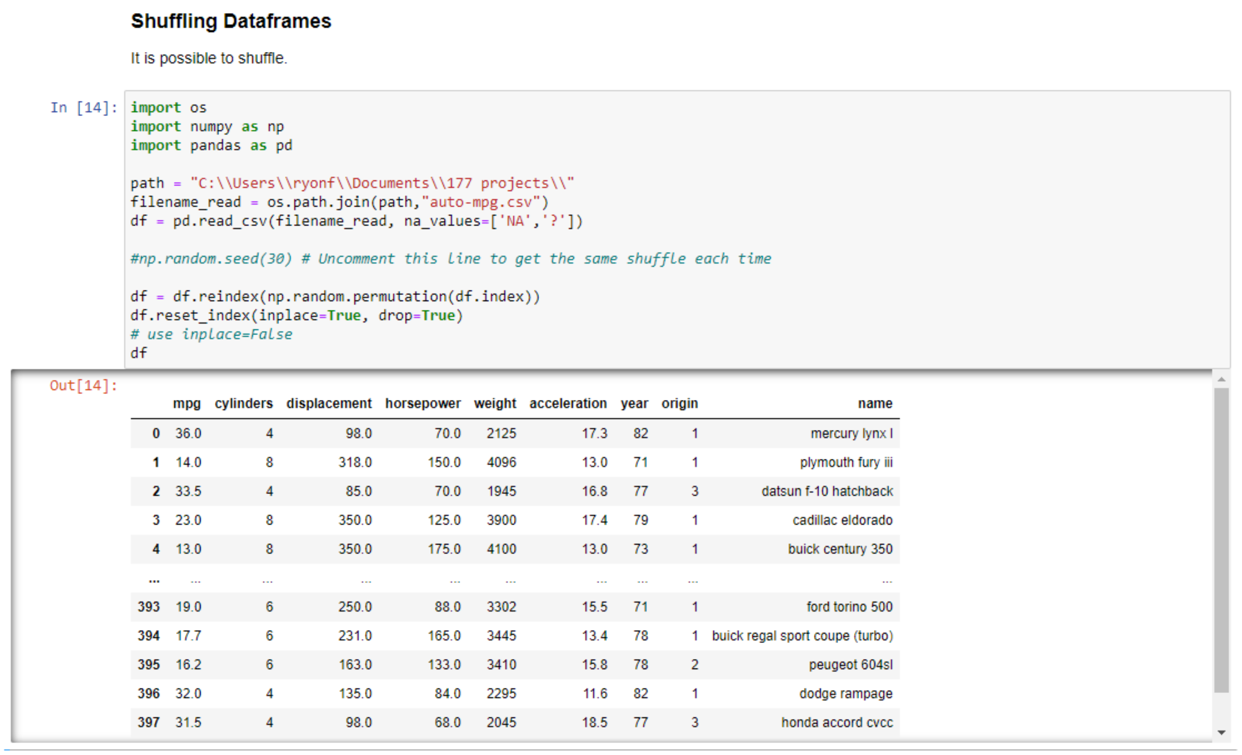
The duplicated() function will return a Boolean array that indicates whether each row is a duplicate of a previous row in the table. The results suggest there are 236 duplicate rows in the breast cancer dataset. For example, the instance with row index 11 has identical attribute values as the instance with row index 28. Although such duplicate rows may correspond to samples for different individuals, in this hypothetical example, we assume that the duplicates are samples taken from the same individual and illustrate below how to remove the duplicated rows.

Code:

```
In [13]: print('Number of rows before discarding duplicates = %d' % (data.shape[0]))
         data2 = data.drop_duplicates()
         print('Number of rows after discarding duplicates = %d' % (data2.shape[0]))
```

```
Number of rows before discarding duplicates = 699
Number of rows after discarding duplicates = 463
```

10. It is also important to shuffle the original set-in order to minimize variance, in the below code that is what's done.



Shuffling Dataframes

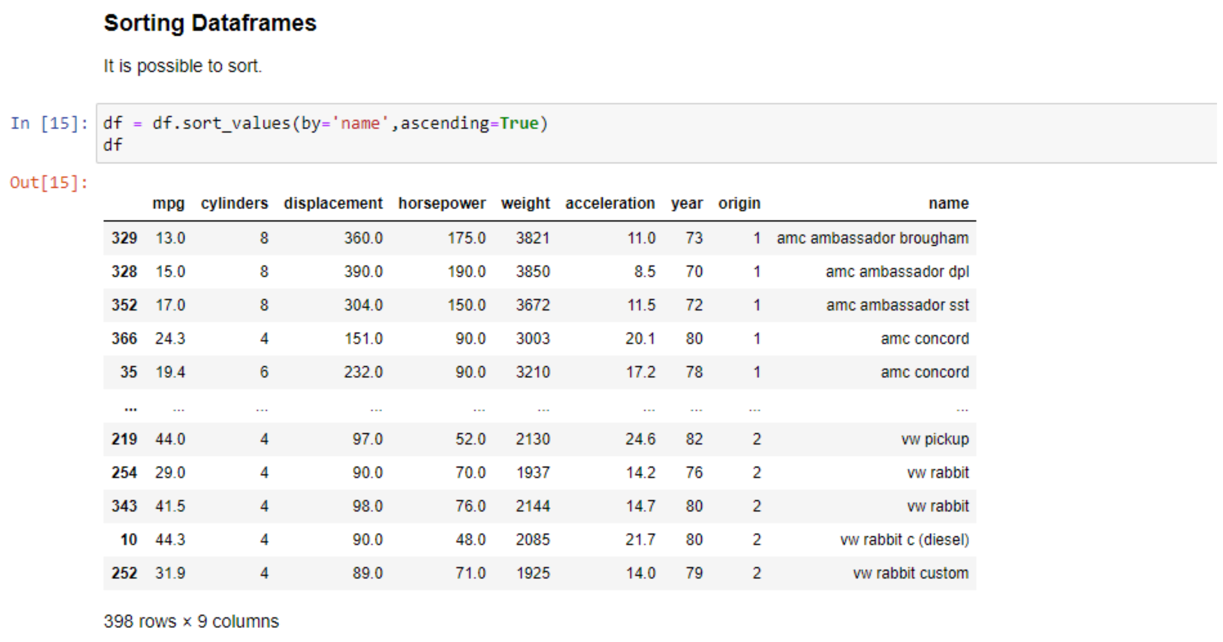
It is possible to shuffle.

In [14]:
```python
import os
import numpy as np
import pandas as pd

path = "C:\\Users\\ryonf\\Documents\\177 projects\\"
filename_read = os.path.join(path,"auto-mpg.csv")
df = pd.read_csv(filename_read, na_values=['NA','?'])

#np.random.seed(30) # Uncomment this line to get the same shuffle each time

df = df.reindex(np.random.permutation(df.index))
df.reset_index(inplace=True, drop=True)
# use inplace=False
df
```

Out[14]:

	mpg	cylinders	displacement	horsepower	weight	acceleration	year	origin	name
0	36.0	4	98.0	70.0	2125	17.3	82	1	mercury lynx l
1	14.0	8	318.0	150.0	4096	13.0	71	1	plymouth fury iii
2	33.5	4	85.0	70.0	1945	16.8	77	3	datsun f-10 hatchback
3	23.0	8	350.0	125.0	3900	17.4	79	1	cadillac eldorado
4	13.0	8	350.0	175.0	4100	13.0	73	1	buick century 350
...	...	...	...	...	...	...	...	...	...
393	19.0	6	250.0	88.0	3302	15.5	71	1	ford torino 500
394	17.7	6	231.0	165.0	3445	13.4	78	1	buick regal sport coupe (turbo)
395	16.2	6	163.0	133.0	3410	15.8	78	2	peugeot 604sl
396	32.0	4	135.0	84.0	2295	11.6	82	1	dodge rampage
397	31.5	4	98.0	68.0	2045	18.5	77	3	honda accord cvcc

11. The below sorts the data frame and then displays it in ascending order.



Sorting Dataframes

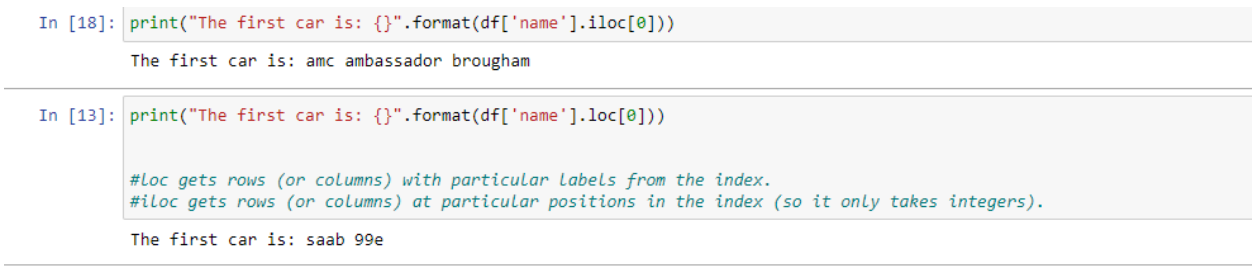
It is possible to sort.

In [15]:
```python
df = df.sort_values(by='name',ascending=True)
df
```

Out[15]:

	mpg	cylinders	displacement	horsepower	weight	acceleration	year	origin	name
329	13.0	8	360.0	175.0	3821	11.0	73	1	amc ambassador brougham
328	15.0	8	390.0	190.0	3850	8.5	70	1	amc ambassador dpl
352	17.0	8	304.0	150.0	3672	11.5	72	1	amc ambassador sst
366	24.3	4	151.0	90.0	3003	20.1	80	1	amc concord
35	19.4	6	232.0	90.0	3210	17.2	78	1	amc concord
...	...	...	...	...	...	...	...	...	...
219	44.0	4	97.0	52.0	2130	24.6	82	2	vw pickup
254	29.0	4	90.0	70.0	1937	14.2	76	2	vw rabbit
343	41.5	4	98.0	76.0	2144	14.7	80	2	vw rabbit
10	44.3	4	90.0	48.0	2085	21.7	80	2	vw rabbit c (diesel)
252	31.9	4	89.0	71.0	1925	14.0	79	2	vw rabbit custom

398 rows × 9 columns



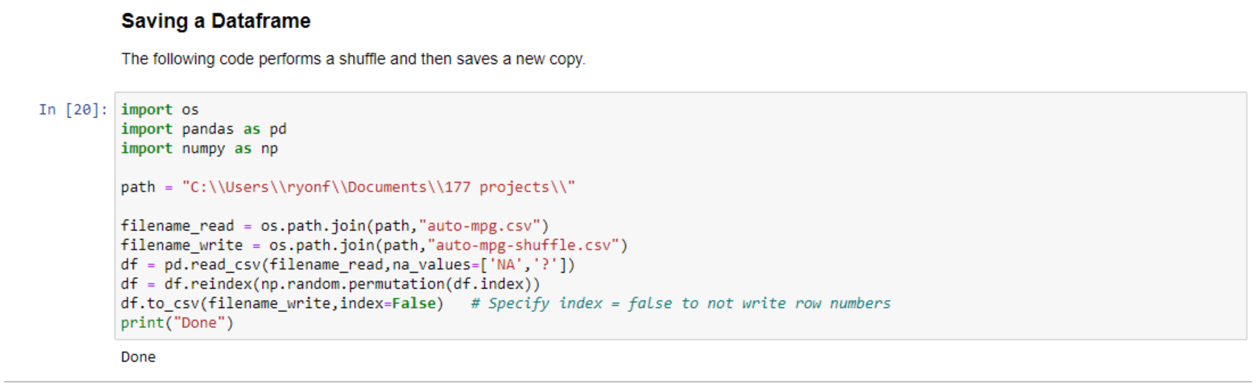
```
In [18]: print("The first car is: {}".format(df['name'].iloc[0]))
```

```
The first car is: amc ambassador brougham
```

```
In [13]: print("The first car is: {}".format(df['name'].loc[0]))


         #loc gets rows (or columns) with particular labels from the index.
         #iloc gets rows (or columns) at particular positions in the index (so it only takes integers).
```

```
The first car is: saab 99e
```

12. Here, the code will shuffle the data and then save a new copy



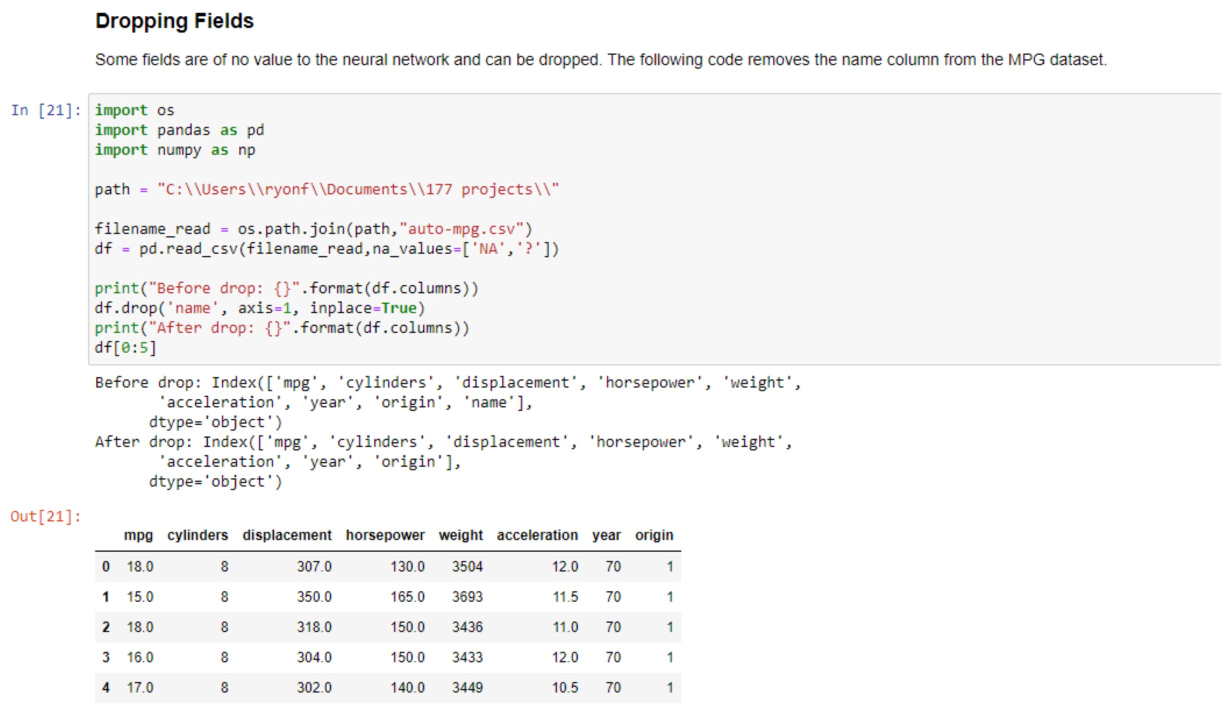
Saving a Dataframe

The following code performs a shuffle and then saves a new copy.

```
In [20]: import os
         import pandas as pd
         import numpy as np

         path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

         filename_read = os.path.join(path,"auto-mpg.csv")
         filename_write = os.path.join(path,"auto-mpg-shuffle.csv")
         df = pd.read_csv(filename_read,na_values=['NA','?'])
         df = df.reindex(np.random.permutation(df.index))
         df.to_csv(filename_write,index=False)    # Specify index = false to not write row numbers
         print("Done")
```

```
Done
```

13. Sometimes certain fields are useless for analysis so we can drop them.



Dropping Fields

Some fields are of no value to the neural network and can be dropped. The following code removes the name column from the MPG dataset.

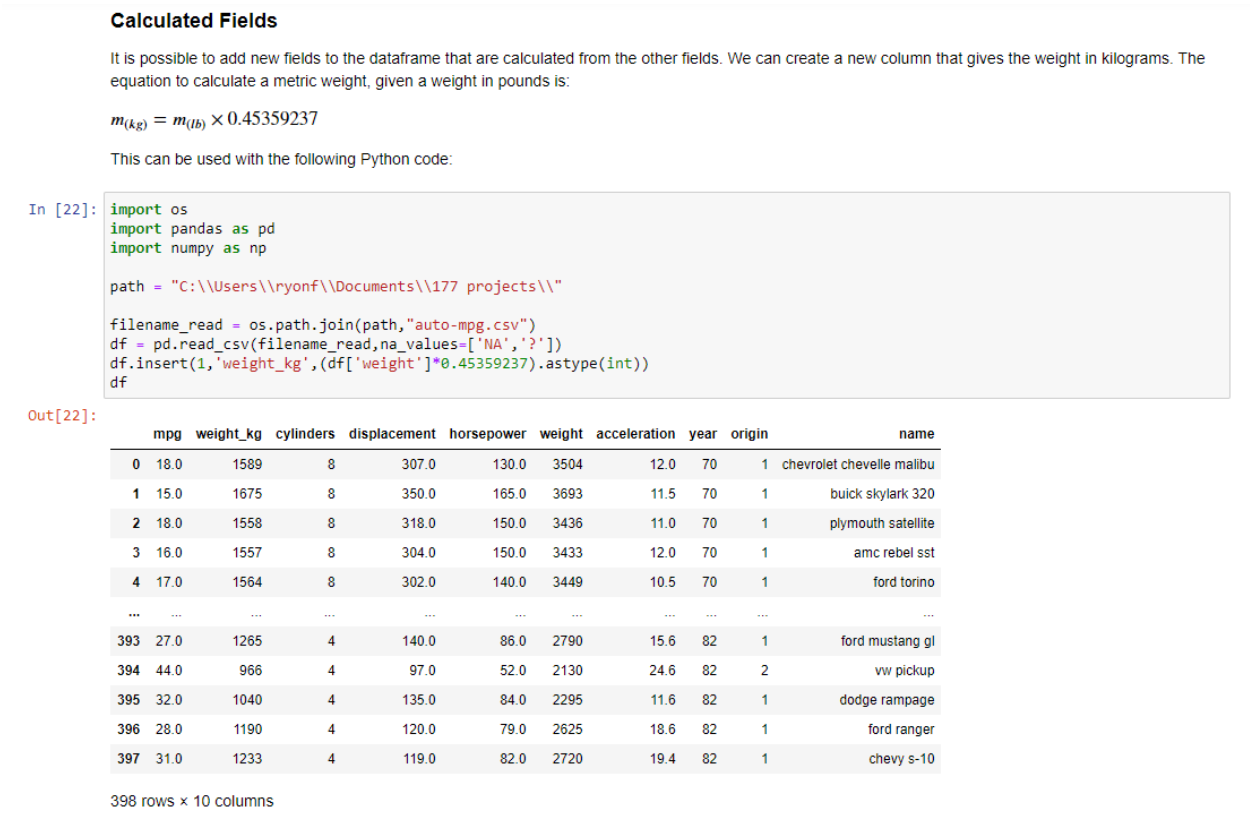
```
In [21]: import os
         import pandas as pd
         import numpy as np

         path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

         filename_read = os.path.join(path,"auto-mpg.csv")
         df = pd.read_csv(filename_read,na_values=['NA','?'])

         print("Before drop: {}".format(df.columns))
         df.drop('name', axis=1, inplace=True)
         print("After drop: {}".format(df.columns))
         df[0:5]
```

```
Before drop: Index(['mpg', 'cylinders', 'displacement', 'horsepower', 'weight',
       'acceleration', 'year', 'origin', 'name'],
      dtype='object')
After drop: Index(['mpg', 'cylinders', 'displacement', 'horsepower', 'weight',
       'acceleration', 'year', 'origin'],
      dtype='object')
```

Out[21]:

	mpg	cylinders	displacement	horsepower	weight	acceleration	year	origin
0	18.0	8	307.0	130.0	3504	12.0	70	1
1	15.0	8	350.0	165.0	3693	11.5	70	1
2	18.0	8	318.0	150.0	3436	11.0	70	1
3	16.0	8	304.0	150.0	3433	12.0	70	1
4	17.0	8	302.0	140.0	3449	10.5	70	1

14. If needed, it’s possible to generate new fields determined by other fields.



Calculated Fields

It is possible to add new fields to the dataframe that are calculated from the other fields. We can create a new column that gives the weight in kilograms. The equation to calculate a metric weight, given a weight in pounds is:

$m_{(kg)} = m_{(lb)} \times 0.45359237$

This can be used with the following Python code:

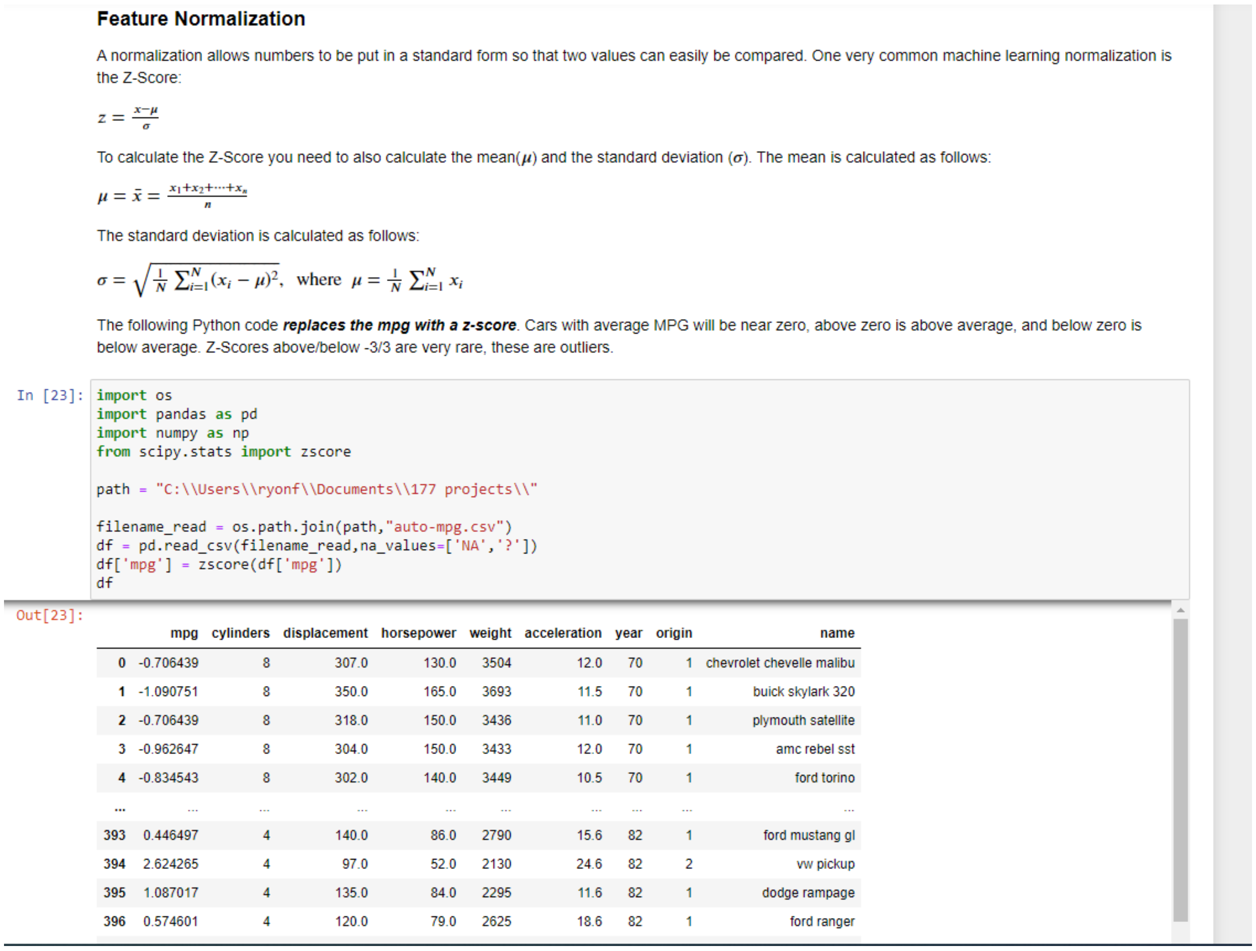
In [22]:
```python
import os
import pandas as pd
import numpy as np

path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

filename_read = os.path.join(path,"auto-mpg.csv")
df = pd.read_csv(filename_read,na_values=['NA','?'])
df.insert(1,'weight_kg',(df['weight']*0.45359237).astype(int))
df
```

Out[22]:

	mpg	weight_kg	cylinders	displacement	horsepower	weight	acceleration	year	origin	name
0	18.0	1589	8	307.0	130.0	3504	12.0	70	1	chevrolet chevelle malibu
1	15.0	1675	8	350.0	165.0	3693	11.5	70	1	buick skylark 320
2	18.0	1558	8	318.0	150.0	3436	11.0	70	1	plymouth satellite
3	16.0	1557	8	304.0	150.0	3433	12.0	70	1	amc rebel sst
4	17.0	1564	8	302.0	140.0	3449	10.5	70	1	ford torino
...	...	...	...	...	...	...	...	...	...	...
393	27.0	1265	4	140.0	86.0	2790	15.6	82	1	ford mustang gl
394	44.0	966	4	97.0	52.0	2130	24.6	82	2	vw pickup
395	32.0	1040	4	135.0	84.0	2295	11.6	82	1	dodge rampage
396	28.0	1190	4	120.0	79.0	2625	18.6	82	1	ford ranger
397	31.0	1233	4	119.0	82.0	2720	19.4	82	1	chevy s-10

398 rows × 10 columns

15. The code below lets us put data in standard form so values can be compared. MPG is replaced with a z-score. This will help us determine outliers.



Feature Normalization

A normalization allows numbers to be put in a standard form so that two values can easily be compared. One very common machine learning normalization is the Z-Score:

$$z = \frac{x-\mu}{\sigma}$$

To calculate the Z-Score you need to also calculate the mean(μ) and the standard deviation (σ). The mean is calculated as follows:

$$\mu = \bar{x} = \frac{x_1+x_2+\cdots+x_n}{n}$$

The standard deviation is calculated as follows:

$$\sigma = \sqrt{\frac{1}{N}\sum_{i=1}^{N}(x_i-\mu)^2}, \text{ where } \mu = \frac{1}{N}\sum_{i=1}^{N} x_i$$

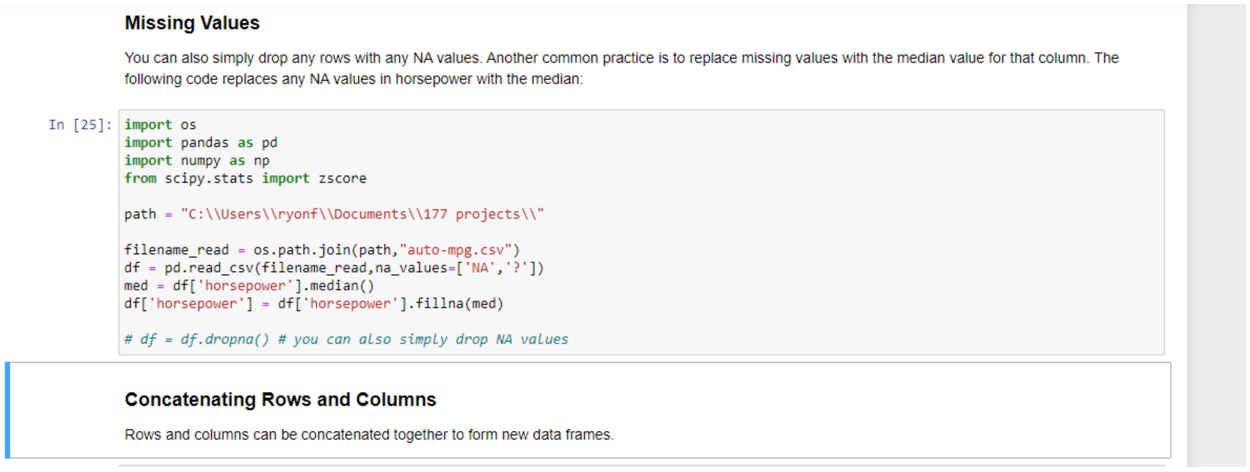
The following Python code ***replaces the mpg with a z-score***. Cars with average MPG will be near zero, above zero is above average, and below zero is below average. Z-Scores above/below -3/3 are very rare, these are outliers.

In [23]:
```
import os
import pandas as pd
import numpy as np
from scipy.stats import zscore

path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

filename_read = os.path.join(path,"auto-mpg.csv")
df = pd.read_csv(filename_read,na_values=['NA','?'])
df['mpg'] = zscore(df['mpg'])
df
```

Out[23]:

	mpg	cylinders	displacement	horsepower	weight	acceleration	year	origin	name
0	-0.706439	8	307.0	130.0	3504	12.0	70	1	chevrolet chevelle malibu
1	-1.090751	8	350.0	165.0	3693	11.5	70	1	buick skylark 320
2	-0.706439	8	318.0	150.0	3436	11.0	70	1	plymouth satellite
3	-0.962647	8	304.0	150.0	3433	12.0	70	1	amc rebel sst
4	-0.834543	8	302.0	140.0	3449	10.5	70	1	ford torino
...	...	...	...	...	...	...	...	...	...
393	0.446497	4	140.0	86.0	2790	15.6	82	1	ford mustang gl
394	2.624265	4	97.0	52.0	2130	24.6	82	2	vw pickup
395	1.087017	4	135.0	84.0	2295	11.6	82	1	dodge rampage
396	0.574601	4	120.0	79.0	2625	18.6	82	1	ford ranger

16. We can drop rows that have missing data or replace them with the median value of that column. In the code below missing values in "horsepower" with its median value.



Missing Values

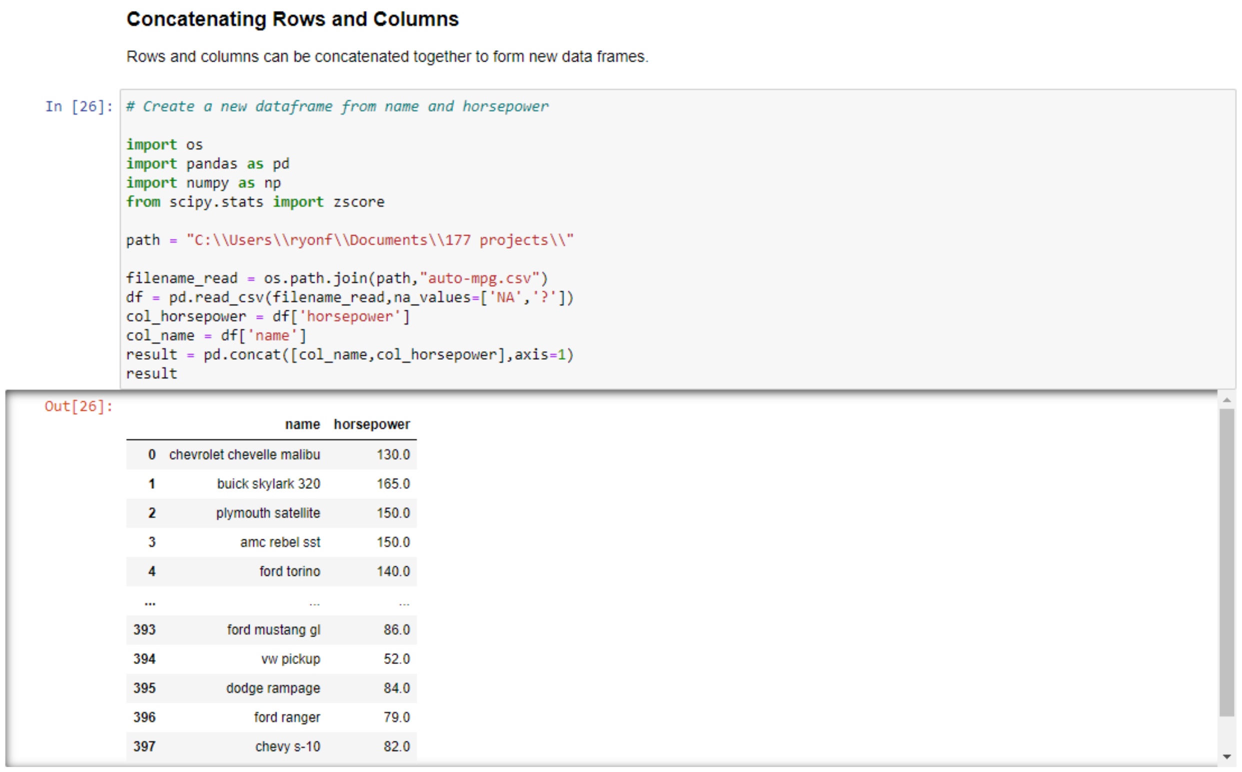
You can also simply drop any rows with any NA values. Another common practice is to replace missing values with the median value for that column. The following code replaces any NA values in horsepower with the median:

In [25]:
```
import os
import pandas as pd
import numpy as np
from scipy.stats import zscore

path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

filename_read = os.path.join(path,"auto-mpg.csv")
df = pd.read_csv(filename_read,na_values=['NA','?'])
med = df['horsepower'].median()
df['horsepower'] = df['horsepower'].fillna(med)

# df = df.dropna() # you can also simply drop NA values
```

Concatenating Rows and Columns

Rows and columns can be concatenated together to form new data frames.

17. This code snippet shows concatenating rows and columns to create a new data frame



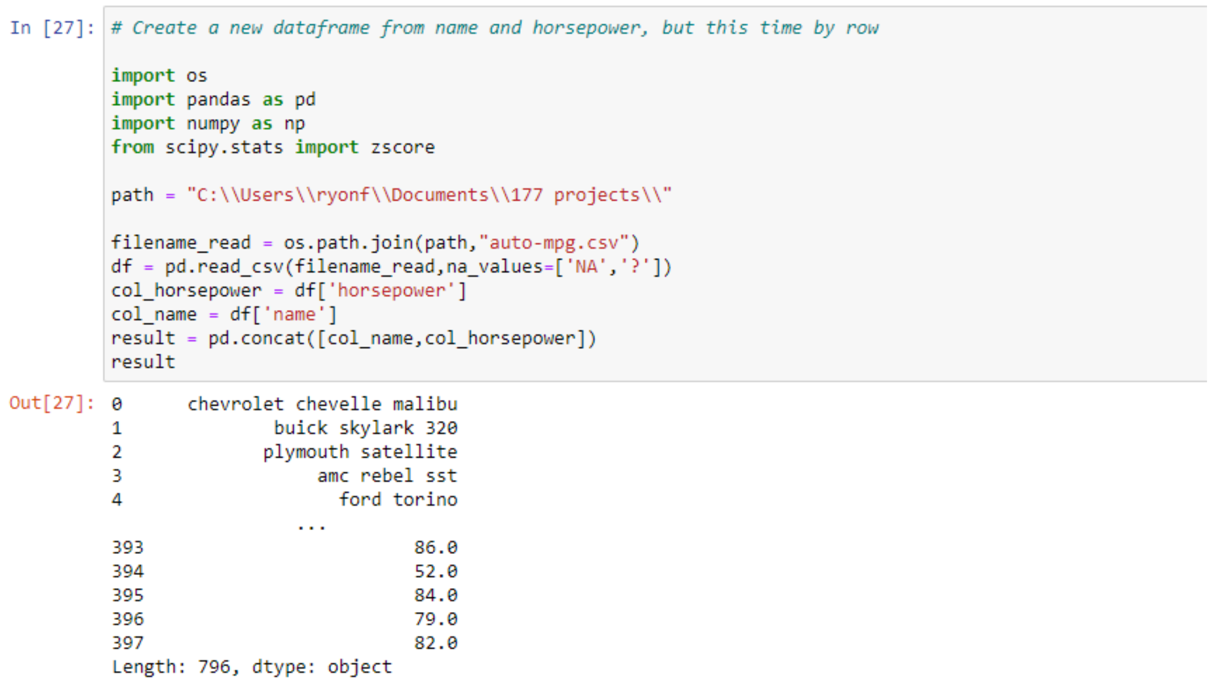
Concatenating Rows and Columns

Rows and columns can be concatenated together to form new data frames.

In [26]:
```
# Create a new dataframe from name and horsepower

import os
import pandas as pd
import numpy as np
from scipy.stats import zscore

path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

filename_read = os.path.join(path,"auto-mpg.csv")
df = pd.read_csv(filename_read,na_values=['NA','?'])
col_horsepower = df['horsepower']
col_name = df['name']
result = pd.concat([col_name,col_horsepower],axis=1)
result
```

Out[26]:

	name	horsepower
0	chevrolet chevelle malibu	130.0
1	buick skylark 320	165.0
2	plymouth satellite	150.0
3	amc rebel sst	150.0
4	ford torino	140.0
...	...	...
393	ford mustang gl	86.0
394	vw pickup	52.0
395	dodge rampage	84.0
396	ford ranger	79.0
397	chevy s-10	82.0



In [27]:
```
# Create a new dataframe from name and horsepower, but this time by row

import os
import pandas as pd
import numpy as np
from scipy.stats import zscore

path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

filename_read = os.path.join(path,"auto-mpg.csv")
df = pd.read_csv(filename_read,na_values=['NA','?'])
col_horsepower = df['horsepower']
col_name = df['name']
result = pd.concat([col_name,col_horsepower])
result
```

Out[27]:
```
0      chevrolet chevelle malibu
1              buick skylark 320
2             plymouth satellite
3                  amc rebel sst
4                    ford torino
                 ...
393                         86.0
394                         52.0
395                         84.0
396                         79.0
397                         82.0
Length: 796, dtype: object
```

Helpful Functions for Tensorflow (Little Gems)

The following functions will be used with TensorFlow to help preprocess the data.

They allow you to build the feature vector in the format that TensorFlow expects from raw data.

(1) Encoding data:

encode_text_dummy - Encode text fields as numeric, such as the iris species as a single field for each class. Three classes would become "0,0,1" "0,1,0" and "1,0,0". Encode non-target features this way. used when the data is part of input (one hot encoding)

encode_text_index - Encode text fields to numeric, such as the iris species as a single numeric field as "0" "1" and "2". Encode the target field for a classification this way. used when data is part of output (label encoding)

(2) Normalizing data:

encode_numeric_zscore - Encode numeric values as a z-score. Neural networks deal well with "normalized" fields only.

encode_numeric_range - Encode a column to a range between the given normalized_low and normalized_high.

(3) Dealing with missing data:

missing_median - Fill all missing values with the median value.

(4) Removing outliers:

remove_outliers - Remove outliers in a certain column with a value beyond X times SD

(5) Creating the feature vector and target vector that * Tensorflow needs*:

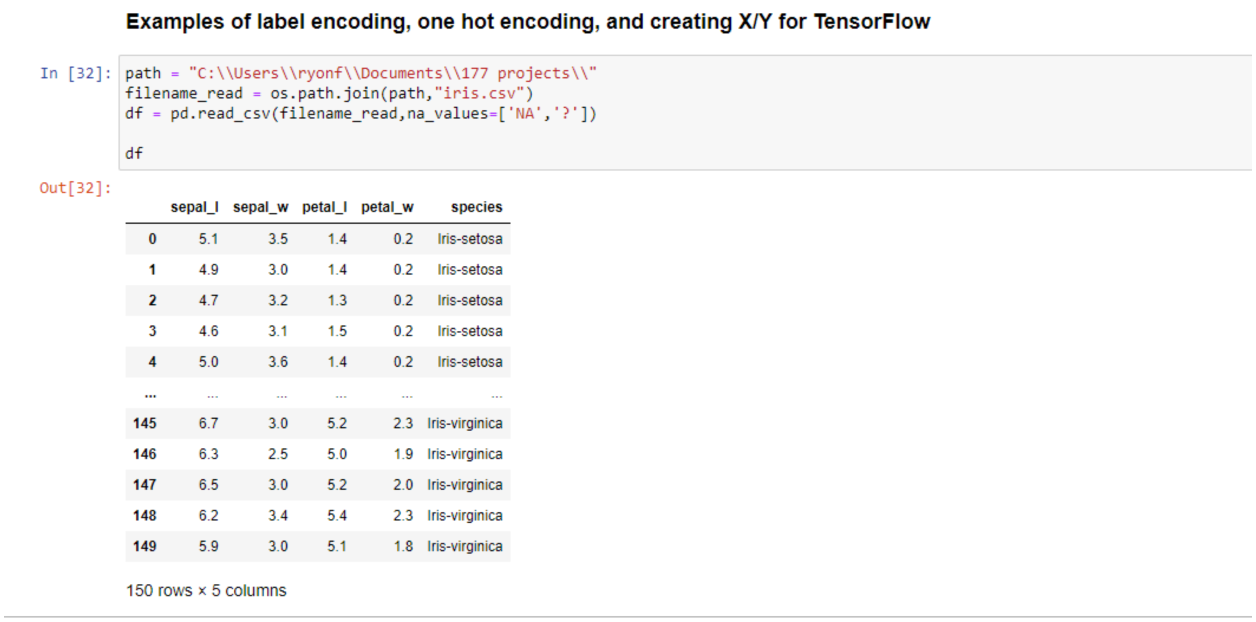
to_xy - Once all fields are encoded to numeric, this function can provide the x and y matrixes that TensorFlow needs to fit the neural network with data.

(6) Other utility functions:

hms_string - Print out an elapsed time string.

chart_regression - Display a chart to show how well a regression performs.

18. Label Encoding



Examples of label encoding, one hot encoding, and creating X/Y for TensorFlow

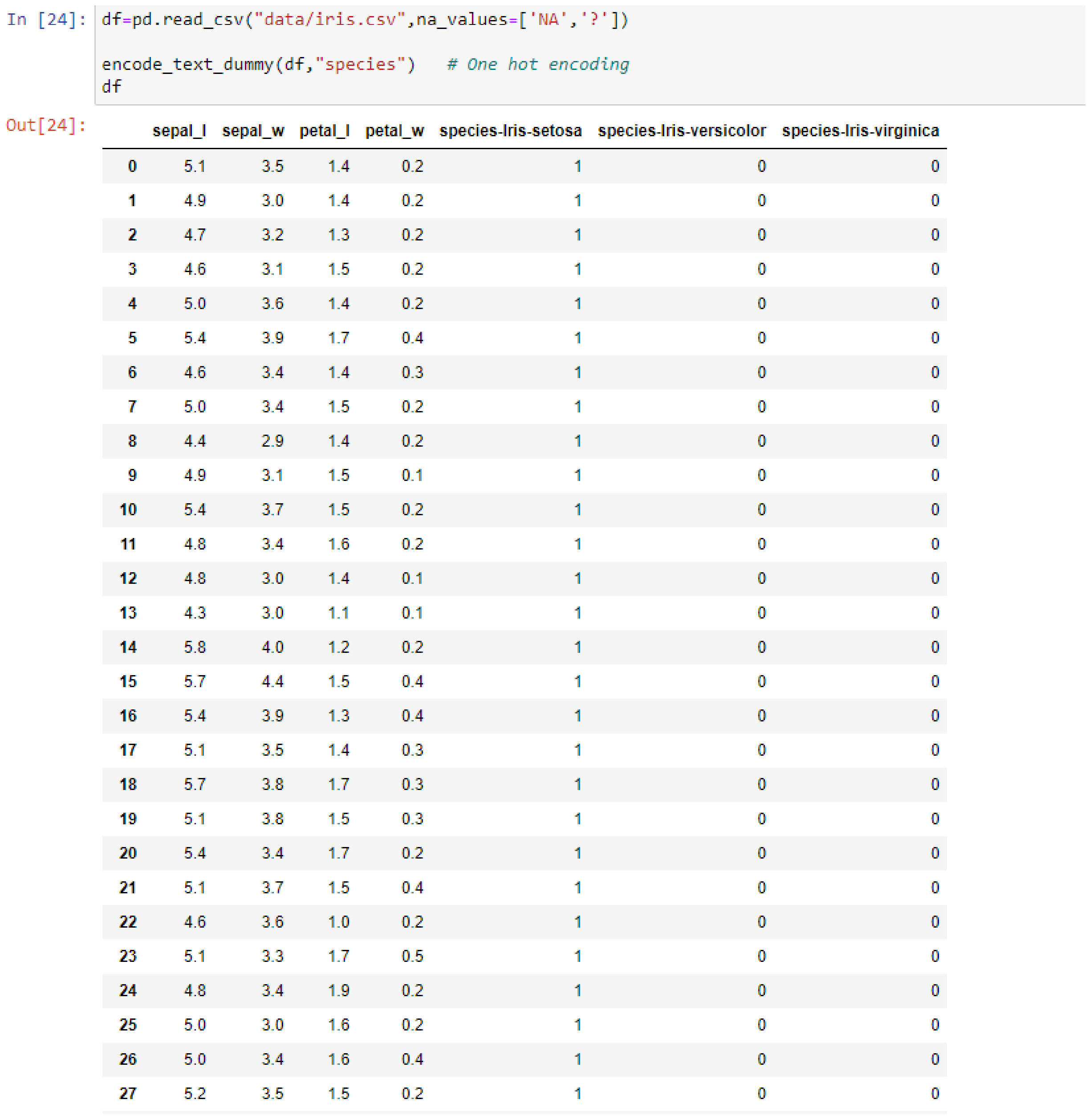
In [32]:
```
path = "C:\\Users\\ryonf\\Documents\\177 projects\\"
filename_read = os.path.join(path,"iris.csv")
df = pd.read_csv(filename_read,na_values=['NA','?'])

df
```

Out[32]:

	sepal_l	sepal_w	petal_l	petal_w	species
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa
...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	Iris-virginica
146	6.3	2.5	5.0	1.9	Iris-virginica
147	6.5	3.0	5.2	2.0	Iris-virginica
148	6.2	3.4	5.4	2.3	Iris-virginica
149	5.9	3.0	5.1	1.8	Iris-virginica

150 rows × 5 columns

19. Hot encoding



```
In [24]: df=pd.read_csv("data/iris.csv",na_values=['NA','?'])

         encode_text_dummy(df,"species")   # One hot encoding
         df
```

Out[24]:

	sepal_l	sepal_w	petal_l	petal_w	species-Iris-setosa	species-Iris-versicolor	species-Iris-virginica
0	5.1	3.5	1.4	0.2	1	0	0
1	4.9	3.0	1.4	0.2	1	0	0
2	4.7	3.2	1.3	0.2	1	0	0
3	4.6	3.1	1.5	0.2	1	0	0
4	5.0	3.6	1.4	0.2	1	0	0
5	5.4	3.9	1.7	0.4	1	0	0
6	4.6	3.4	1.4	0.3	1	0	0
7	5.0	3.4	1.5	0.2	1	0	0
8	4.4	2.9	1.4	0.2	1	0	0
9	4.9	3.1	1.5	0.1	1	0	0
10	5.4	3.7	1.5	0.2	1	0	0
11	4.8	3.4	1.6	0.2	1	0	0
12	4.8	3.0	1.4	0.1	1	0	0
13	4.3	3.0	1.1	0.1	1	0	0
14	5.8	4.0	1.2	0.2	1	0	0
15	5.7	4.4	1.5	0.4	1	0	0
16	5.4	3.9	1.3	0.4	1	0	0
17	5.1	3.5	1.4	0.3	1	0	0
18	5.7	3.8	1.7	0.3	1	0	0
19	5.1	3.8	1.5	0.3	1	0	0
20	5.4	3.4	1.7	0.2	1	0	0
21	5.1	3.7	1.5	0.4	1	0	0
22	4.6	3.6	1.0	0.2	1	0	0
23	5.1	3.3	1.7	0.5	1	0	0
24	4.8	3.4	1.9	0.2	1	0	0
25	5.0	3.0	1.6	0.2	1	0	0
26	5.0	3.4	1.6	0.4	1	0	0
27	5.2	3.5	1.5	0.2	1	0	0

20. Encoding the labels prior to calling to_xy()

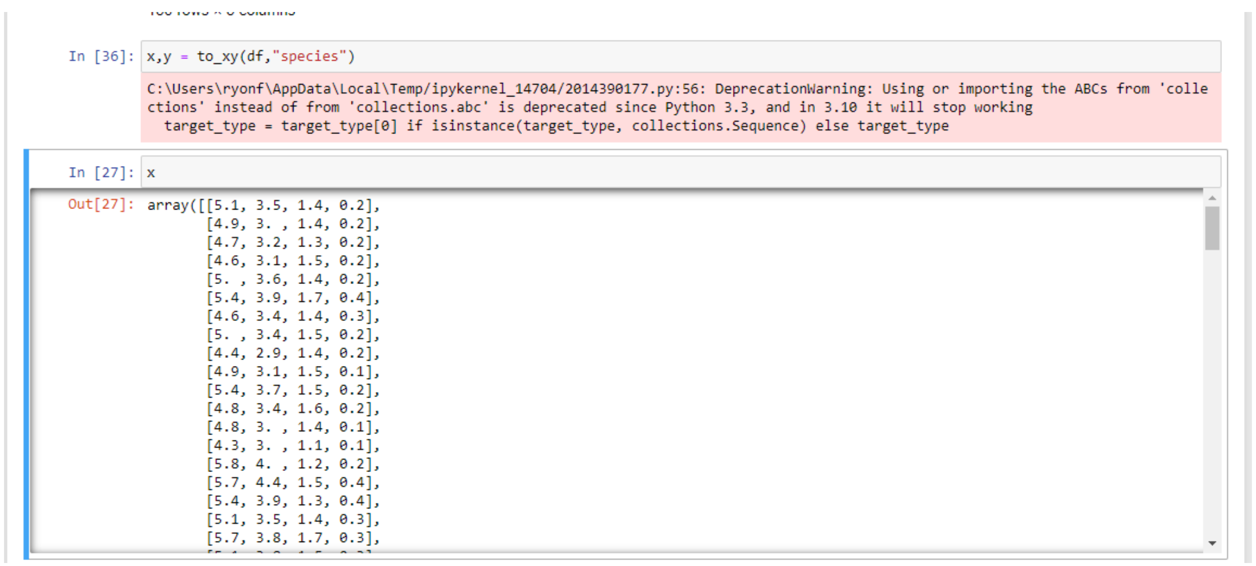
Make sure you encode the lables first before you call to_xy()

```
In [35]:

path = "C:\\Users\\ryonf\\Documents\\177 projects\\"
filename_read = os.path.join(path,"iris.csv")
df = pd.read_csv(filename_read,na_values=['NA','?'])

encode_text_index(df,"species")    # encoding first before you call to_xy()

df
```

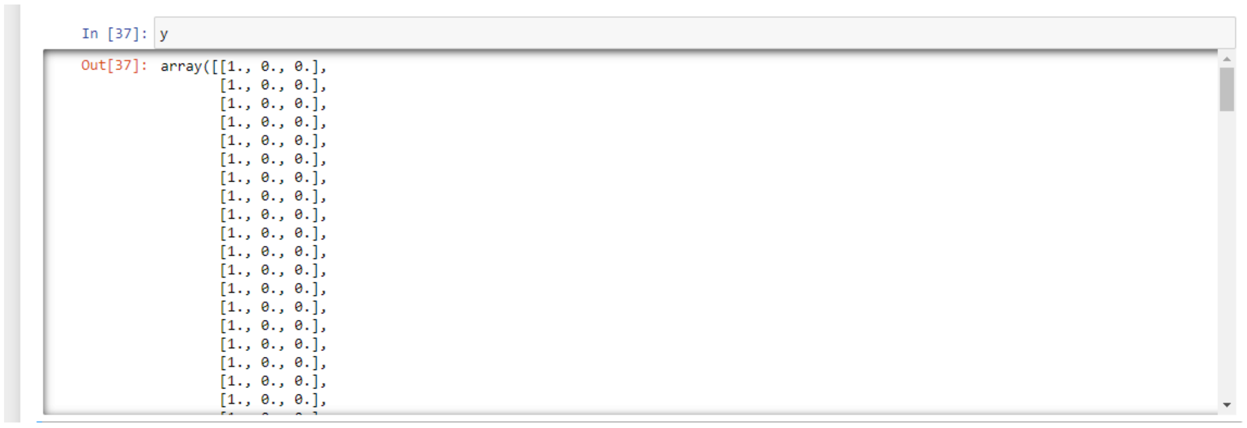
Out[35]:

	sepal_l	sepal_w	petal_l	petal_w	species
0	5.1	3.5	1.4	0.2	0
1	4.9	3.0	1.4	0.2	0
2	4.7	3.2	1.3	0.2	0
3	4.6	3.1	1.5	0.2	0
4	5.0	3.6	1.4	0.2	0
...	...	...	...	...	...
145	6.7	3.0	5.2	2.3	2
146	6.3	2.5	5.0	1.9	2
147	6.5	3.0	5.2	2.0	2
148	6.2	3.4	5.4	2.3	2
149	5.9	3.0	5.1	1.8	2

150 rows × 5 columns

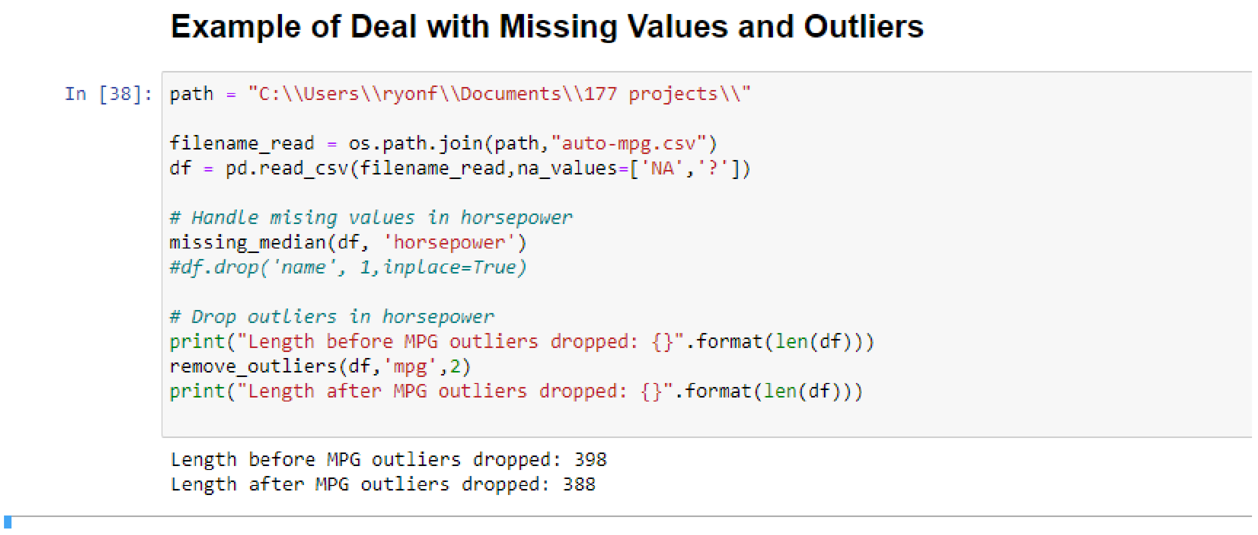


```
In [36]: x,y = to_xy(df,"species")

C:\Users\ryonf\AppData\Local\Temp/ipykernel_14704/2014390177.py:56: DeprecationWarning: Using or importing the ABCs from 'colle
ctions' instead of from 'collections.abc' is deprecated since Python 3.3, and in 3.10 it will stop working
  target_type = target_type[0] if isinstance(target_type, collections.Sequence) else target_type

In [27]: x

Out[27]: array([[5.1, 3.5, 1.4, 0.2],
                [4.9, 3. , 1.4, 0.2],
                [4.7, 3.2, 1.3, 0.2],
                [4.6, 3.1, 1.5, 0.2],
                [5. , 3.6, 1.4, 0.2],
                [5.4, 3.9, 1.7, 0.4],
                [4.6, 3.4, 1.4, 0.3],
                [5. , 3.4, 1.5, 0.2],
                [4.4, 2.9, 1.4, 0.2],
                [4.9, 3.1, 1.5, 0.1],
                [5.4, 3.7, 1.5, 0.2],
                [4.8, 3.4, 1.6, 0.2],
                [4.8, 3. , 1.4, 0.1],
                [4.3, 3. , 1.1, 0.1],
                [5.8, 4. , 1.2, 0.2],
                [5.7, 4.4, 1.5, 0.4],
                [5.4, 3.9, 1.3, 0.4],
                [5.1, 3.5, 1.4, 0.3],
                [5.7, 3.8, 1.7, 0.3],
```



```
In [37]: y

Out[37]: array([[1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
                [1., 0., 0.],
```

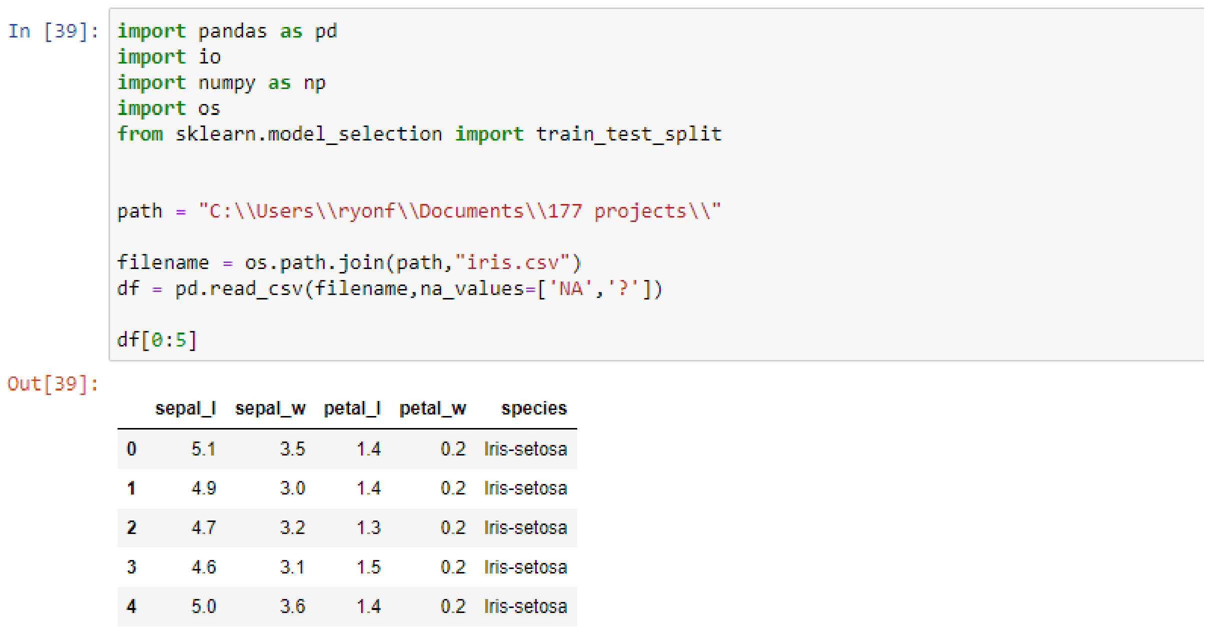
21. Missing values and outliers example.



Example of Deal with Missing Values and Outliers

```
In [38]: path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

         filename_read = os.path.join(path,"auto-mpg.csv")
         df = pd.read_csv(filename_read,na_values=['NA','?'])

         # Handle mising values in horsepower
         missing_median(df, 'horsepower')
         #df.drop('name', 1,inplace=True)

         # Drop outliers in horsepower
         print("Length before MPG outliers dropped: {}".format(len(df)))
         remove_outliers(df,'mpg',2)
         print("Length after MPG outliers dropped: {}".format(len(df)))

         Length before MPG outliers dropped: 398
         Length after MPG outliers dropped: 388
```

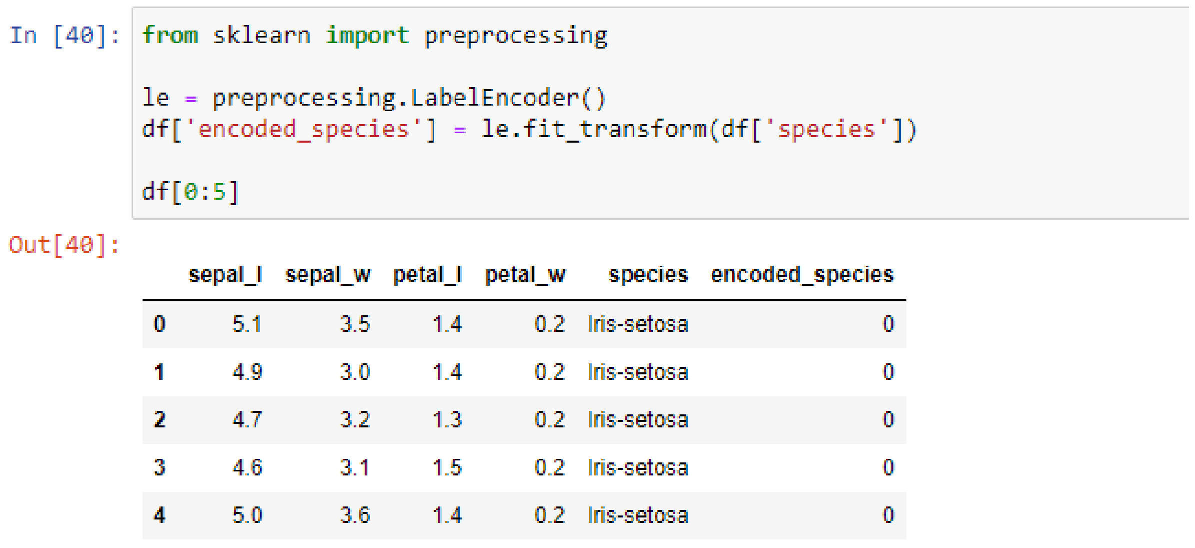
22. Training and test split. Training data/ test split is when the data is split into a percentage of 80% for training and 20% for validation as seen in this code snippet.



In [39]:
```python
import pandas as pd
import io
import numpy as np
import os
from sklearn.model_selection import train_test_split


path = "C:\\Users\\ryonf\\Documents\\177 projects\\"

filename = os.path.join(path,"iris.csv")
df = pd.read_csv(filename,na_values=['NA','?'])

df[0:5]
```

Out[39]:

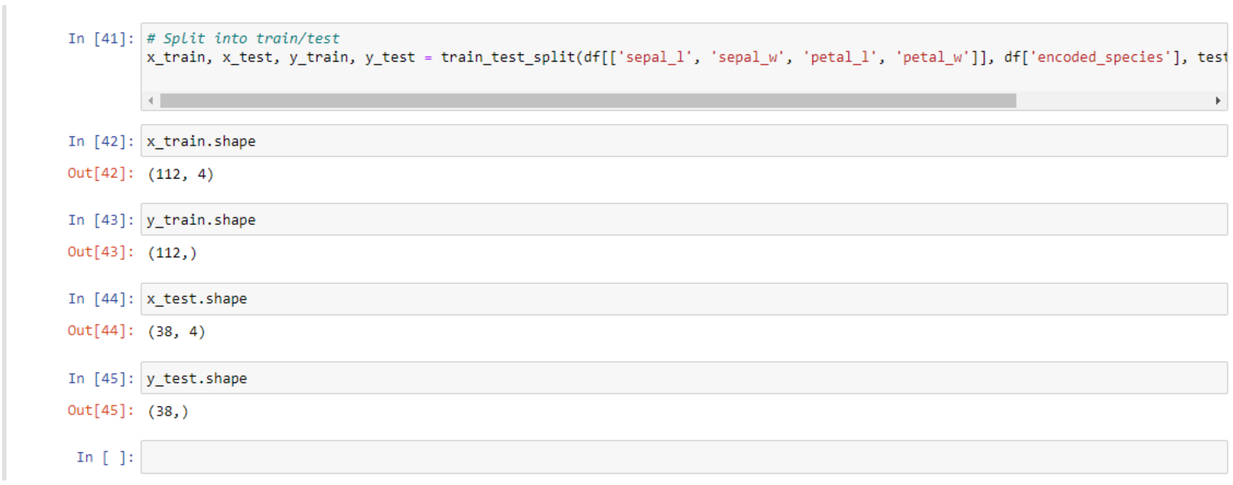
	sepal_l	sepal_w	petal_l	petal_w	species
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa



In [40]:
```python
from sklearn import preprocessing

le = preprocessing.LabelEncoder()
df['encoded_species'] = le.fit_transform(df['species'])

df[0:5]
```

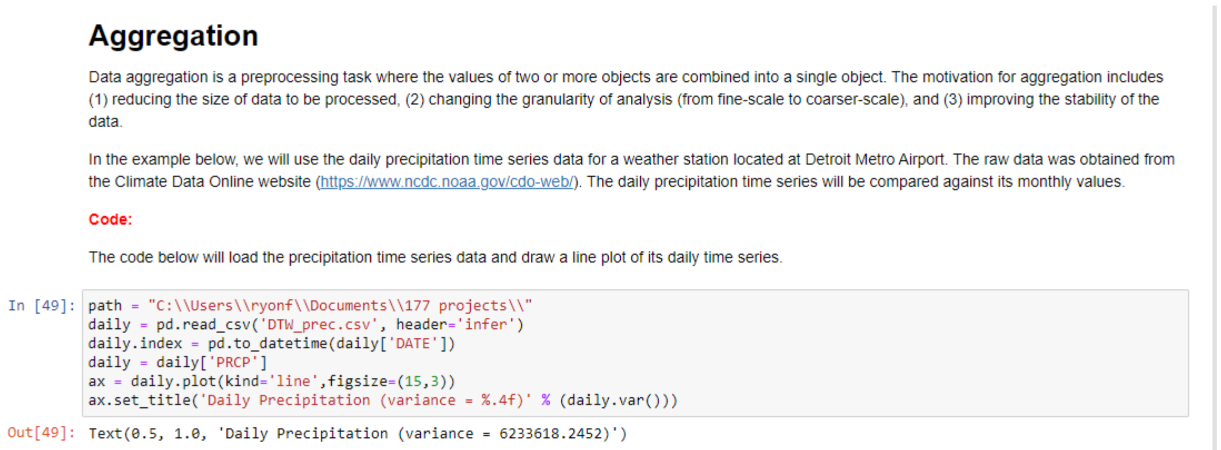
Out[40]:

	sepal_l	sepal_w	petal_l	petal_w	species	encoded_species
0	5.1	3.5	1.4	0.2	Iris-setosa	0
1	4.9	3.0	1.4	0.2	Iris-setosa	0
2	4.7	3.2	1.3	0.2	Iris-setosa	0
3	4.6	3.1	1.5	0.2	Iris-setosa	0
4	5.0	3.6	1.4	0.2	Iris-setosa	0



```
In [41]: # Split into train/test
         x_train, x_test, y_train, y_test = train_test_split(df[['sepal_l', 'sepal_w', 'petal_l', 'petal_w']], df['encoded_species'], test

In [42]: x_train.shape
Out[42]: (112, 4)

In [43]: y_train.shape
Out[43]: (112,)

In [44]: x_test.shape
Out[44]: (38, 4)

In [45]: y_test.shape
Out[45]: (38,)

In [ ]:
```

23. Aggregation is when values of two or more objects are combined. This can help reduce data size, change granularity of analysis and improve the stability of data. Below is an example of grouping by day, month and year.



Aggregation

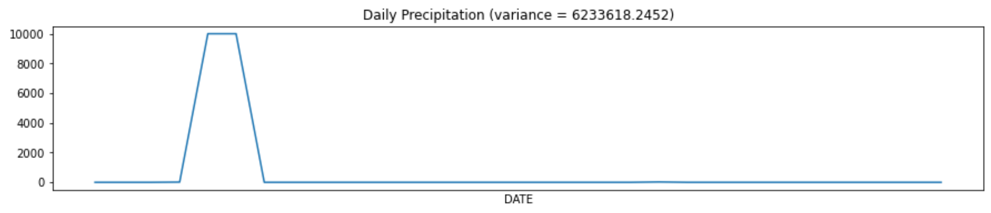
Data aggregation is a preprocessing task where the values of two or more objects are combined into a single object. The motivation for aggregation includes (1) reducing the size of data to be processed, (2) changing the granularity of analysis (from fine-scale to coarser-scale), and (3) improving the stability of the data.

In the example below, we will use the daily precipitation time series data for a weather station located at Detroit Metro Airport. The raw data was obtained from the Climate Data Online website (https://www.ncdc.noaa.gov/cdo-web/). The daily precipitation time series will be compared against its monthly values.

Code:

The code below will load the precipitation time series data and draw a line plot of its daily time series.

```
In [49]: path = "C:\\Users\\ryonf\\Documents\\177 projects\\"
         daily = pd.read_csv('DTW_prec.csv', header='infer')
         daily.index = pd.to_datetime(daily['DATE'])
         daily = daily['PRCP']
         ax = daily.plot(kind='line',figsize=(15,3))
         ax.set_title('Daily Precipitation (variance = %.4f)' % (daily.var()))
Out[49]: Text(0.5, 1.0, 'Daily Precipitation (variance = 6233618.2452)')
```



```
In [50]: daily
```

```
Out[50]: DATE
1970-01-01 00:00:00.020100101       0
1970-01-01 00:00:00.020100102       0
1970-01-01 00:00:00.020100103       0
1970-01-01 00:00:00.020100104      15
1970-01-01 00:00:00.020100105    9999
1970-01-01 00:00:00.020100106    9999
1970-01-01 00:00:00.020100107       0
1970-01-01 00:00:00.020100108       0
1970-01-01 00:00:00.020100109       0
1970-01-01 00:00:00.020100110       0
1970-01-01 00:00:00.020100111       0
1970-01-01 00:00:00.020100112       0
1970-01-01 00:00:00.020100113       0
1970-01-01 00:00:00.020100114       0
1970-01-01 00:00:00.020100115       0
1970-01-01 00:00:00.020100116       0
1970-01-01 00:00:00.020100117       0
1970-01-01 00:00:00.020100118       0
1970-01-01 00:00:00.020100119       0
1970-01-01 00:00:00.020100120       0
1970-01-01 00:00:00.020100121      25
1970-01-01 00:00:00.020100122       0
1970-01-01 00:00:00.020100123       0
1970-01-01 00:00:00.020100124       0
1970-01-01 00:00:00.020100125       0
1970-01-01 00:00:00.020100126       0
1970-01-01 00:00:00.020100127       0
1970-01-01 00:00:00.020100128       0
1970-01-01 00:00:00.020100129       0
1970-01-01 00:00:00.020100130       0
1970-01-01 00:00:00.020100131       0
Name: PRCP, dtype: int64
```

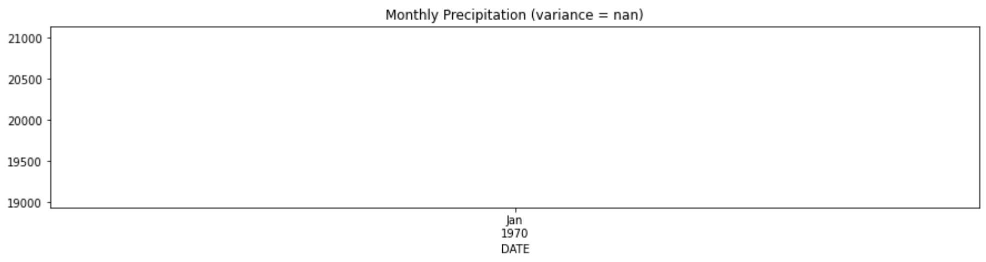
Observe that the daily time series appear to be quite chaotic and varies significantly from one time step to another. The time series can be grouped and aggregated by month to obtain the total monthly precipitation values. The resulting time series appears to vary more smoothly compared to the daily time series.

Code:

```
In [51]: monthly = daily.groupby(pd.Grouper(freq='M')).sum()
         ax = monthly.plot(kind='line',figsize=(15,3))
         ax.set_title('Monthly Precipitation (variance = %.4f)' % (monthly.var()))
```

```
C:\Users\ryonf\anaconda3\lib\site-packages\pandas\plotting\_matplotlib\core.py:1200: UserWarning: Attempting to set identical l
eft == right == 0.0 results in singular transformations; automatically expanding.
  ax.set_xlim(left, right)
```

```
Out[51]: Text(0.5, 1.0, 'Monthly Precipitation (variance = nan)')
```



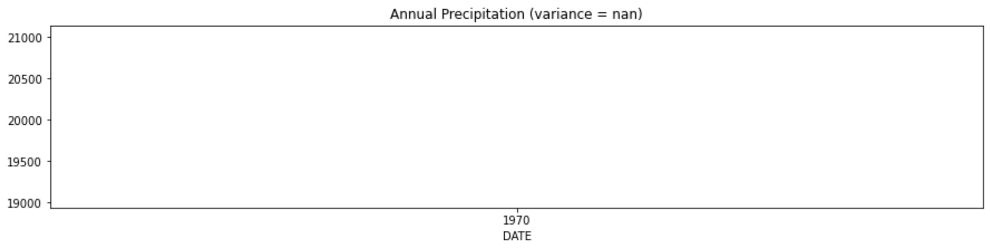
In the example below, the daily precipitation time series are grouped and aggregated by year to obtain the annual precipitation values.

Code:

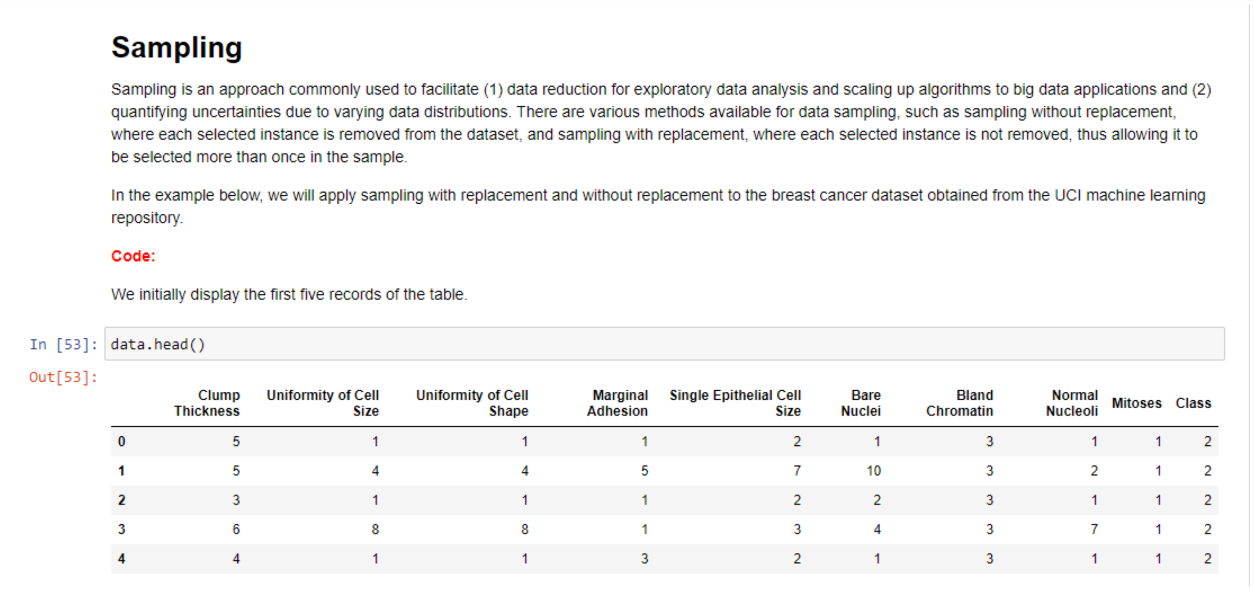
```
In [52]: annual = daily.groupby(pd.Grouper(freq='Y')).sum()
         ax = annual.plot(kind='line',figsize=(15,3))
         ax.set_title('Annual Precipitation (variance = %.4f)' % (annual.var()))
```

```
C:\Users\ryonf\anaconda3\lib\site-packages\pandas\plotting\_matplotlib\core.py:1200: UserWarning: Attempting to set identical l
eft == right == 0.0 results in singular transformations; automatically expanding.
  ax.set_xlim(left, right)
```

```
Out[52]: Text(0.5, 1.0, 'Annual Precipitation (variance = nan)')
```



24. Sampling is an approach commonly used to facilitate (1) data reduction for exploratory data analysis and scaling up algorithms to big data applications and (2) quantifying uncertainties due to varying data distributions. An example is, sampling without replacement, where each selected instance is removed from the dataset, and sampling with replacement, where each selected instance is not removed, thus allowing it to be selected more than once in the sample.



Sampling

Sampling is an approach commonly used to facilitate (1) data reduction for exploratory data analysis and scaling up algorithms to big data applications and (2) quantifying uncertainties due to varying data distributions. There are various methods available for data sampling, such as sampling without replacement, where each selected instance is removed from the dataset, and sampling with replacement, where each selected instance is not removed, thus allowing it to be selected more than once in the sample.

In the example below, we will apply sampling with replacement and without replacement to the breast cancer dataset obtained from the UCI machine learning repository.

Code:

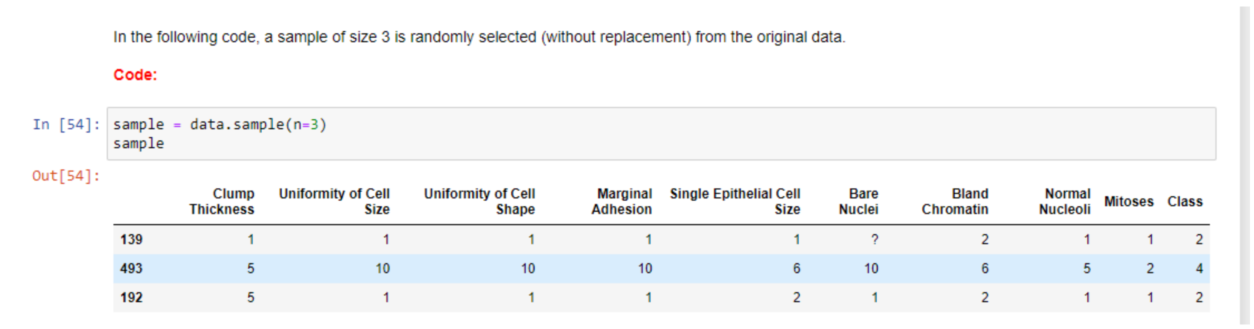
We initially display the first five records of the table.

```
In [53]: data.head()
```

Out[53]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
0	5	1	1	1	2	1	3	1	1	2
1	5	4	4	5	7	10	3	2	1	2
2	3	1	1	1	2	2	3	1	1	2
3	6	8	8	1	3	4	3	7	1	2
4	4	1	1	3	2	1	3	1	1	2

A sample of size of 3 randomly selected from the original data.



In the following code, a sample of size 3 is randomly selected (without replacement) from the original data.

Code:

```
In [54]: sample = data.sample(n=3)
         sample
```

Out[54]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
139	1	1	1	1	1	?	2	1	1	2
493	5	10	10	10	6	10	6	5	2	4
192	5	1	1	1	2	1	2	1	1	2

Randomly select 1% of the data

In the next example, we randomly select 1% of the data (without replacement) and display the selected samples. The random_state argument of the function specifies the seed value of the random number generator.

Code:

```
In [55]: sample = data.sample(frac=0.01, random_state=1)
         sample
```

Out[55]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
584	5	1	1	6	3	1	1	1	1	2
417	1	1	1	1	2	1	2	1	1	2
606	4	1	1	2	2	1	1	1	1	2
349	4	2	3	5	3	8	7	6	1	4
134	3	1	1	1	3	1	2	1	1	2
502	4	1	1	2	2	1	2	1	1	2
117	4	5	5	10	4	10	7	5	8	4

Sampling with replacement

Finally, we perform a sampling with replacement to create a sample whose size is equal to 1% of the entire data. You should be able to observe duplicate instances in the sample by increasing the sample size.

Code:

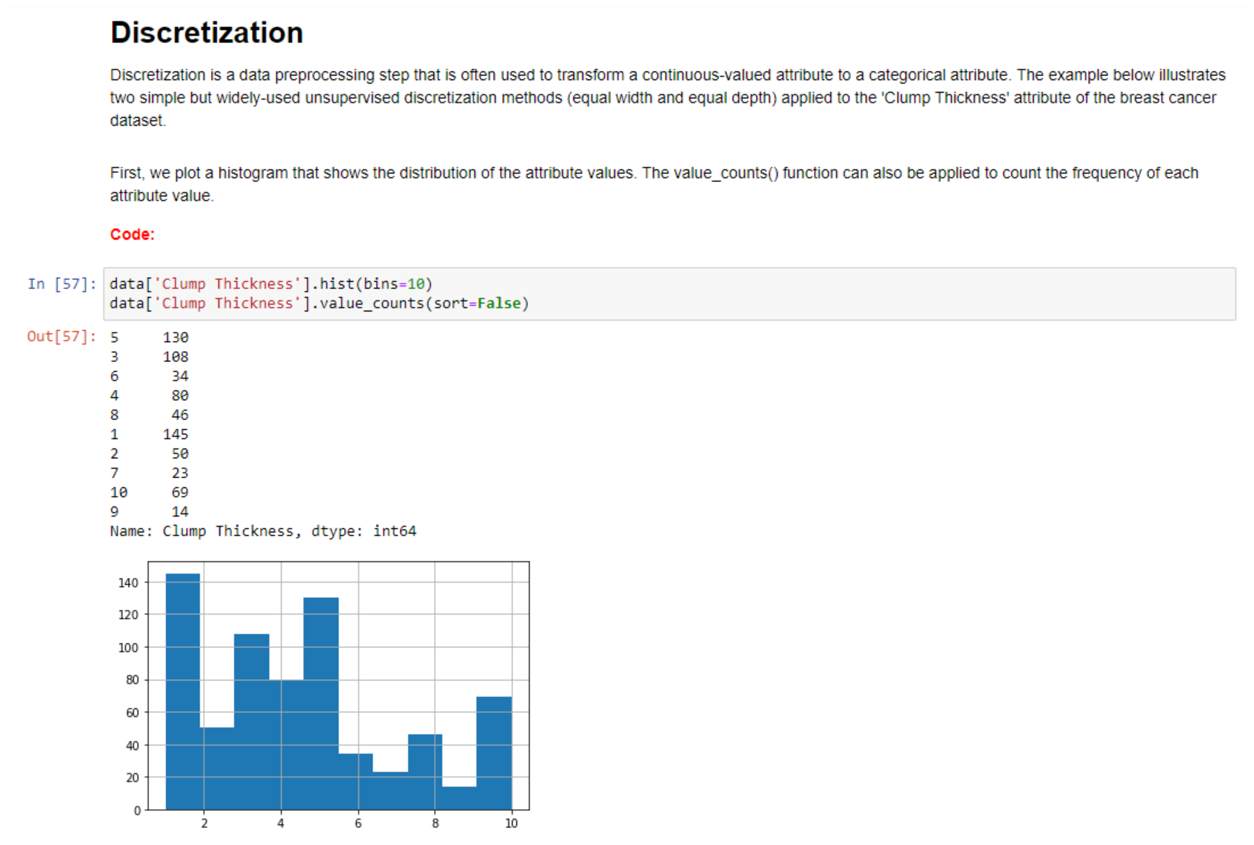
```
In [56]: sample = data.sample(frac=0.01, replace=True, random_state=1)
         sample
```

Out[56]:

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Normal Nucleoli	Mitoses	Class
37	6	2	1	1	1	1	7	1	1	2
235	3	1	4	1	2	?	3	1	1	2
72	1	3	3	2	2	1	7	2	1	2
645	3	1	1	1	2	1	2	1	1	2
144	2	1	1	1	2	1	2	1	1	2
129	1	1	1	1	10	1	1	1	1	2
583	3	1	1	1	2	1	1	1	1	2

25. Discretization is a data preprocessing step that is often used to transform a continuous-valued attribute to a categorical attribute.

    Below, a histogram is plotted that shows the distribution of attribute values.



Discretization

Discretization is a data preprocessing step that is often used to transform a continuous-valued attribute to a categorical attribute. The example below illustrates two simple but widely-used unsupervised discretization methods (equal width and equal depth) applied to the 'Clump Thickness' attribute of the breast cancer dataset.

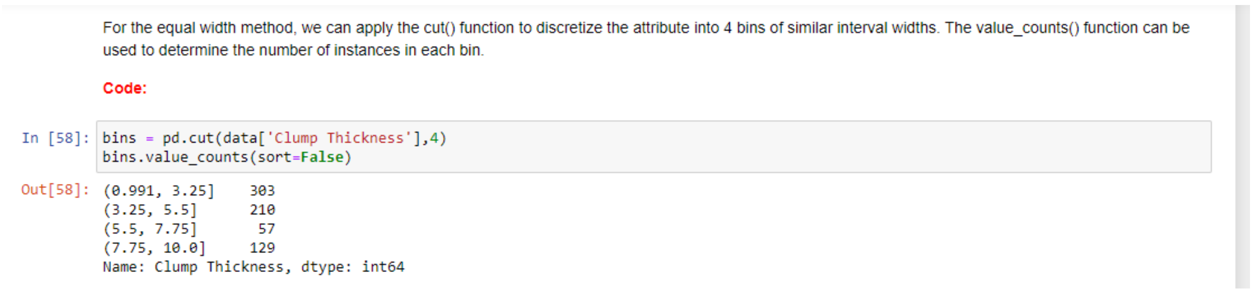
First, we plot a histogram that shows the distribution of the attribute values. The value_counts() function can also be applied to count the frequency of each attribute value.

Code:

In [57]:
```
data['Clump Thickness'].hist(bins=10)
data['Clump Thickness'].value_counts(sort=False)
```

Out[57]:
```
5     130
3     108
6      34
4      80
8      46
1     145
2      50
7      23
10     69
9      14
Name: Clump Thickness, dtype: int64
```

discretize the attribute into 4 bins of similar interval widths. The value_counts() function can be used to determine the number of instances in each bin.



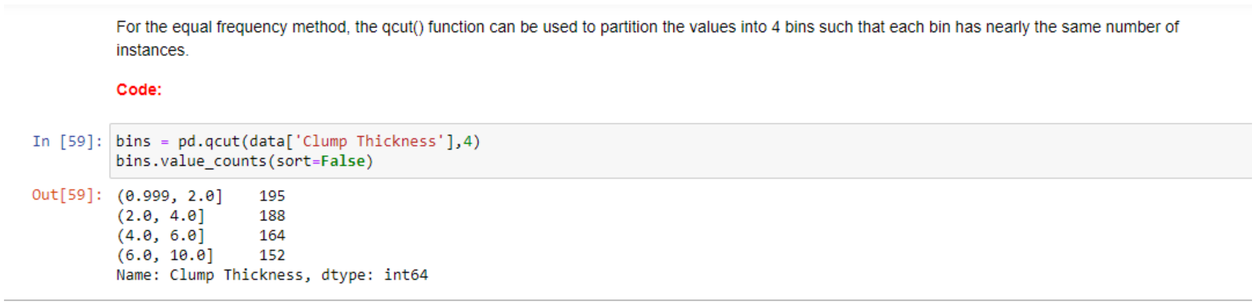
For the equal width method, we can apply the cut() function to discretize the attribute into 4 bins of similar interval widths. The value_counts() function can be used to determine the number of instances in each bin.

Code:

In [58]:
```
bins = pd.cut(data['Clump Thickness'],4)
bins.value_counts(sort=False)
```

Out[58]:
```
(0.991, 3.25]    303
(3.25, 5.5]      210
(5.5, 7.75]       57
(7.75, 10.0]     129
Name: Clump Thickness, dtype: int64
```

For the equal frequency method, the qcut() function can be used to partition the values into 4 bins such that each bin has nearly the same number of instances



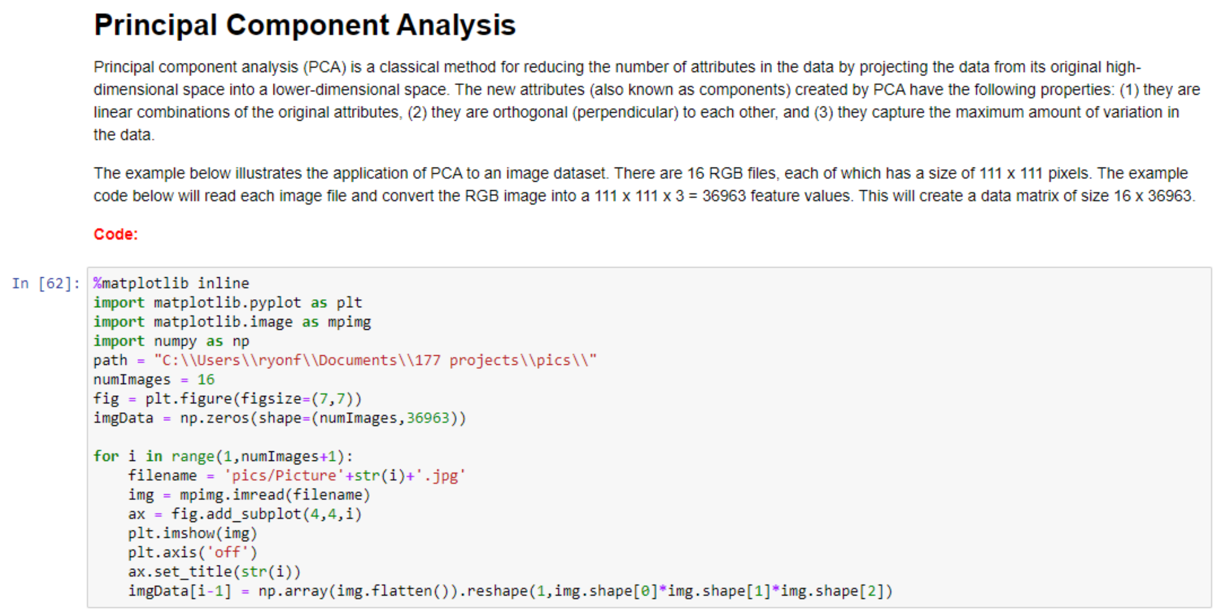
For the equal frequency method, the qcut() function can be used to partition the values into 4 bins such that each bin has nearly the same number of instances.

Code:

```
In [59]: bins = pd.qcut(data['Clump Thickness'],4)
         bins.value_counts(sort=False)
```

```
Out[59]: (0.999, 2.0]     195
         (2.0, 4.0]       188
         (4.0, 6.0]       164
         (6.0, 10.0]      152
         Name: Clump Thickness, dtype: int64
```

Principal component analysis (PCA) is a classical method for reducing the number of attributes in the data by projecting the data from its original high-dimensional space into a lower-dimensional space. The new attributes (also known as components) created by PCA have the following properties: (1) they are linear combinations of the original attributes, (2) they are orthogonal (perpendicular) to each other, and (3) they capture the maximum amount of variation in the data. The example below illustrates the application of PCA to an image dataset. There are 16 RGB files, each of which has a size of 111 x 111 pixels. The example code below will read each image file and convert the RGB image into a 111 x 111 x 3 = 36963 feature values. This will create a data matrix of size 16 x 36963.



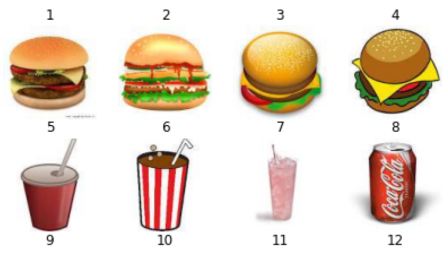
Principal Component Analysis

Principal component analysis (PCA) is a classical method for reducing the number of attributes in the data by projecting the data from its original high-dimensional space into a lower-dimensional space. The new attributes (also known as components) created by PCA have the following properties: (1) they are linear combinations of the original attributes, (2) they are orthogonal (perpendicular) to each other, and (3) they capture the maximum amount of variation in the data.

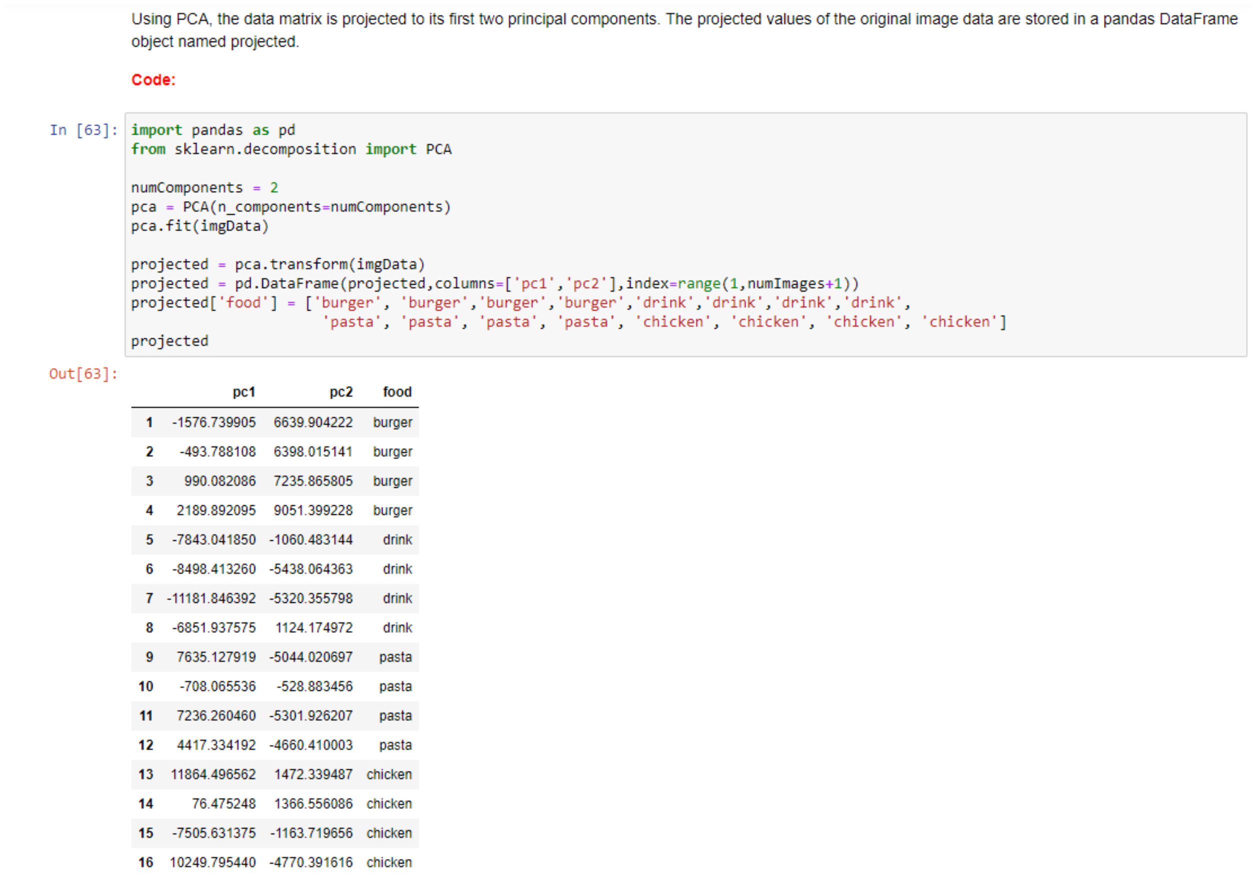
The example below illustrates the application of PCA to an image dataset. There are 16 RGB files, each of which has a size of 111 x 111 pixels. The example code below will read each image file and convert the RGB image into a 111 x 111 x 3 = 36963 feature values. This will create a data matrix of size 16 x 36963.

Code:

```
In [62]: %matplotlib inline
         import matplotlib.pyplot as plt
         import matplotlib.image as mpimg
         import numpy as np
         path = "C:\\Users\\ryonf\\Documents\\177 projects\\pics\\"
         numImages = 16
         fig = plt.figure(figsize=(7,7))
         imgData = np.zeros(shape=(numImages,36963))

         for i in range(1,numImages+1):
             filename = 'pics/Picture'+str(i)+'.jpg'
             img = mpimg.imread(filename)
             ax = fig.add_subplot(4,4,i)
             plt.imshow(img)
             plt.axis('off')
             ax.set_title(str(i))
             imgData[i-1] = np.array(img.flatten()).reshape(1,img.shape[0]*img.shape[1]*img.shape[2])
```



Using PCA, the data matrix is projected to its first two principal components. The projected values of the original image data are stored in a pandas DataFrame object named projected



Using PCA, the data matrix is projected to its first two principal components. The projected values of the original image data are stored in a pandas DataFrame object named projected.

Code:

```
In [63]: import pandas as pd
         from sklearn.decomposition import PCA

         numComponents = 2
         pca = PCA(n_components=numComponents)
         pca.fit(imgData)

         projected = pca.transform(imgData)
         projected = pd.DataFrame(projected,columns=['pc1','pc2'],index=range(1,numImages+1))
         projected['food'] = ['burger', 'burger','burger','burger','drink','drink','drink','drink',
                              'pasta', 'pasta', 'pasta', 'pasta', 'chicken', 'chicken', 'chicken', 'chicken']
         projected
```

Out[63]:

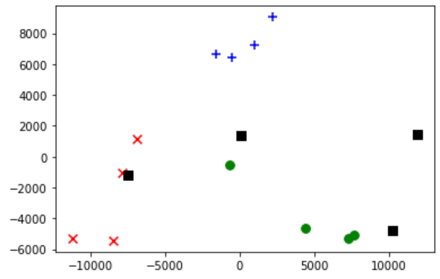
	pc1	pc2	food
1	-1576.739905	6639.904222	burger
2	-493.788108	6398.015141	burger
3	990.082086	7235.865805	burger
4	2189.892095	9051.399228	burger
5	-7843.041850	-1060.483144	drink
6	-8498.413260	-5438.064363	drink
7	-11181.846392	-5320.355798	drink
8	-6851.937575	1124.174972	drink
9	7635.127919	-5044.020697	pasta
10	-708.065536	-528.883456	pasta
11	7236.260460	-5301.926207	pasta
12	4417.334192	-4660.410003	pasta
13	11864.496562	1472.339487	chicken
14	76.475248	1366.556086	chicken
15	-7505.631375	-1163.719656	chicken
16	10249.795440	-4770.391616	chicken

Draw a scatter plot to display the projected values. Observe that the images of burgers, drinks, and pastas are all projected to the same region. However, the images for fried chicken (shown as black squares in the diagram) are harder to discriminate.

Finally, we draw a scatter plot to display the projected values. Observe that the images of burgers, drinks, and pastas are all projected to the same region. However, the images for fried chicken (shown as black squares in the diagram) are harder to discriminate.

Code:

In [64]:
```
import matplotlib.pyplot as plt

colors = {'burger':'b', 'drink':'r', 'pasta':'g', 'chicken':'k'}
markerTypes = {'burger':'+', 'drink':'x', 'pasta':'o', 'chicken':'s'}

for foodType in markerTypes:
    d = projected[projected['food']==foodType]
    plt.scatter(d['pc1'],d['pc2'],c=colors[foodType],s=60,marker=markerTypes[foodType])
```



In [ ]: