CSE 572: Lab 2

This lab contains a Data Exploration module and a practice exercise in which you will use some of the operations from the Data Exploration module.

To execute and make changes to this notebook, click File > Save a copy to save your own version in your Google Drive or Github. Read the step-by-step instructions below carefully. To execute the code, click on each cell below and press the SHIFT-ENTER keys simultaneously or by clicking the Play button.

When you finish executing all code/exercises, save your notebook then download a copy (.ipynb file). Submit 1) a link to your Colab notebook and 2) the .ipynb file on Canvas.

Data Exploration

The following tutorial contains examples of Python code for data exploration. You should refer to the "Data Exploration" chapter of the "Introduction to Data Mining" book (available at https://www-users.cs.umn.edu/~kumar001/dmbook/index.php) to understand some of the concepts introduced in this tutorial notebook.

Data exploration refers to the preliminary investigation of data in order to better understand its specific characteristics. There are two key motivations for data exploration:

1. To help users select the appropriate preprocessing and data analysis techniques to be used.
2. To make use of humans' abilities to recognize patterns in the data.

1. Summary Statistics

Summary statistics are quantities, such as the mean and standard deviation, that capture various characteristics of a potentially large set of values with a single number or a small set of numbers. In this tutorial, we will use the Iris sample data, which contains information on 150 Iris flowers, 50 each from one of three Iris species: Setosa, Versicolour, and Virginica. Each flower is characterized by five attributes:

- sepal length in centimeters
- sepal width in centimeters
- petal length in centimeters
- petal width in centimeters
- class (Setosa, Versicolour, Virginica)

In this tutorial, you will learn how to:

- Load a CSV data file into a Pandas DataFrame object.
- Compute various summary statistics from the DataFrame.

1. First, you need to download the Iris dataset from the UCI machine learning repository.

Code: The following code uses Pandas to read the CSV file and store them in a DataFrame object named data. Next, it will display the first five rows of the data frame.

```
import pandas as pd

data = pd.read_csv('http://archive.ics.uci.edu/ml/machine-learning-databases/iris/iris.data',header=None)
data.columns = ['sepal length', 'sepal width', 'petal length', 'petal width', 'class']

data.head()
```

How big is this dataset? Print the number of samples/records and attributes.

```
print('There are {} samples and {} attributes in this dataset.'.format(data.shape[0], data.shape[1]))
```

```
    There are 150 samples and 5 attributes in this dataset.
```

2. For each quantitative attribute, calculate its average, standard deviation, minimum, and maximum values.

Code:

```
from pandas.api.types import is_numeric_dtype

for col in data.columns:
    if is_numeric_dtype(data[col]):
        print('%s:' % (col))
        print('\t Mean = %.2f' % data[col].mean())
        print('\t Standard deviation = %.2f' % data[col].std())
        print('\t Minimum = %.2f' % data[col].min())
        print('\t Maximum = %.2f' % data[col].max())
```

```
    sepal length:
             Mean = 5.84
             Standard deviation = 0.83
             Minimum = 4.30
             Maximum = 7.90
    sepal width:
             Mean = 3.05
             Standard deviation = 0.43
             Minimum = 2.00
             Maximum = 4.40
    petal length:
             Mean = 3.76
             Standard deviation = 1.76
             Minimum = 1.00
             Maximum = 6.90
    petal width:
             Mean = 1.20
             Standard deviation = 0.76
             Minimum = 0.10
             Maximum = 2.50
```

3. For the qualitative attribute (class), count the frequency for each of its distinct values.

Code:

```
data['class'].value_counts()
```

```
    Iris-setosa        50
    Iris-versicolor    50
    Iris-virginica     50
    Name: class, dtype: int64
```

4. It is also possible to display the summary for all the attributes simultaneously in a table using the describe() function. If an attribute is quantitative, it will display its mean, standard deviation and various quantiles (including minimum, median, and maximum) values. If an attribute is qualitative, it will display its number of unique values and the top (most frequent) values.

Code:

```
data.describe(include='all')
```

	sepal length	sepal width	petal length	petal width	class
count	150.000000	150.000000	150.000000	150.000000	150
unique	NaN	NaN	NaN	NaN	3
top	NaN	NaN	NaN	NaN	Iris-setosa
freq	NaN	NaN	NaN	NaN	50

Note that count refers to the number of non-missing values for each attribute.

std	0.828066	0.433594	1.764420	0.763161	NaN

5. For multivariate statistics, you can compute the covariance and correlation between pairs of attributes.

Code:

50%	5.800000	3.000000	4.350000	1.300000	NaN

```
print('Covariance:')
data.cov()
```

```
Covariance:
```

	sepal length	sepal width	petal length	petal width
sepal length	0.685694	-0.039268	1.273682	0.516904
sepal width	-0.039268	0.188004	-0.321713	-0.117981
petal length	1.273682	-0.321713	3.113179	1.296387
petal width	0.516904	-0.117981	1.296387	0.582414

```
print('Correlation:')
data.corr()
```

```
Correlation:
```

	sepal length	sepal width	petal length	petal width
sepal length	1.000000	-0.109369	0.871754	0.817954
sepal width	-0.109369	1.000000	-0.420516	-0.356544
petal length	0.871754	-0.420516	1.000000	0.962757
petal width	0.817954	-0.356544	0.962757	1.000000

Question 1: Which two features have the strongest correlation? (ignore the diagonals, which show each feature's correlation with itself)

Answer:

The Strongest correlation is between **petal width and petal length which is 0.962757**

2. Data Visualization

Data visualization is the display of information in a graphic or tabular format. Successful visualization requires that the data (information) be converted into a visual format so that the characteristics of the data and the relationships among data items or attributes can be analyzed or reported.

In this tutorial, you will learn how to display the Iris data created in Section 3.1.

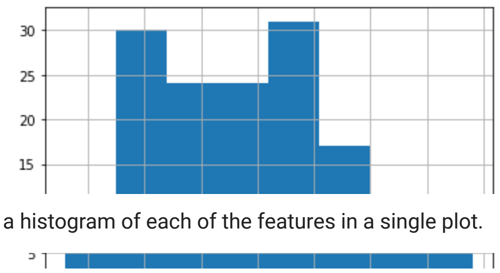
1. First, we will display the histogram for the sepal length attribute by discretizing it into 8 separate bins and counting the frequency for each bin.

Code:

```
%matplotlib inline

data['sepal length'].hist(bins=8)
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f1531f09f10>
```

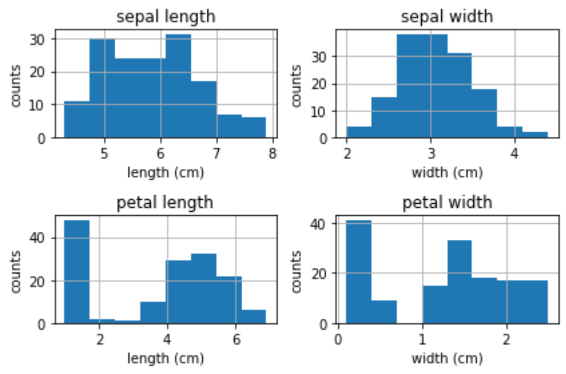


Plot a histogram of each of the features in a single plot.

```
import matplotlib.pyplot as plt
fig, axes = plt.subplots(nrows=2, ncols=2)

for i, col in enumerate(data.columns[:4]):
    data[col].hist(bins=8, ax=axes.flat[i])
    axes.flat[i].set_title(col)
    if 'length' in col:
        axes.flat[i].set_xlabel('length (cm)')
    elif 'width' in col:
        axes.flat[i].set_xlabel('width (cm)')
    axes.flat[i].set_ylabel('counts')

fig.tight_layout()
```



Question 2: What do these histograms tells us about the distribution of the values of each feature in our dataset? Are they uniformly distributed, Gaussian-distributed, or other? Do they appear to have one mode, or multiple? Describe the distribution of each of the features.

Note: You do not need to quantitatively compute the distribution or do a statistical test for this question. Just describe its appearance.

Answer:

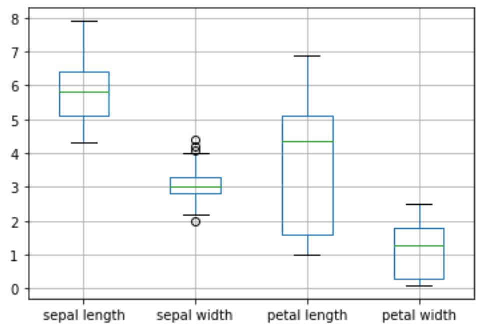
1. There are two separate modes in petal length and petal width
2. Also two modes that are possibly distinct but close in proximity in sepal length.
3. The distributions are **primarily Gaussian**.

2. A boxplot can also be used to show the distribution of values for each attribute.

Code:

```
data.boxplot()
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f152f84ae20>
```

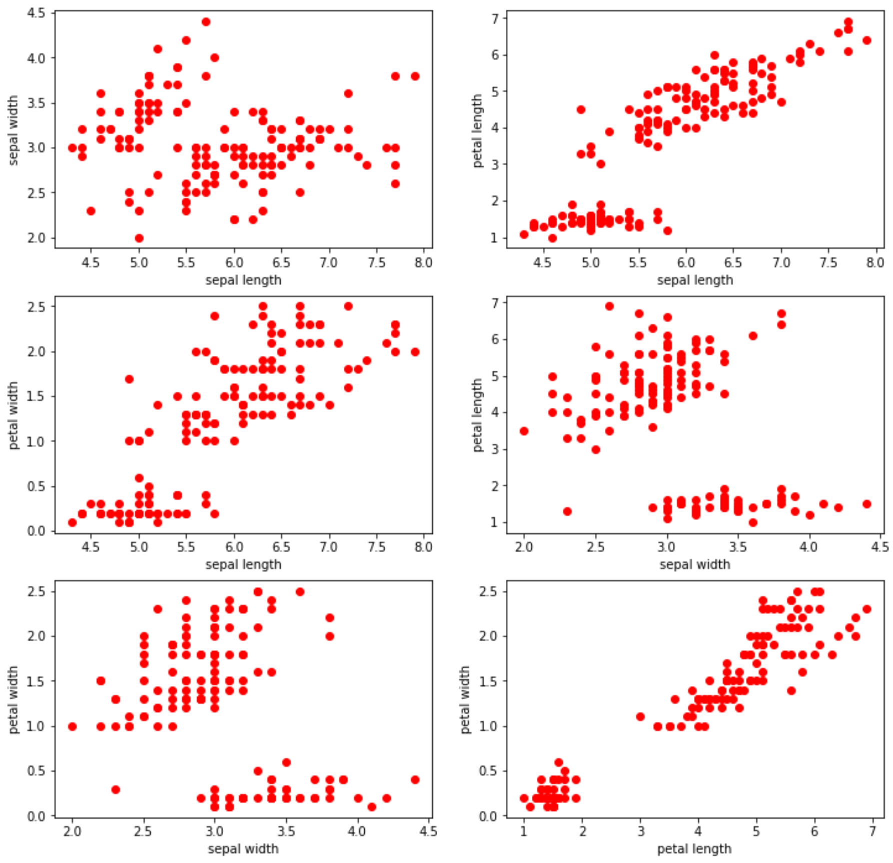


3. For each pair of attributes, we can use a scatter plot to visualize their joint distribution.

Code:

```
import matplotlib.pyplot as plt

fig, axes = plt.subplots(3, 2, figsize=(12,12))
index = 0
for i in range(3):
    for j in range(i+1,4):
        ax1 = int(index/2)
        ax2 = index % 2
        axes[ax1][ax2].scatter(data[data.columns[i]], data[data.columns[j]], color='red')
        axes[ax1][ax2].set_xlabel(data.columns[i])
        axes[ax1][ax2].set_ylabel(data.columns[j])
        index = index + 1
```

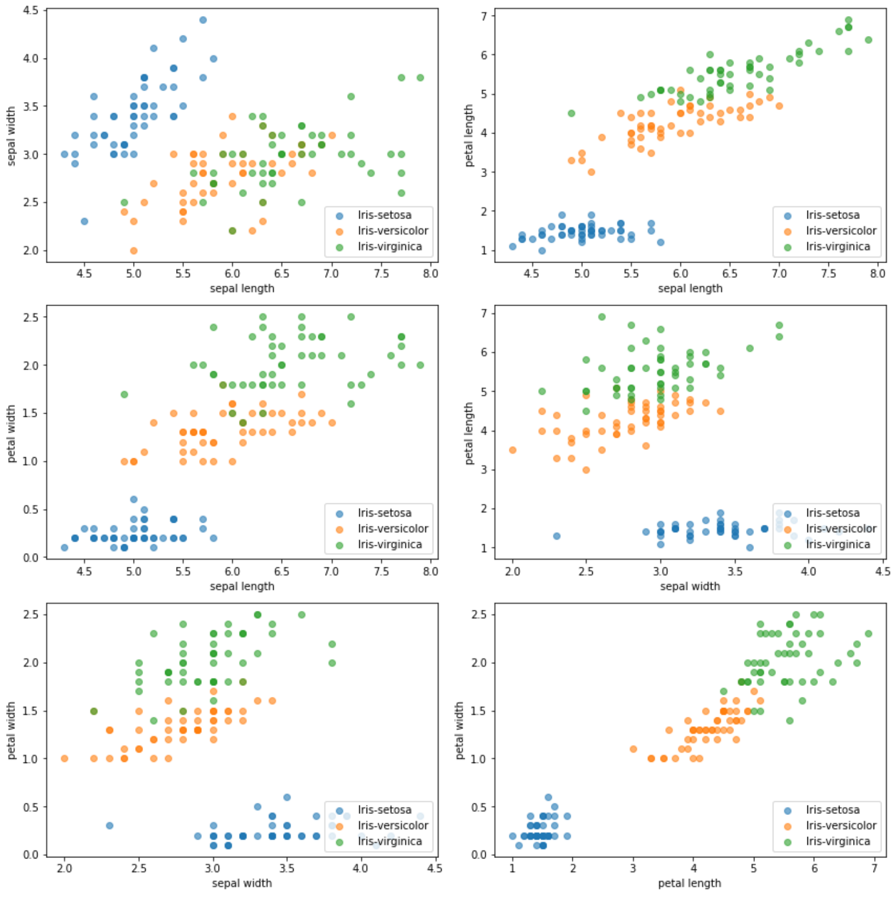


4. If we color the scatter plot points by the class value for each sample, we can see if the classes are clustered in any of the attribute pairs.

Code:

```
fig, axes = plt.subplots(3, 2, figsize=(12,12))
index = 0
for i in range(3):
    for j in range(i+1,4):
        ax1 = int(index/2)
        ax2 = index % 2
        for iris in data['class'].unique():
            axes[ax1][ax2].scatter(data[data['class'] == iris][data.columns[i]],
                                   data[data['class'] == iris][data.columns[j]],
                                   label=iris,
                                   alpha=0.6)
        axes[ax1][ax2].set_xlabel(data.columns[i])
        axes[ax1][ax2].set_ylabel(data.columns[j])
        axes[ax1][ax2].legend(loc='lower right')
        index = index + 1
```

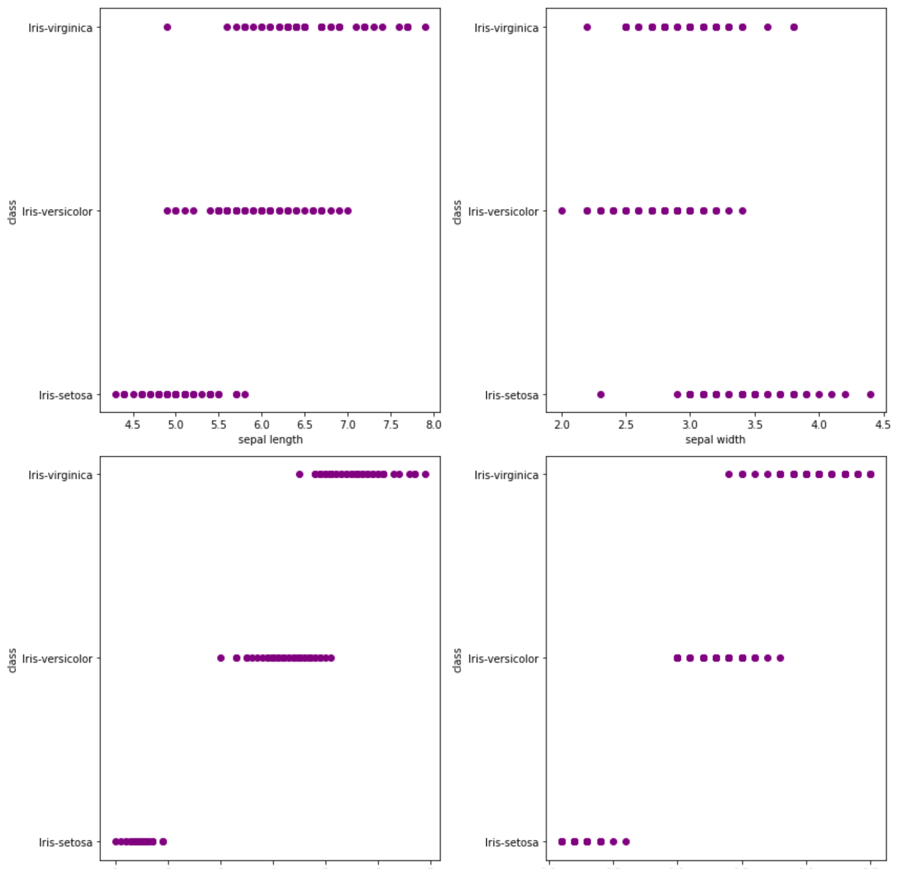
```
fig.tight_layout()
```



5. To see which features are the best and weakest predictors of the iris class, we can visualize the feature value and class value as a scatter plot.

Code:

```
fig, axes = plt.subplots(2, 2, figsize=(12,12))
index = 0
for col_name in data.columns[:-1]:
        ax1 = int(index/2)
        ax2 = index % 2
        axes[ax1][ax2].scatter(data[col_name], data['class'], color='purple')
        axes[ax1][ax2].set_xlabel(col_name)
        axes[ax1][ax2].set_ylabel('class')
        index = index + 1
fig.tight_layout()
```



Question 3: Study these plots and review your responses to Questions 1 and 2. Which features are the best predictors of the iris class? The weakest predictors? Which combination of two features separates the classes best?

Answer:

By referring to the colored scatter graphs above, if we see last graph which is petal length and petal width, we can see the classes are clearly seperable. Hence, Petal length or petal width are the best predictors of the iris class.

1. Strongest Clustering and Predictors: Petal width and Petal Length combined.
2. Weakest Clustering and Predictors: Sepal Length and Sepal Width: by refeering to very first colored graph, all classes seem to be inseprable also from each other and last scatter plot shows overlapping.

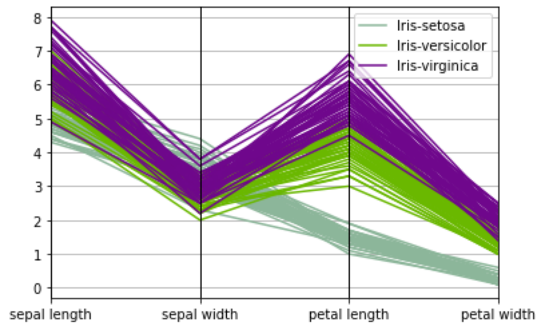
4. Parallel coordinates can be used to display all the data points simultaneously. Parallel coordinates have one coordinate axis for each attribute, but the different axes are parallel to one other instead of perpendicular, as is traditional. Furthermore, an object is represented as a line instead of as a point. In the example below, the distribution of values for each class can be identified in a separate color.

Code:

```
from pandas.plotting import parallel_coordinates
%matplotlib inline

parallel_coordinates(data, 'class')
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f152f76a610>
```



Question 4: Which of the classes are more similar to each other in terms of their attribute distributions (i.e., their lines overlap most)? If you had to come up with a set of rules for distinguishing between iris-setosa, iris-versicolor, and iris-virginica based on their attribute values, what are some rules you might propose?

Answer:

1. From the graph above we can see that, iris-virginica and iris-versicolor lines are overlapping the most and thus these classes are most similar to each other.
2. Rules to distiguish between the classes can be -
    1. Iris-setosa if petal length < ~2.7,
    2. Iris-virginica if petal length > ~5,
    3. Iris-versicolor otherwise
    4. Iris-Setosa if petal-width <~0.7
    5. Iris-Virginica if petal-width < 1.8
    6. Iris-Versicolor if petal-width < otherwise Observing Sepal-length and Sepal-width it is really hard to determine the classes, hence we should go withcombination of other rules to determine the best possible class.

4. Data Quality Issues

Poor data quality can have an adverse effect on data mining. Among the common data quality issues include noise, outliers, missing values, and duplicate data. This section presents examples of Python code to alleviate some of these data quality problems. We begin with an example dataset from the UCI machine learning repository containing information about breast cancer patients. We will first download the dataset using Pandas read_csv() function and display its first 5 data points.

Code:

Question 5: View the documentation for the Wisconsin Breast Cancer dataset here. Who collected this dataset? When did they collect it?

Answer:

The dataset is created by Dr. WIlliam H. Wolberg (physician) University of Wisconsin Hospitals Madison, Wisconsin, USA. It was collected and revised between 1989-1991. It was donated in 1992

```
data = pd.read_csv('https://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wisconsin/breast-cancer-wisconsin.data', header=N
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
```

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

Print the value counts for the Class attribute.

```
# YOUR CODE HERE
data['Class'].value_counts()
```

```
2    458
4    241
Name: Class, dtype: int64
```

Question 6: What does a Class value of 2 indicate? What does 4 indicate?

Answer:

The value of 2 indicates its benign, and 4 is malignant.

4.1.1 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:

```
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
```

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:

```
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
```

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:

```
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
```

4.1.2 Outliers

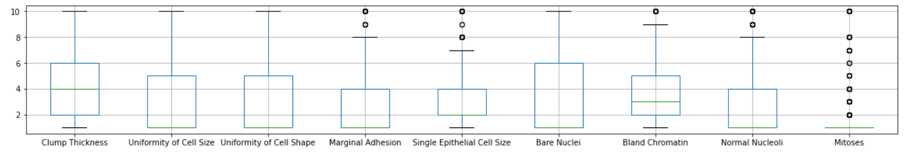
Outliers are data instances with characteristics that are considerably different from the rest of the dataset. In the example code below, we will draw a boxplot to identify the columns in the table that contain outliers. Note that the values in all columns (except for 'Bare Nuclei') are originally stored 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:

```
%matplotlib inline

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

```
    /usr/local/lib/python3.8/dist-packages/matplotlib/cbook/__init__.py:1376: VisibleDepreca
      X = np.atleast_1d(X.T if isinstance(X, np.ndarray) else np.asarray(X))
    <matplotlib.axes._subplots.AxesSubplot at 0x7f152f72ec10>
```



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. To standardize variables, you calculate the mean and standard deviation for a variable. Then, for each observed value of the variable, you subtract the mean and divide by the standard deviation. This results in standard scores that represent the number of standard deviations above or below the mean that a specific observation falls. For instance, a standardized value of 2 indicates that the observation falls 2 standard deviations above the mean.

Note that missing values (NaN) are not affected by the standardization process.

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

Code:

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

```
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 outliers = %d' % (Z2.shape[0]))
```

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

4.1.3 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.

```
dups = data.duplicated()
print('Number of duplicate rows = %d' % (dups.sum()))
data[dups]
```

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

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	Bare Nuclei	Bland Chromatin	Norma Nucleol
28	2	1	1	1	2	1	2	
35	2	1	1	1	2	1	2	
48	4	1	1	3	2	1	3	
64	1	1	1	1	2	1	2	
66	4	1	1	1	2	1	3	
...	...	...	...	...	...	...	...	
686	1	1	1	1	2	1	1	
688	4	1	1	1	2	1	1	
690	1	1	1	3	2	1	1	
692	3	1	1	1	2	1	1	
695	2	1	1	1	2	1	1	

The duplicated() function will return a Boolean array that indicates whether each row is a duplicate of a previous row in the table:

```
dups
```

```
    0      False
    1      False
    2      False
    3      False
    4      False
           ...
    694    False
    695     True
    696    False
    697    False
    698    False
    Length: 699, dtype: bool
```

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.

```
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
```

Now, combine all of these pre-processing steps to clean the dataset by 1) dropping the rows that have NaN values, 2) dropping the duplicate rows, and then 3) removing outliers with Z score Z > 3 or Z <= -3.

```
# YOUR CODE HERE
# 1
data_clean = data.dropna()
data_clean.shape

# 2
data_clean = data_clean.drop_duplicates()
data_clean.shape

# 3 reading comment aove bare nuclie is . Note that the values in all columns (except for 'Bare Nuclei') are originally stored as 'int64' whe
data_clean = data_clean.drop(['Class'],axis=1)
data_clean['Bare Nuclei'] = pd.to_numeric(data_clean['Bare Nuclei'])
ValueOfZ = (data_clean-data_clean.mean())/data_clean.std()
data_clean = ValueOfZ.loc[((ValueOfZ > -3).sum(axis=1)==9) & ((ValueOfZ <= 3).sum(axis=1)==9),:]
data_clean.shape

     (435, 9)
```

Question 7: How many rows/samples are left after applying all three steps?

Answer:

435

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