Analysis of Iris Dataset

The **Iris dataset** is a multivariate dataset introduced by the British statistician and biologist Ronald Fisher in 1936. More information about this can be found on wikipedia (https://en.wikipedia.org/wiki/Iris_flower_data_set).

Importing the Libraries

In this section we import all the libraries required for analysis.

In [1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

%matplotlib inline

sns.set()
```

In [2]:
```
from sklearn.datasets import load_iris

import itertools
```

In [3]:
```
# Importing metrics for evaluation
from sklearn.metrics import confusion_matrix
from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score

from sklearn import model_selection
from sklearn.model_selection import train_test_split

from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.svm import SVC
from sklearn.cluster import KMeans

from matplotlib.colors import ListedColormap

from pandas.tools.plotting import scatter_matrix
```

Dataset

The dataset contains 150 observations of iris species/classes, 50 samples from each of three species of Iris (*Iris setosa*, *Iris virginica* and *Iris versicolor*). Four features are recorded for each sample: the length and the width of the sepals and petals, in centimeters.

The dataset is publically available at UCI Machine Learning Repository (https://archive.ics.uci.edu/ml/datasets/Iris). It is also available within the packages scikit-learn and seaborn.

We can import that data in one of the following three ways. We will also rename the columns in each case:

1- From the UCI Machine Learning Repository:

We obtain a dataframe from the dataset as follows:

In [4]:
```
df = pd.read_csv("https://archive.ics.uci.edu/ml/machine-learning-databases/iris/
                  names=['sepalLength', 'sepalWidth', 'petalLength', 'petalWidth',

# if already downloaded in the working directory
#df = pd.read_csv("iris.data", header=None,names=['sepalLength', 'sepalWidth', 'p

df.head()
```

Out[4]:

	sepalLength	sepalWidth	petalLength	petalWidth	class
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

2- From Seaborn package:

We obtain the dataframe from the dataset as follows:

In [5]:
```
df = sns.load_dataset('iris')
df.columns = ['sepalLength', 'sepalWidth', 'petalLength', 'petalWidth', 'class']
df.head()
```

Out[5]:

	sepalLength	sepalWidth	petalLength	petalWidth	class
0	5.1	3.5	1.4	0.2	setosa
1	4.9	3.0	1.4	0.2	setosa
2	4.7	3.2	1.3	0.2	setosa
3	4.6	3.1	1.5	0.2	setosa
4	5.0	3.6	1.4	0.2	setosa

3- From scikit-learn package:

In this case we obtain the features and target in separate arrays.

```
In [6]: iris = load_iris()
```

```
In [7]: iris.data[:5]
```

```
Out[7]: 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]])
```

```
In [8]: iris.target[:5]
```

```
Out[8]: array([0, 0, 0, 0, 0])
```

Looking at the data

Confirm the number of rows and columns in the dataset:

```
In [9]: df.shape
```

```
Out[9]: (150, 5)
```

So the data has 150 rows and 5 columns.

Summary Statistics:

```
In [10]: df.describe()
```

Out[10]:

	sepalLength	sepalWidth	petalLength	petalWidth
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.057333	3.758000	1.199333
std	0.828066	0.435866	1.765298	0.762238
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000
75%	6.400000	3.300000	5.100000	1.800000
max	7.900000	4.400000	6.900000	2.500000

Information about the data

```
In [11]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
sepalLength    150 non-null float64
sepalWidth     150 non-null float64
petalLength    150 non-null float64
petalWidth     150 non-null float64
class          150 non-null object
dtypes: float64(4), object(1)
memory usage: 5.9+ KB
```

Check the type of each attribute:

```
In [12]: df.dtypes
```

```
Out[12]: sepalLength    float64
         sepalWidth     float64
         petalLength    float64
         petalWidth     float64
         class           object
         dtype: object
```

Check the number of unique classes of Iris:

```
In [13]: df['class'].unique()
```

```
Out[13]: array(['setosa', 'versicolor', 'virginica'], dtype=object)
```

Class distribution

```
In [14]: df['class'].value_counts()
```

```
Out[14]: versicolor    50
         setosa        50
         virginica     50
         Name: class, dtype: int64
```

```
In [15]: # We can also do the above as follows:
         df.groupby('class').size()
```

```
Out[15]: class
         setosa        50
         versicolor    50
         virginica     50
         dtype: int64
```

Check for missing values in the dataset:

```
In [16]: df.isnull().any() # True/False for missing value for each column separately
         #df.isnull().values.sum() #Gives total number of missing values
         #df.isnull().any().any()  #True if any column has a missing value, False otherwis
```

```
Out[16]: sepalLength    False
         sepalWidth     False
         petalLength    False
         petalWidth     False
         class          False
         dtype: bool
```

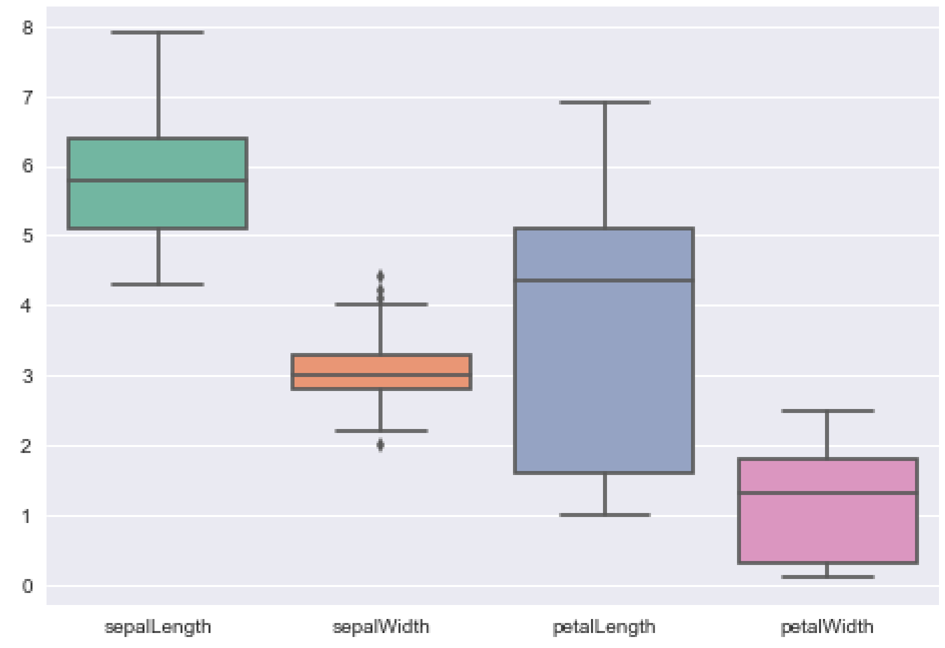
So the dataset does not have any missing values.

Visualization

Boxplots

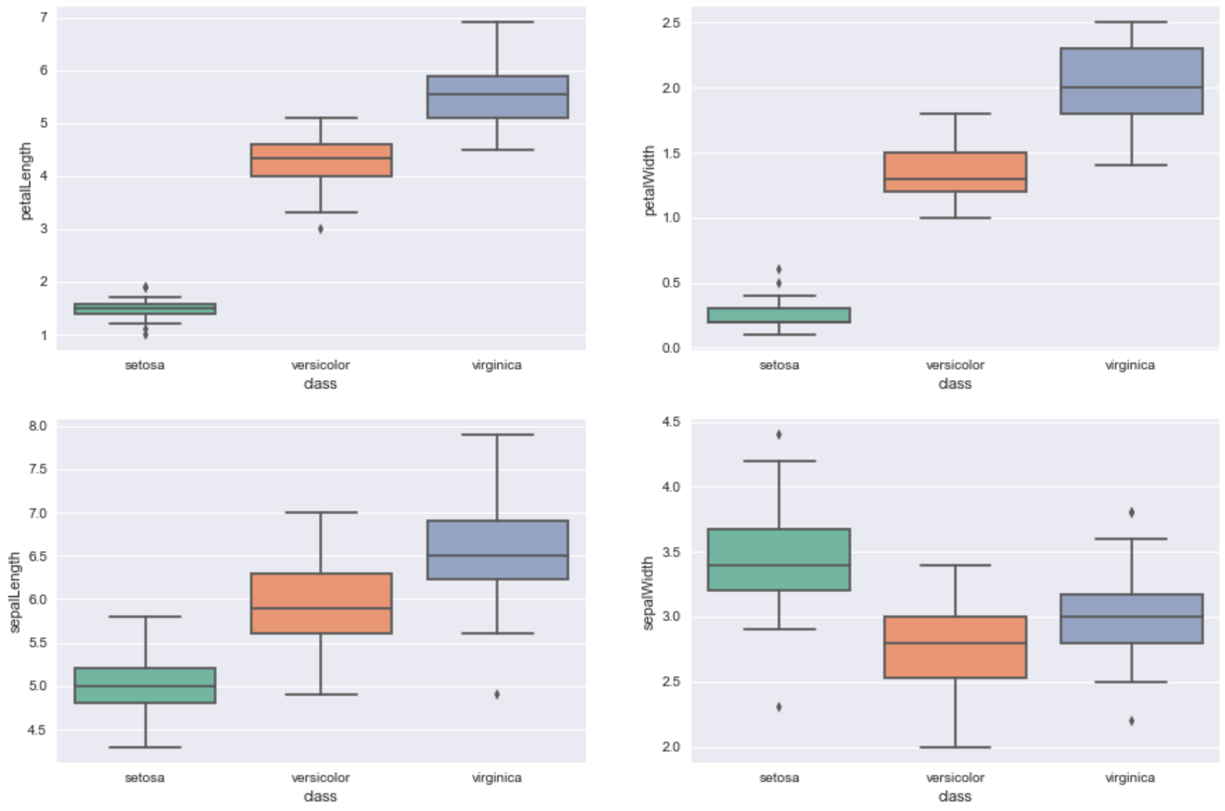
Draw a boxplot for each numeric variable in a DataFrame:

```
In [17]: sns.boxplot(data=df, palette="Set2") # palette is to change the default colour sc
         sns.plt.show()
         # for horizontal orientation: sns.boxplot(data=df, orient="h")
```



We can also compare the box plots for each class of Iris, for each numeric variable for each class:

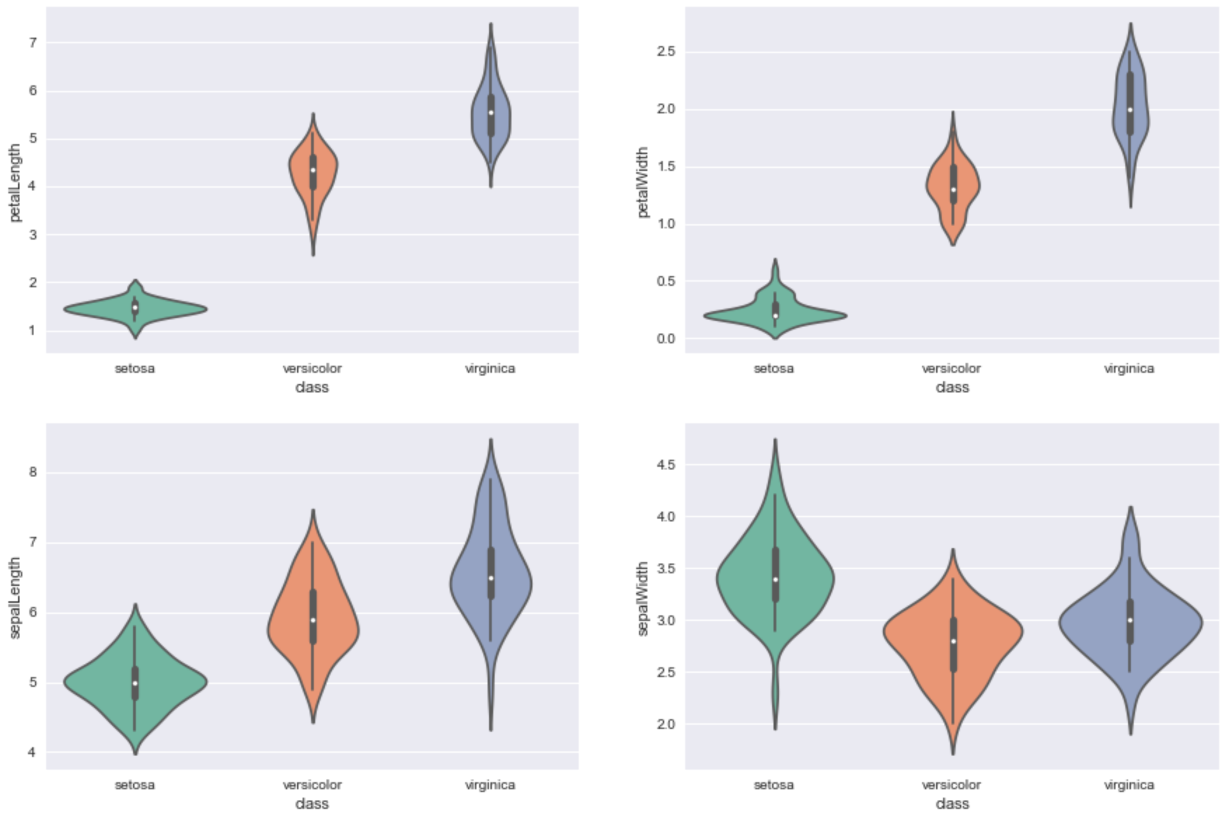
```
In [18]: plt.figure(figsize=(15,10))
         plt.subplot(2,2,1)
         sns.boxplot(x='class',y='petalLength',data=df, palette="Set2")
         plt.subplot(2,2,2)
         sns.boxplot(x='class',y='petalWidth',data=df, palette="Set2")
         plt.subplot(2,2,3)
         sns.boxplot(x='class',y='sepalLength',data=df, palette="Set2")
         plt.subplot(2,2,4)
         sns.boxplot(x='class',y='sepalWidth',data=df, palette="Set2")
         sns.plt.show()
```



Violin Plots

Simlarly, we can also have a look at the violin plots for each class of Iris.

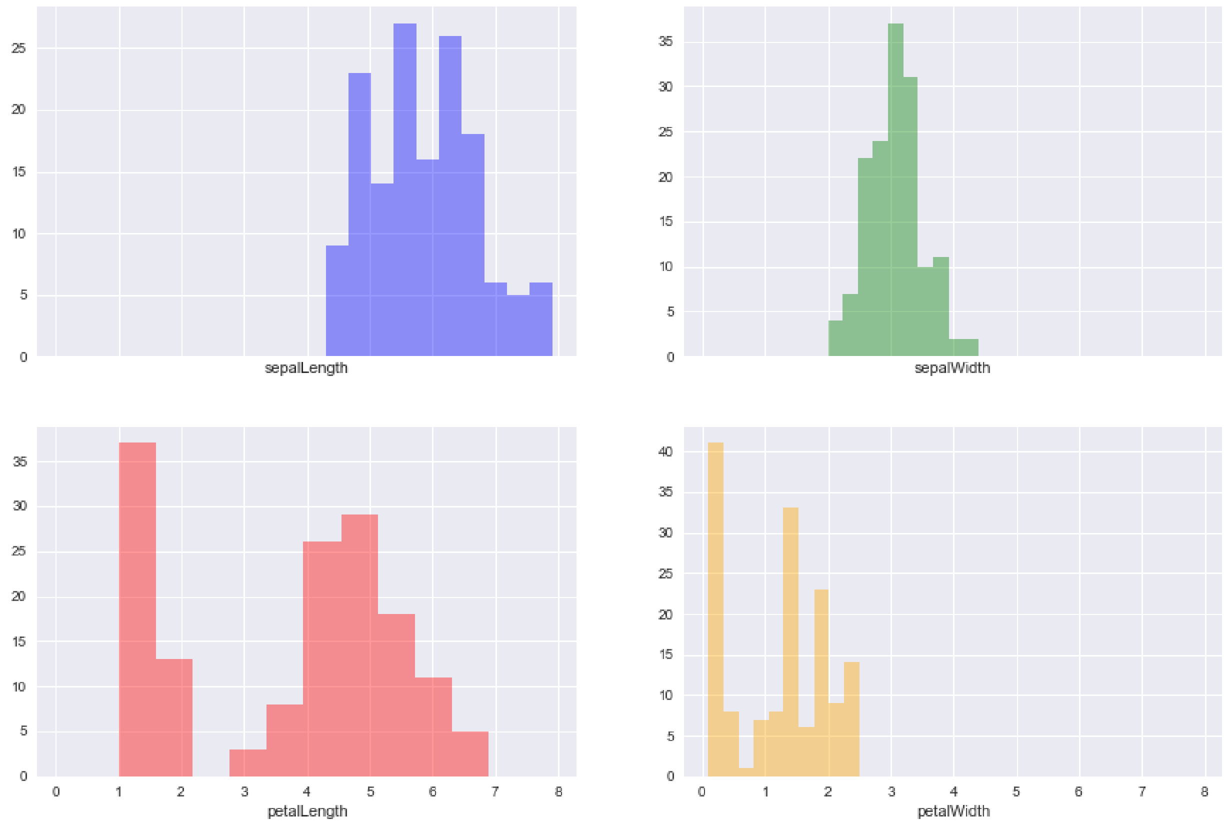
```
In [19]: plt.figure(figsize=(15,10))
         plt.subplot(2,2,1)
         sns.violinplot(x='class',y='petalLength',data=df, palette="Set2")
         plt.subplot(2,2,2)
         sns.violinplot(x='class',y='petalWidth',data=df, palette="Set2")
         plt.subplot(2,2,3)
         sns.violinplot(x='class',y='sepalLength',data=df, palette="Set2")
         plt.subplot(2,2,4)
         sns.violinplot(x='class',y='sepalWidth',data=df, palette="Set2")
         sns.plt.show()
```



Histograms

We can also create a histogram of each input variable to get an idea of the distribution.

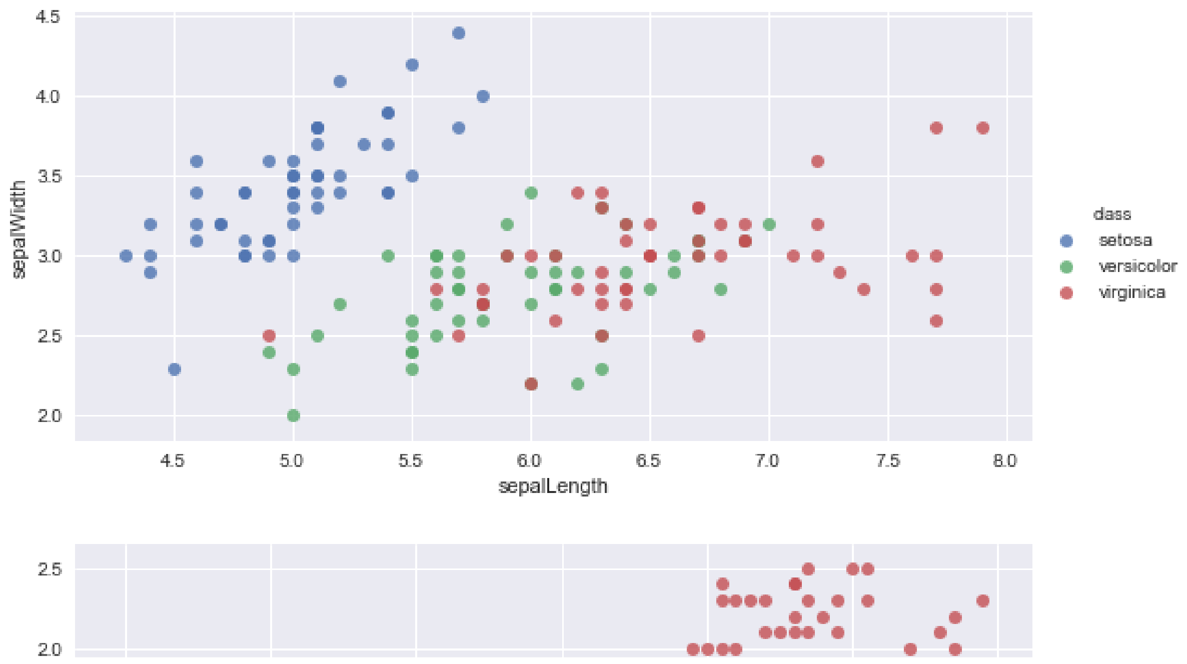
```
In [20]: f, axes = plt.subplots(2, 2, figsize=(15, 10), sharex=True)
         sns.distplot( df["sepalLength"] , color="blue", ax=axes[0, 0], kde=False, bins=10
         sns.distplot( df["sepalWidth"] , color="green", ax=axes[0, 1], kde=False, bins=10
         sns.distplot( df["petalLength"] , color="red", ax=axes[1, 0], kde=False, bins=10)
         sns.distplot( df["petalWidth"] , color="orange", ax=axes[1, 1], kde=False, bins=1
         sns.plt.show()
```



At first sight, Petal length and petal width seem to diverge from the normal distribution.

Scatter Plots

In [21]:
```
# Create scatterplot of dataframe
sns.lmplot('sepalLength', 'sepalWidth', data=df, fit_reg=False, hue="class", size
sns.lmplot('petalLength', 'petalWidth', data=df, fit_reg=False, hue="class", size
sns.lmplot('petalLength', 'sepalLength', data=df, fit_reg=False, hue="class", siz
sns.lmplot('petalLength', 'sepalWidth', data=df, fit_reg=False, hue="class", size
sns.lmplot('petalWidth', 'sepalLength', data=df, fit_reg=False, hue="class", size
sns.lmplot('petalWidth', 'sepalWidth', data=df, fit_reg=False, hue="class", size=
sns.plt.show()
```

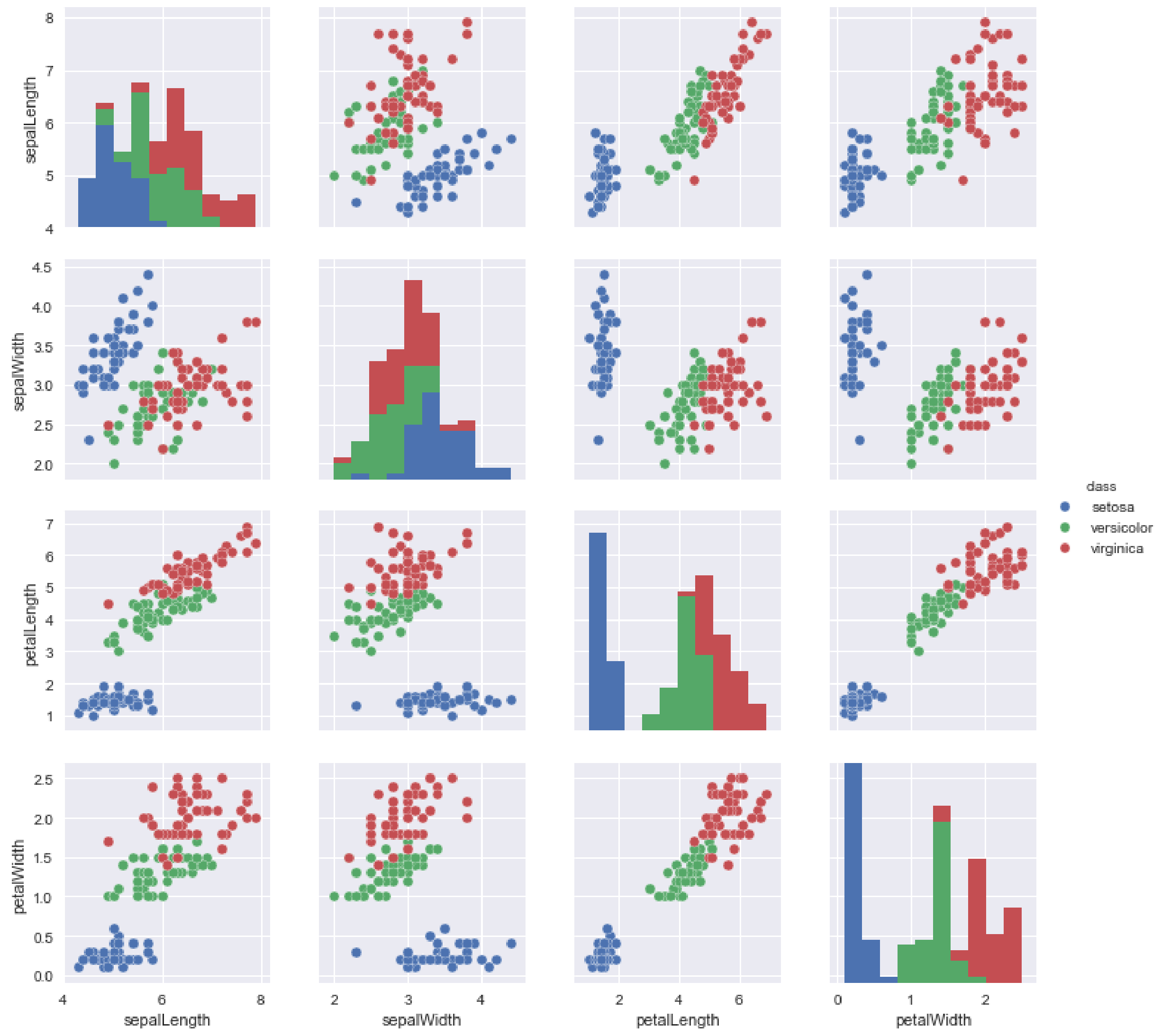


From the scatter plot, we can see that the class setosa is separataed from the other two classes across all attributes combinations.

Pair Plot

We can also compare scatter plots and histograms using pair plots, and observe the bivariate relation between each pair of attributes/features:

In [22]:
```
# Using seaborn pairplot to see the bivariate relation between each pair of featu
sns.pairplot(df, hue="class")
sns.plt.show()
```



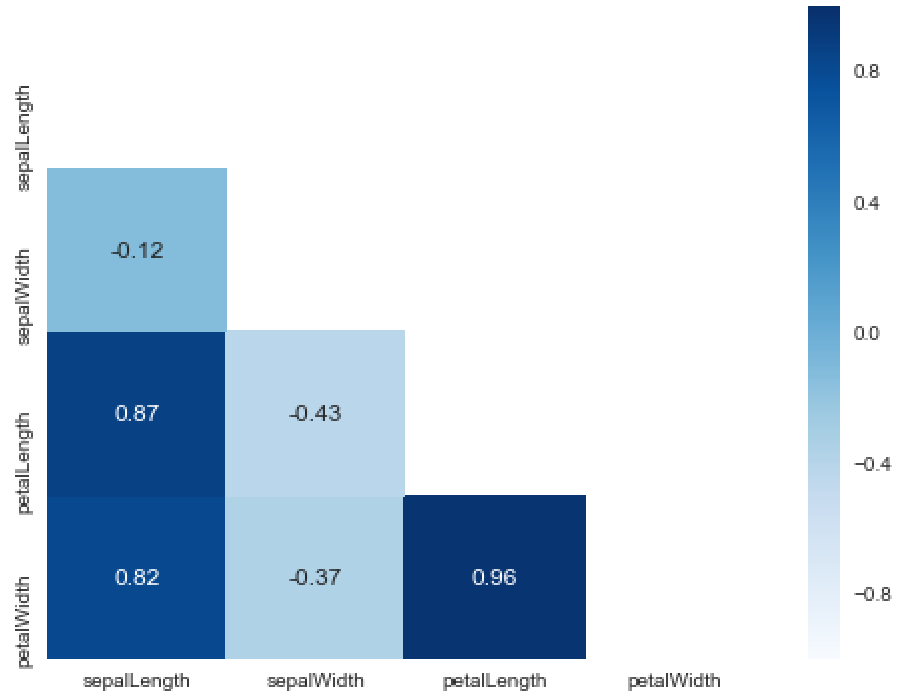
Correlations

We now look at the correlation between each pair of features:

In [23]:
```
corr = df.corr(method="pearson") #returns a dataframe, so it can be reused. metho
print(corr)
```

```
             sepalLength  sepalWidth  petalLength  petalWidth
sepalLength     1.000000   -0.117570     0.871754    0.817941
sepalWidth     -0.117570    1.000000    -0.428440   -0.366126
petalLength     0.871754   -0.428440     1.000000    0.962865
petalWidth      0.817941   -0.366126     0.962865    1.000000
```

```
In [24]: plt.figure(figsize=(8,6))
         mask = np.zeros_like(corr)
         mask[np.triu_indices_from(mask)] = True
         with sns.axes_style("white"):
             sns.heatmap(corr, xticklabels=corr.columns.values, yticklabels=corr.columns.v
                         annot=True, mask=mask)  #cmap = 'viridis'
         sns.plt.show()
```



According to the correlation matrix results, we see that the petal Length and petal Width have a very high positive correlation which can also be seen in the scatter plots above.

Modeling and Prediction

Split the data into train and test sets

```
In [25]: # Seperating the data into dependent and independent variables
         X = df.iloc[:, :-1].values
         y = df.iloc[:, -1].values

         # Splitting the dataset into the Training set and Test set
         X_train, X_test, y_train, y_test = model_selection.train_test_split(X, y, test_si
```

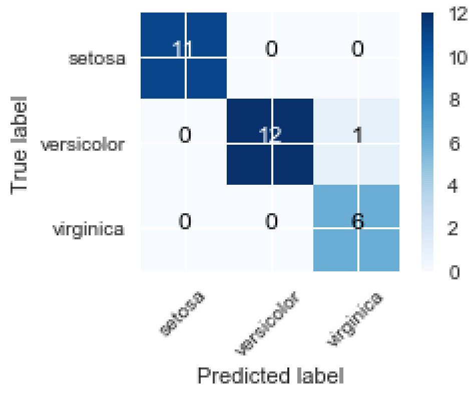
```
In [26]: # Selecting the seed and the evaluation metric
         seed = 0
         scoring = 'accuracy'
```

In [27]:
```
#Function to plot confusion matrix
def plot_confusion_matrix(cm, classes, normalize=False, cmap=plt.cm.Blues):
    """
    This function prints and plots the confusion matrix.
    Normalization can be applied by setting `normalize=True`.
    """

    plt.figure(figsize=(4,3))
    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    fmt = '.2f' if normalize else 'd'
    thresh = cm.max() / 2.
    for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
        plt.text(j, i, format(cm[i, j], fmt),
                 horizontalalignment="center",
                 color="white" if cm[i, j] > thresh else "black")

    plt.ylabel('True label')
    plt.xlabel('Predicted label')
    plt.tight_layout()
    plt.show()
```

LogisticRegression

```
In [28]: # LogisticRegression
         LR_classifier = LogisticRegression()
         LR_classifier.fit(X_train, y_train)

         y_pred = LR_classifier.predict(X_test)

         # Summary of the predictions made by the classifier
         print(classification_report(y_test, y_pred), "\n")

         # Accuracy score
         print('accuracy is', accuracy_score(y_pred,y_test))

         #confusion matrix
         cm = confusion_matrix(y_test, y_pred)
         #plt.figure()
         plot_confusion_matrix(cm, classes=df['class'].unique())
```

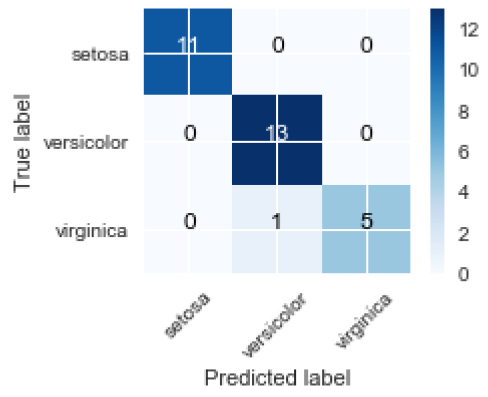
```
             precision    recall  f1-score   support

     setosa       1.00      1.00      1.00        11
 versicolor       1.00      0.92      0.96        13
  virginica       0.86      1.00      0.92         6

avg / total       0.97      0.97      0.97        30


accuracy is 0.9666666666666667
```



Naive Bayes

In [29]:
```
# Naive Bayes
NB_classifier = GaussianNB()
NB_classifier.fit(X_train, y_train)

y_pred = NB_classifier.predict(X_test)

# Summary of the predictions made by the classifier
print(classification_report(y_test, y_pred), "\n")

# Accuracy score
print('accuracy is', accuracy_score(y_pred,y_test))

#confusion matrix
cm = confusion_matrix(y_test, y_pred)
plot_confusion_matrix(cm, classes=df['class'].unique())
plt.show()
```

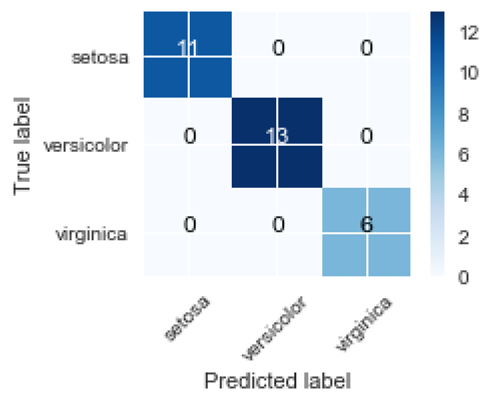
```
             precision    recall  f1-score   support

     setosa       1.00      1.00      1.00        11
 versicolor       0.93      1.00      0.96        13
  virginica       1.00      0.83      0.91         6

avg / total       0.97      0.97      0.97        30


accuracy is 0.9666666666666667
```



Support Vector Machine (SVM)

In [30]:
```python
# Support Vector Machine's
SVM_classifier = SVC()
SVM_classifier.fit(X_train, y_train)

y_pred = SVM_classifier.predict(X_test)

# Summary of the predictions made by the classifier
print(classification_report(y_test, y_pred), "\n")

# Accuracy score
print('accuracy is', accuracy_score(y_pred,y_test))

#confusion matrix
cm = confusion_matrix(y_test, y_pred)
plot_confusion_matrix(cm, classes=df['class'].unique())
plt.show()
```

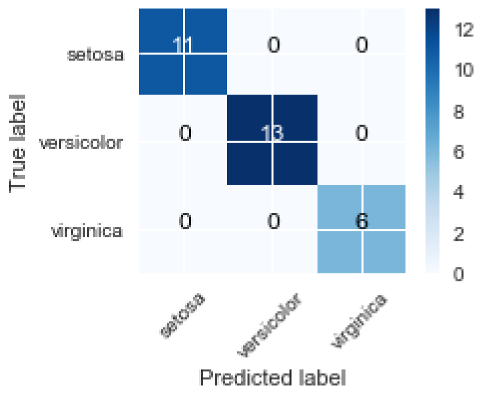
```
             precision    recall  f1-score   support

     setosa       1.00      1.00      1.00        11
 versicolor       1.00      1.00      1.00        13
  virginica       1.00      1.00      1.00         6

avg / total       1.00      1.00      1.00        30


accuracy is 1.0
```



Decision Tree

In [31]:
```
# Decision Tree
DT_classifier = DecisionTreeClassifier()

DT_classifier.fit(X_train, y_train)

y_pred = DT_classifier.predict(X_test)

# Summary of the predictions made by the classifier
print(classification_report(y_test, y_pred), "\n")

# Accuracy score
print('accuracy is', accuracy_score(y_pred,y_test))

#confusion matrix
cm = confusion_matrix(y_test, y_pred)
plot_confusion_matrix(cm, classes=df['class'].unique())
plt.show()
```

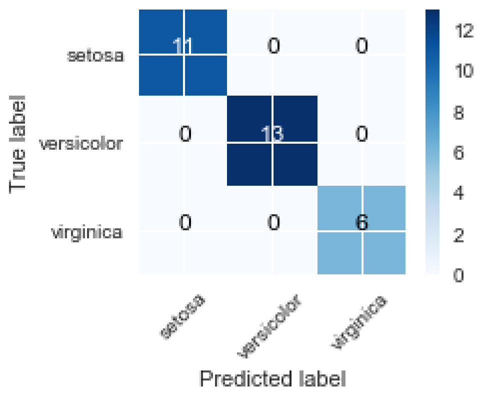
```
             precision    recall  f1-score   support

     setosa       1.00      1.00      1.00        11
 versicolor       1.00      1.00      1.00        13
  virginica       1.00      1.00      1.00         6

avg / total       1.00      1.00      1.00        30


accuracy is 1.0
```



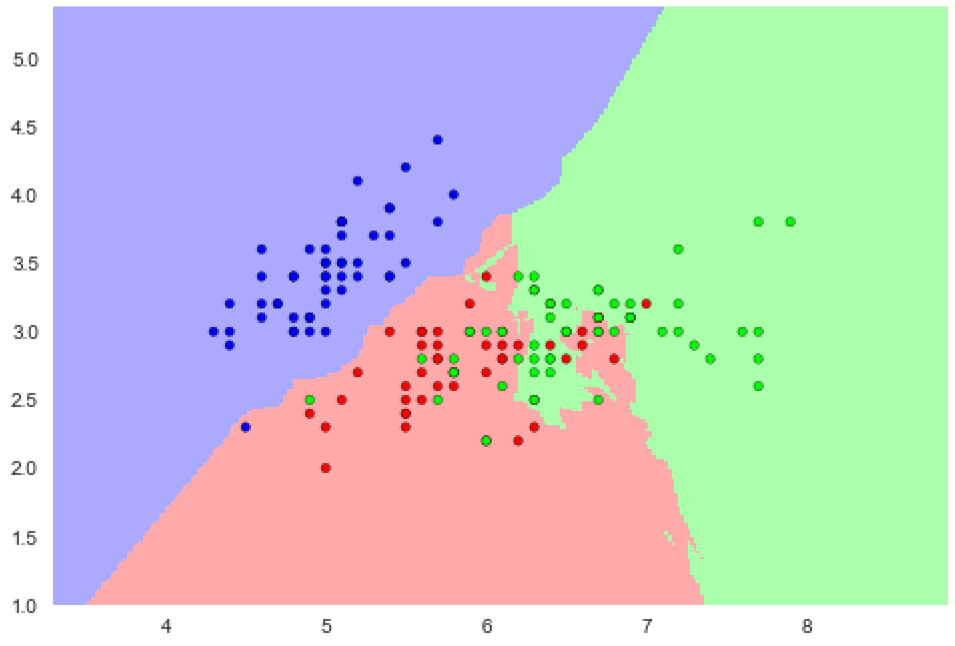
In [32]:
```
#### K-Nearest Neighbours
```

```
In [33]: # K-Nearest Neighbours
         n_nbrs = 8
         KNN_classifier = KNeighborsClassifier(n_neighbors=n_nbrs)
         KNN_classifier.fit(X_train, y_train)

         y_pred = KNN_classifier.predict(X_test)

         # Summary of the predictions made by the classifier
         print(classification_report(y_test, y_pred), "\n")

         # Accuracy score
         print('accuracy is', accuracy_score(y_pred,y_test))

         #confusion matrix
         cm = confusion_matrix(y_test, y_pred)
         plot_confusion_matrix(cm, classes=df['class'].unique())
         plt.show()
```

```
             precision    recall  f1-score   support

     setosa       1.00      1.00      1.00        11
 versicolor       1.00      1.00      1.00        13
  virginica       1.00      1.00      1.00         6

avg / total       1.00      1.00      1.00        30


accuracy is 1.0
```



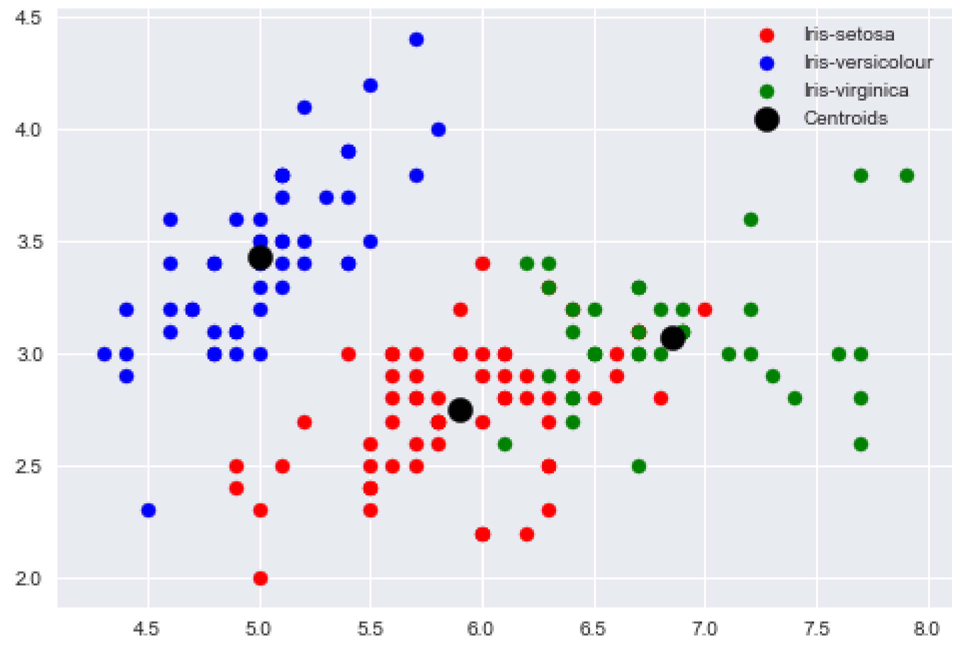
In [34]:
```
# we only take the first two features. We could avoid this ugly slicing by using 
X1 = df.iloc[:, :2].values
y1 = df.iloc[:, -1].astype('category').cat.codes.values

h = .02  # step size in the mesh

# Create color maps
cmap_light = ListedColormap(['#AAAAFF', '#FFAAAA', '#AAFFAA'])
cmap_bold = ListedColormap(['#0000FF', '#FF0000', '#00FF00'])

# we create an instance of Neighbours Classifier and fit the data.
KNN_classifier.fit(X1, y1)

# Plot the decision boundary. For that, we will assign a color to each
# point in the mesh [x_min, x_max]x[y_min, y_max].
x_min, x_max = X1[:, 0].min() - 1, X1[:, 0].max() + 1
y_min, y_max = X1[:, 1].min() - 1, X1[:, 1].max() + 1
x, y = np.meshgrid(np.arange(x_min, x_max, h), np.arange(y_min, y_max, h))
Z = KNN_classifier.predict(np.c_[x.ravel(), y.ravel()])

# Put the result into a color plot
Z = Z.reshape(x.shape)
plt.figure()
plt.pcolormesh(x, y, Z, cmap=cmap_light)

# Plot also the training points
plt.scatter(X1[:, 0], X1[:, 1], c=y1, cmap=cmap_bold, edgecolor='k', s=20)
plt.xlim(x.min(), x.max())
plt.ylim(y.min(), y.max())
plt.show()
```



KMeans Clustering

```
In [35]: kmeans = KMeans(n_clusters = 3, init = 'k-means++', max_iter = 300, n_init = 10,
         y_kmeans = kmeans.fit_predict(X)
```

```
In [36]: #Visualising the clusters
         plt.scatter(X[y_kmeans == 0, 0], X[y_kmeans == 0, 1], s = 50, c = 'red', label =
         plt.scatter(X[y_kmeans == 1, 0], X[y_kmeans == 1, 1], s = 50, c = 'blue', label =
         plt.scatter(X[y_kmeans == 2, 0], X[y_kmeans == 2, 1], s = 50, c = 'green', label

         #Plotting the centroids of the clusters
         plt.scatter(kmeans.cluster_centers_[:, 0], kmeans.cluster_centers_[:,1], s = 150,

         plt.legend()
         plt.show()
```


Iris-setosa
Iris-versicolour
Iris-virginica
Centroids