COSC 3337 : Data Science I

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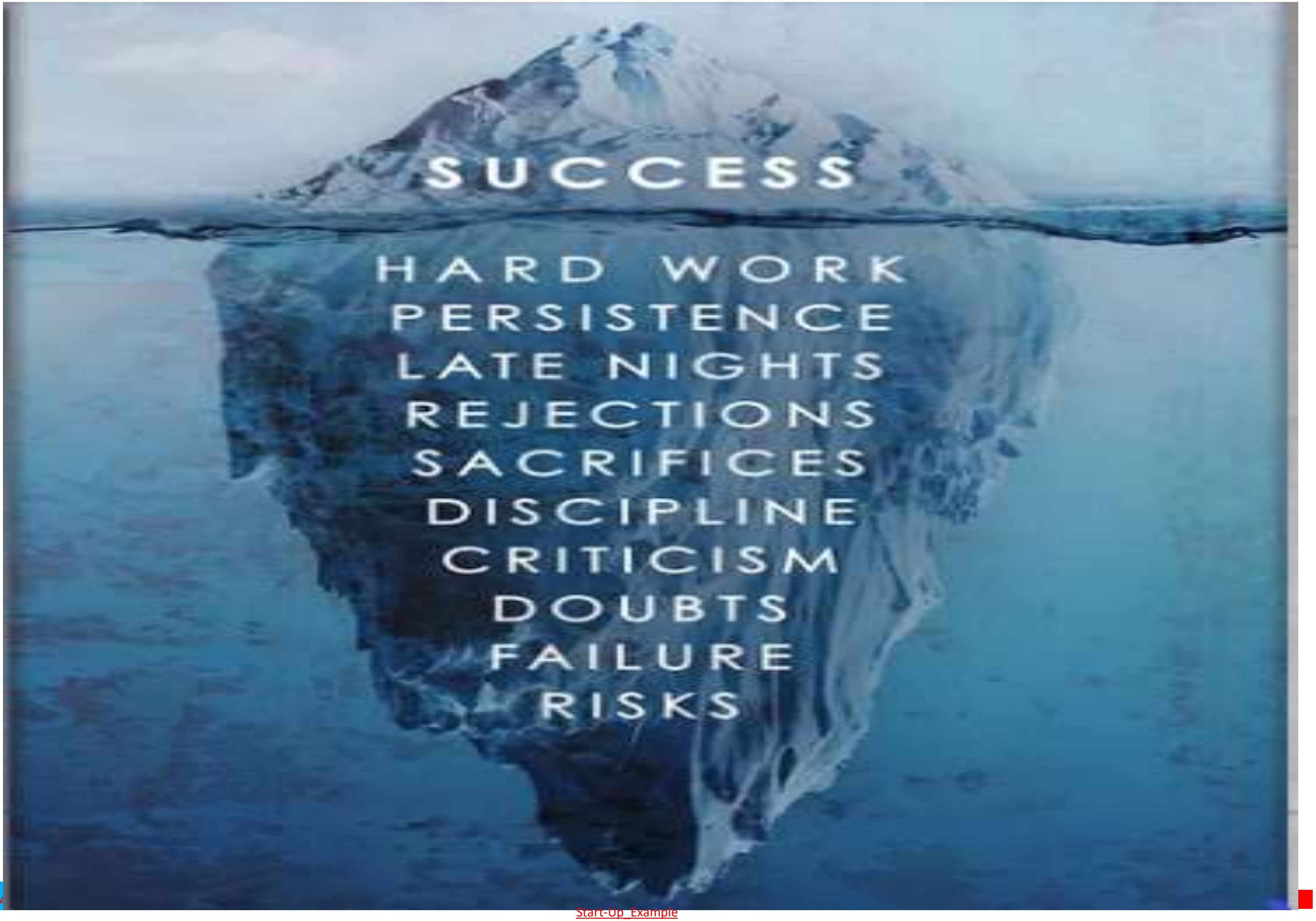
Start-Up_Example


SUCCESS
HARD WORK
PERSISTENCE
LATE NIGHTS
REJECTIONS
SACRIFICES
DISCIPLINE
CRITICISM
DOUBTS
FAILURE
RISKS

Outline

Getting started

Setting up python environment

At first, we need to set up our environment.

```
pip install numpy pandas matplotlib sklearn
```

```python
# We need pandas to import and use .csv files
import pandas as pd

# numpy is used for various numeric operations
import numpy as np

# matplotlib lets us draw nice plots
import matplotlib.pyplot as plt

# We will use several modules of sklearn package
# that is a "swiss knife" ML toolset for python
from sklearn import cluster, metrics, decomposition
```

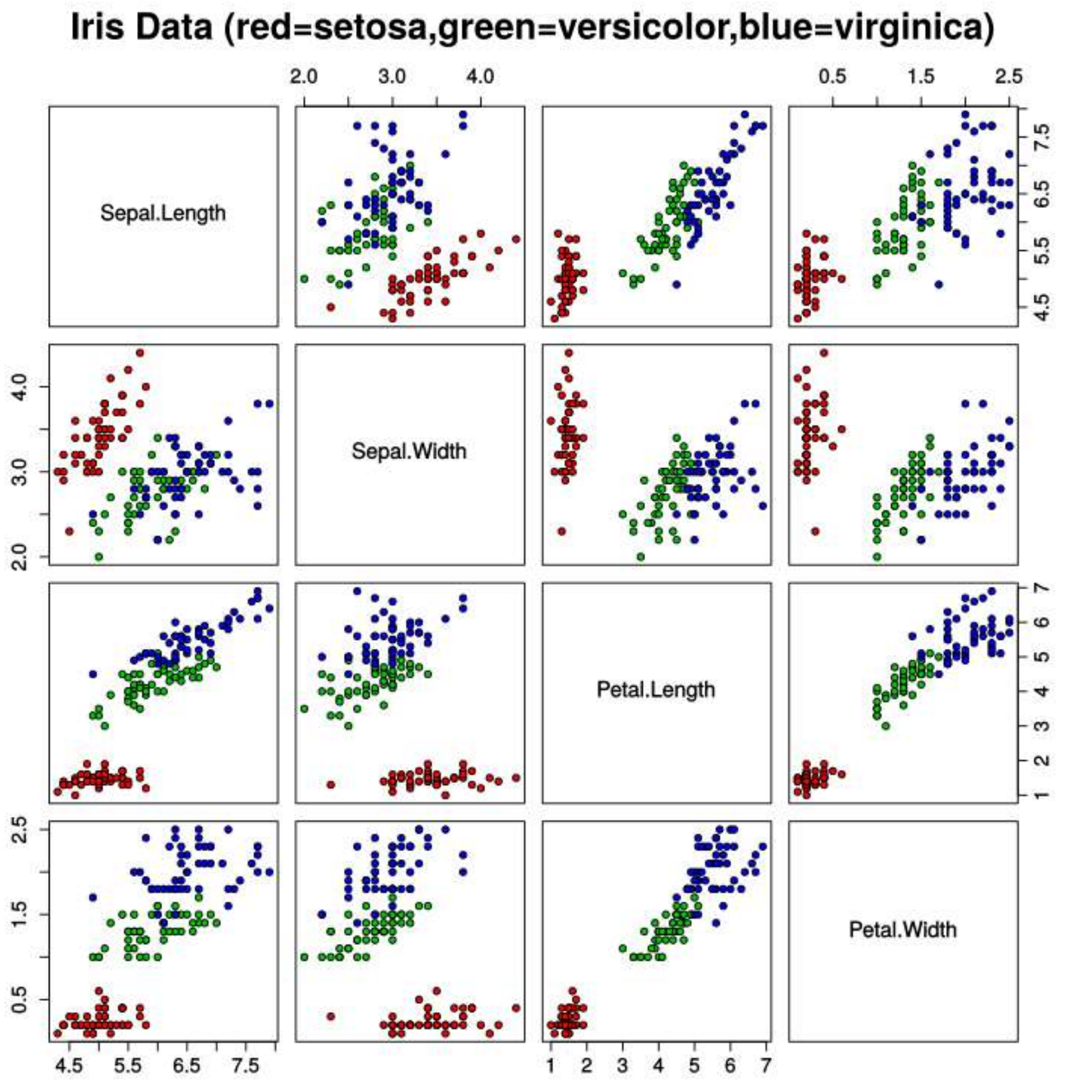
Get the Iris dataset

Example data for clustering

The Iris flower data set is a multivariate data set introduced by the British statistician and biologist Ronal Fisher in 1936.

You can read more about it on Wikipedia's page
https://en.wikipedia.org/wiki/Iris_flower_data_set

You can find the `.csv` file easily; I got it from
https://raw.githubusercontent.com/vincentarelbundock/Rdatasets/master/csv/datasets/iris.csv



Get the Iris dataset

Now, we are ready to load the `.csv` file into the interpreter using `pandas` package.

```
# Using pandas library to load csv file
# into a DataFrame object
ourData = pd.read_csv("iris.csv")

# Created object `ourData` contains
# a funny and famous data set of flowers.
# At first, we need to explore,
# what is in this data set.
# For this, pandas package provides
# several very useful functions
```

Explore the Iris dataset

Trying useful functions from `pandas`

The first useful command is `head()`
It returns first several lines of a dataframe. Very useful to get an idea of what kind of data you have!

```
ourData.head()
```

```
#    Unnamed: 0  Sepal.Length  Sepal.Width  Petal.Length  Petal.Width Species
# 0           1           5.1          3.5           1.4          0.2  setosa
# 1           2           4.9          3.0           1.4          0.2  setosa
# 2           3           4.7          3.2           1.3          0.2  setosa
# 3           4           4.6          3.1           1.5          0.2  setosa
# 4           5           5.0          3.6           1.4          0.2  setosa
```

Explore the Iris dataset

Trying useful functions from `pandas`

Second command, `info()` , can give a more precise information on what data types we operate on.

`irisData.info()`

- The dataset has 150 entries
- Sepal and petal parameters are floating-point numbers
- Species is recognized as object type – in fact, this is a text

```
# <class 'pandas.core.frame.DataFrame'>
# Int64Index: 150 entries, 0 to 149
# Data columns (total 6 columns):
# Unnamed: 0        150 non-null int64
# Sepal.Length      150 non-null float64
# Sepal.Width       150 non-null float64
# Petal.Length      150 non-null float64
# Petal.Width       150 non-null float64
# Species           150 non-null object
# dtypes: float64(4), int64(1), object(1)
# memory usage: 8.2+ KB
```

Explore the Iris dataset

Trying useful functions from `pandas`

The last command is more advanced: `ourData.describe()`.

```
ourData.describe()
```

This command gives some statistical information about numeric values in your dataset.

It is useful to understand what is the range of your values.

#	Unnamed: 0	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
# count	150.000000	150.000000	150.000000	150.000000	150.000000
# mean	75.500000	5.843333	3.057333	3.758000	1.199333
# std	43.445368	0.828066	0.435866	1.765298	0.762238
# min	1.000000	4.300000	2.000000	1.000000	0.100000
# 25%	38.250000	5.100000	2.800000	1.600000	0.300000
# 50%	75.500000	5.800000	3.000000	4.350000	1.300000
# 75%	112.750000	6.400000	3.300000	5.100000	1.800000
# max	150.000000	7.900000	4.400000	6.900000	2.500000

Explore the Iris dataset

Trying useful functions from `pandas`

But what about the last column `Species`?

We've seen these are textual values. Now, let us see what kinds of values does this column have?

```
# Get unique values in the column
species = ourData.Species.unique()

print(species)
```

```
# ['setosa' 'versicolor' 'virginica']
```

Draw some plots

Using `matlplotlib`

Let's try to plot something!

```
# plot different species in different colours
colors = ['g', 'r', 'b', 'c', 'm', 'k']
species_dict = dict(zip(species, colors))
plt.scatter( ourData['Sepal.Length']
           , ourData['Sepal.Width']
           , c=ourData['Species']
                .apply(lambda x: species_dict[x])
           )
# use either
#    plt.show() # to draw on-screen
# or
#    plt.savefig("filename") # to save picture
plt.savefig("real-labels.png")
```

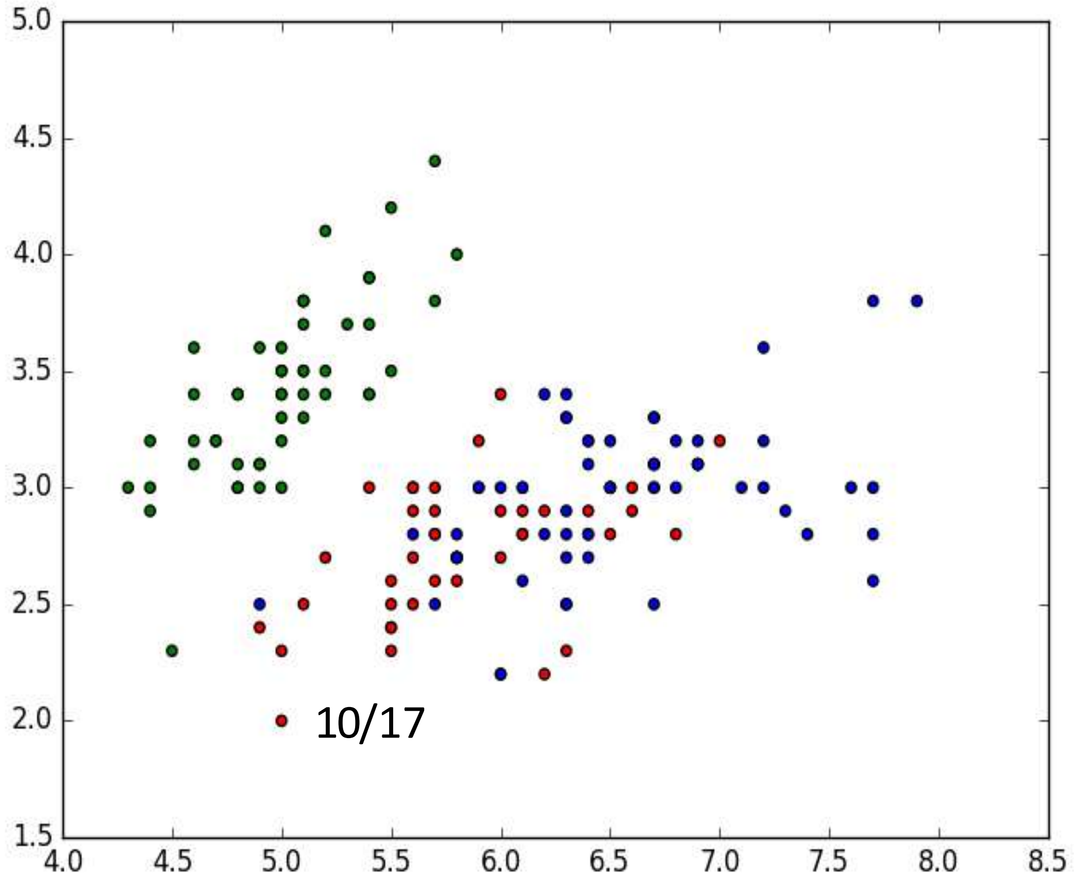
In this example I map names of the species onto colors.

Play with this code a little bit changing the columns to plot. This gives you an insight how the data looks like.

Draw some plots

Using `matlplotlib`

...And here is how the result looks like



Prepare data

Split input and labels

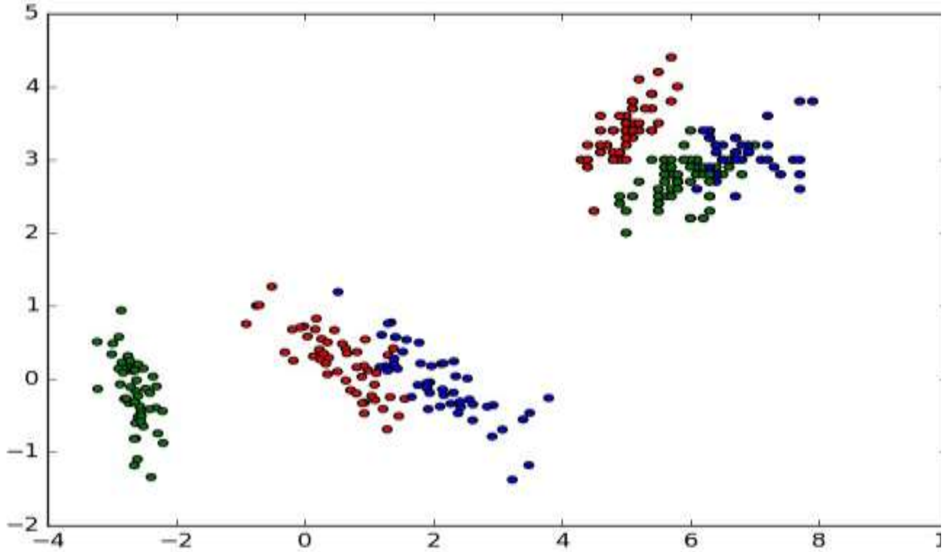
```
# Here is our data, but without species information
ourDataNoLabels
  = pd.DataFrame( ourData
                , columns=[ 'Sepal.Length'
                          , 'Sepal.Width'
                          , 'Petal.Length'
                          , 'Petal.Width'
                          ]
                )
```

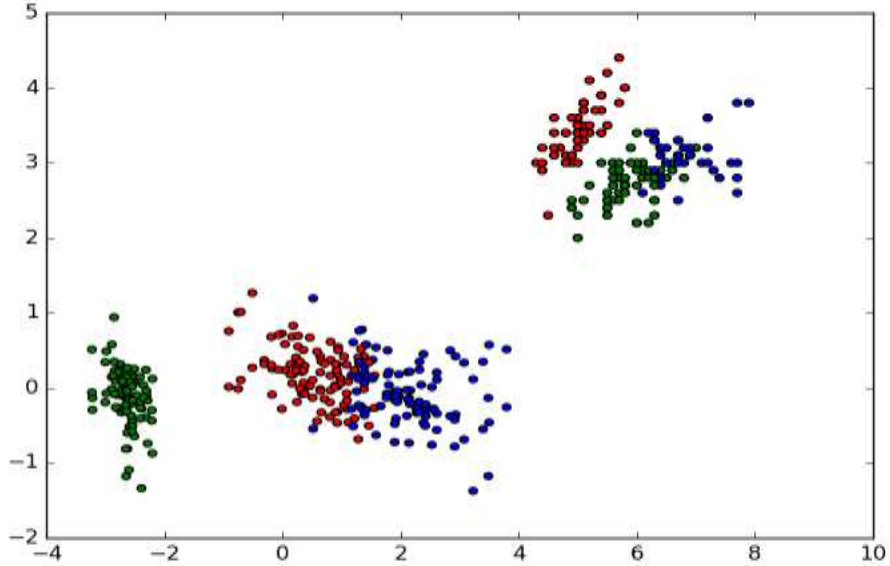
Copy the data to a new variable `ourDataNoLabels`.
We will play like we don't know the labels and want to estimate them.

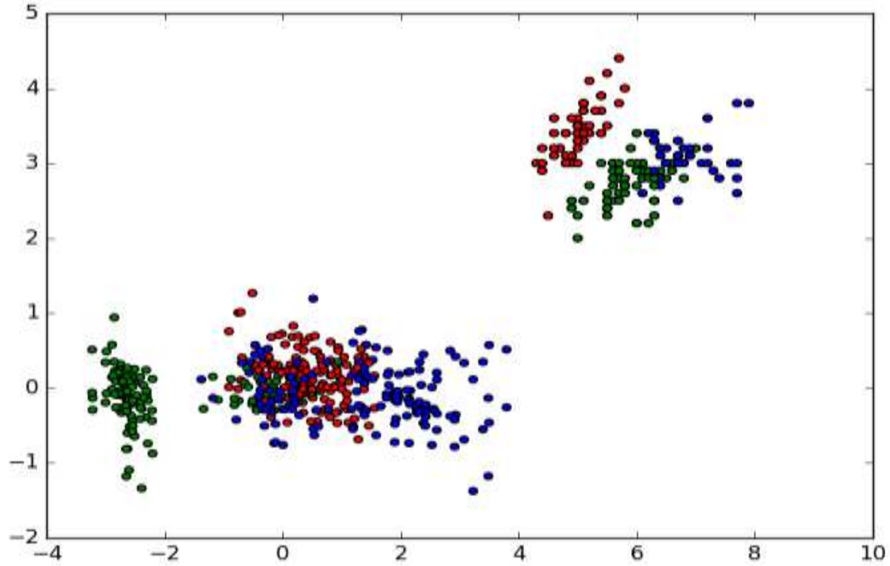
Draw some plots

Using `matplotlib`

...And here are the plots







Principal Component analysis

Using `sklearn.decomposition`

This code performs PCA (lines 3-7).
(Most of the code is just to draw three plots).

Principal component transform is a procedure that rotates point space in such a way that points variance is the biggest along X-axis, the second is along Y-axis, and so on.

The method is simple but very powerful for data exploration. If data have many dimensions (i.e. 50) it is very convenient to look only at 2-5 most significant dimensions. Otherwise visual inspection of the data would be too difficult.

```
1  # Run Principal Component Analysis
2  # to get more understanding how our data looks like
3  ourDataReduced
4    = decomposition
5      .PCA(n_components=3)
6      .fit_transform(ourDataNoLabels)
7  plt.scatter( ourDataReduced[:,0]
8             , ourDataReduced[:,1]
9             , c=ourData['Species']
10                .apply(lambda x: species_dict[x]))
11 plt.savefig("real-pca-1-2.png")
12 plt.scatter( ourDataReduced[:,0]
13            , ourDataReduced[:,2]
14            , c=ourData['Species']
15                .apply(lambda x: species_dict[x]))
16 plt.savefig("real-pca-1-3.png")
17 plt.scatter( ourDataReduced[:,1]
18            , ourDataReduced[:,2]
19            , c=ourData['Species']
20                .apply(lambda x: species_dict[x]))
21 plt.savefig("real-pca-2-3.png")
```

Principal Component analysis

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17 plt.scatter( ourDataReduced[:,1]
18       12/17 , ourDataReduced[:,2]
19            , c=ourData['Species']
20              .apply(lambda x: species_dict[x]))
21 plt.savefig("real-pca-2-3.png")
```

K-means clustering

Using `sklearn.cluster`

Finally, we are ready for some clustering!

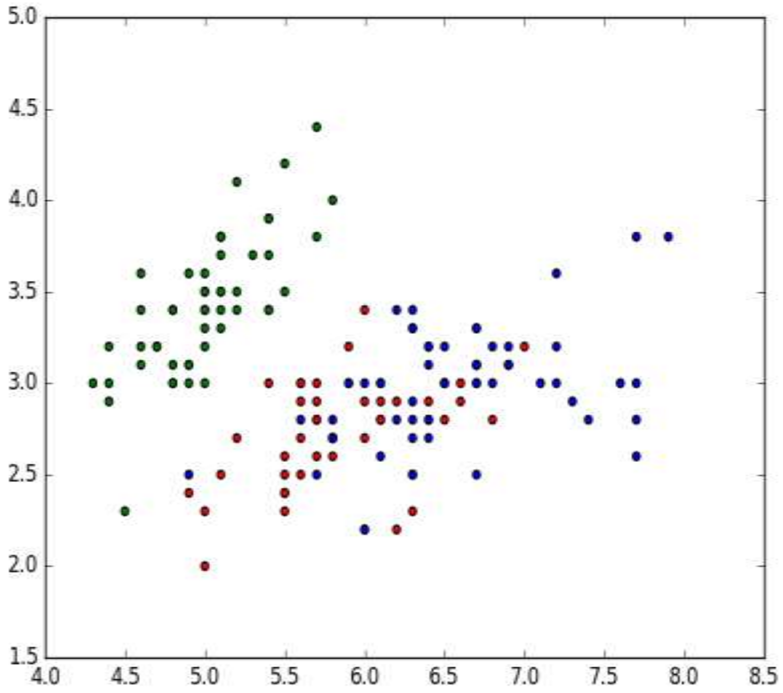
```
# We know that there must be 3 different clusters
#                                          - species of flowers.
# So let's give this hint to the algorithm
kmeans = cluster.KMeans(3)
                   .fit(np.array(ourDataNoLabels))
foundLabels
   = pd.DataFrame( kmeans.labels_
                  , columns=['K-means clusters'])

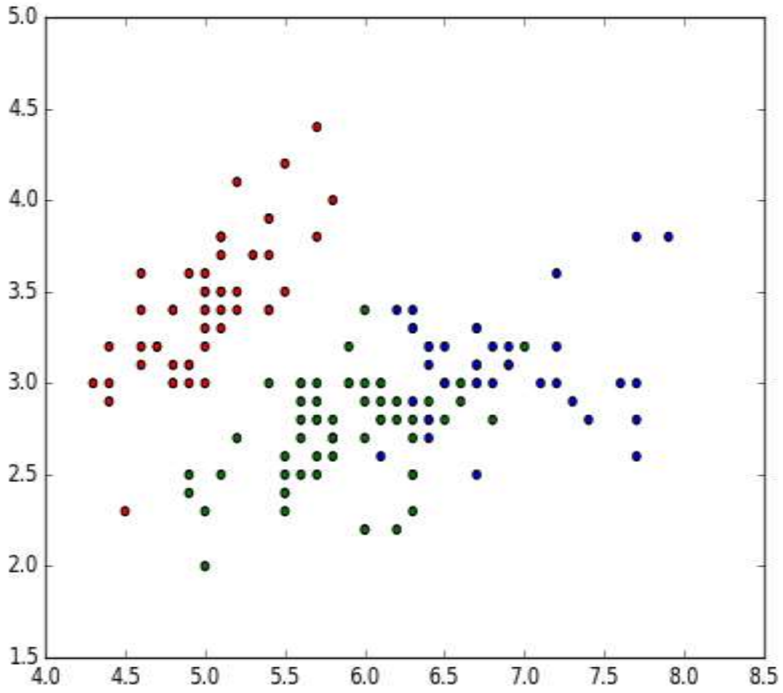

plt.scatter( ourData['Sepal.Length']
            , ourData['Sepal.Width']
            , c=foundLabels['K-means clusters']
                 .apply(lambda x: colors[x])
            )
plt.savefig("predicted-labels.png")
```

K-means clustering

Using `sklearn.cluster`

Let's compare plots...





...would you say this is a good result?

Assess clustering quality

Using `pandas`

A very good way to assess performance of an unsupervised clustering algorithm is to look at co-occurrence tables.

```
mat = pd.crosstab( ourData['Species']
                 , foundLabels['K-means clusters']
                 )
print(mat)
```

Package `pandas` provides a special function `crosstab()` that calculates how many times a value from one column occurs together with a value from another column.

```
# K-means clusters    0   1   2
# Species
# setosa              0  50   0
# versicolor         48   0   2
# virginica          14   0  36
```

So, what would be a conclusion now?

Bonus: DBSCAN

Using `sklearn.cluster`

This code does everything the same way as KMeans clustering example.

```
dbscan = cluster.DBSCAN()
                      .fit(np.array(ourDataNoLabels))
foundLabels['DBSCAN clusters']
     = pd.DataFrame( dbscan.labels_
                     , columns=['DBSCAN clusters'])
plt.scatter( ourData['Sepal.Length']
           , ourData['Sepal.Width']
           , c=foundLabels['DBSCAN clusters']
                     .apply(lambda x: colors[x]))
plt.savefig("predicted-labels2.png")
mat = pd.crosstab( ourData['Species']
                 , foundLabels['DBSCAN clusters'])
print(mat)
```

Try it! And compare the results.
Which algorithm performs better?