

Python Code for Chapter 2 of Introduction to Data Mining

1.Data Preparation

Load necessary packages.

```
1. @Load packages
2. import pandas as pd
3. from pandas import Series, DataFrame
4. import numpy as np
5. from sklearn.datasets import load_iris
6. import matplotlib.pyplot as plt
7. import seaborn as sns
```

Load Iris dataset and store it in a dataframe.

```
1. data=load_iris()
2. data.target.shape=(len(data.data),1)
3. #concatenate the target column and the feature columns
4. new_data=np.concatenate((data.data,data.target),axis=1)
5. iris=pd.DataFrame(new_data,columns=
    ['sepal_length','sepal_width','petal_length','petal_width','target'])
```

Let us take a look at the iris dataframe.

```
1. print(iris.head(10))
```

	sepal_length	sepal_width	petal_length	petal_width	target
0	5.1	3.5	1.4	0.2	0.0
1	4.9	3.0	1.4	0.2	0.0
2	4.7	3.2	1.3	0.2	0.0
3	4.6	3.1	1.5	0.2	0.0
4	5.0	3.6	1.4	0.2	0.0
5	5.4	3.9	1.7	0.4	0.0
6	4.6	3.4	1.4	0.3	0.0
7	5.0	3.4	1.5	0.2	0.0
8	4.4	2.9	1.4	0.2	0.0
9	4.9	3.1	1.5	0.1	0.0

```
[ 0.92154126  0.04875355  0.01851016  0.00716384  0.00403119]
```

2. Data Quality

Check the basic statistics of iris dataset.

```
1. print(iris.info())
2. print(iris.describe())
```

Note that no missing values in iris dataset.

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 150 entries, 0 to 149
Data columns (total 5 columns):
sepal_length    150 non-null float64
sepal_width     150 non-null float64
petal_length    150 non-null float64
petal_width     150 non-null float64
target         150 non-null float64
dtypes: float64(5)
memory usage: 5.9 KB
None
```

	sepal_length	sepal_width	petal_length	petal_width	target
count	150.000000	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667	1.000000
std	0.828066	0.433594	1.764420	0.763161	0.819232
min	4.300000	2.000000	1.000000	0.100000	0.000000
25%	5.100000	2.800000	1.600000	0.300000	0.000000
50%	5.800000	3.000000	4.350000	1.300000	1.000000
75%	6.400000	3.300000	5.100000	1.800000	2.000000
max	7.900000	4.400000	6.900000	2.500000	2.000000

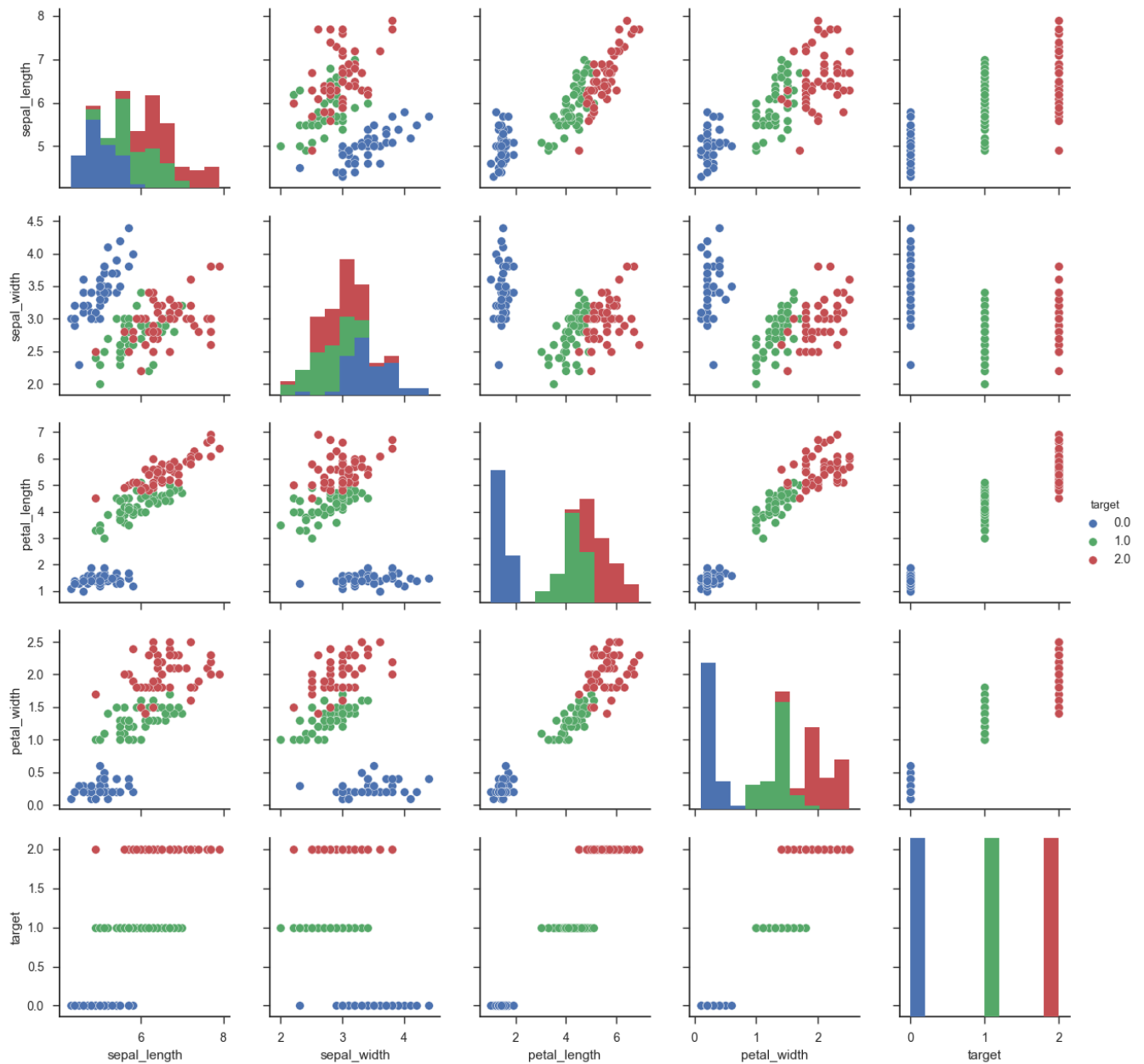
Inspect the scatter matrix plot of iris dataset.

```
1. #The scatter-matrix of iris
2. sns.set(style="ticks")
3. sns.pairplot(iris,hue="target")
```

```

4. plt.savefig("Scatter Matrix.png")
5. plt.show()

```



Check the duplicated rows and remove them.

```

1. print('number of duplicated:',iris.duplicated().sum())
2. iris=iris.drop_duplicates()

```

number of duplicated: 3

3. Aggregation

Aggregate by species using mean.

```
1. grouped_mean=iris.groupby('target').mean()  
2. print(grouped_mean)
```

target	sepal_length	sepal_width	petal_length	petal_width
0.0	5.010417	3.431250	1.462500	0.250000
1.0	5.936000	2.770000	4.260000	1.326000
2.0	6.604082	2.979592	5.561224	2.028571

Aggregate by species using mean.

```
1. grouped_median=iris.groupby('target').median()  
2. print(grouped_median)
```

target	sepal_length	sepal_width	petal_length	petal_width
0.0	5.0	3.4	1.50	0.2
1.0	5.9	2.8	4.35	1.3
2.0	6.5	3.0	5.60	2.0

[0.92154126 0.04875355 0.01851016 0.00716384 0.00403119]

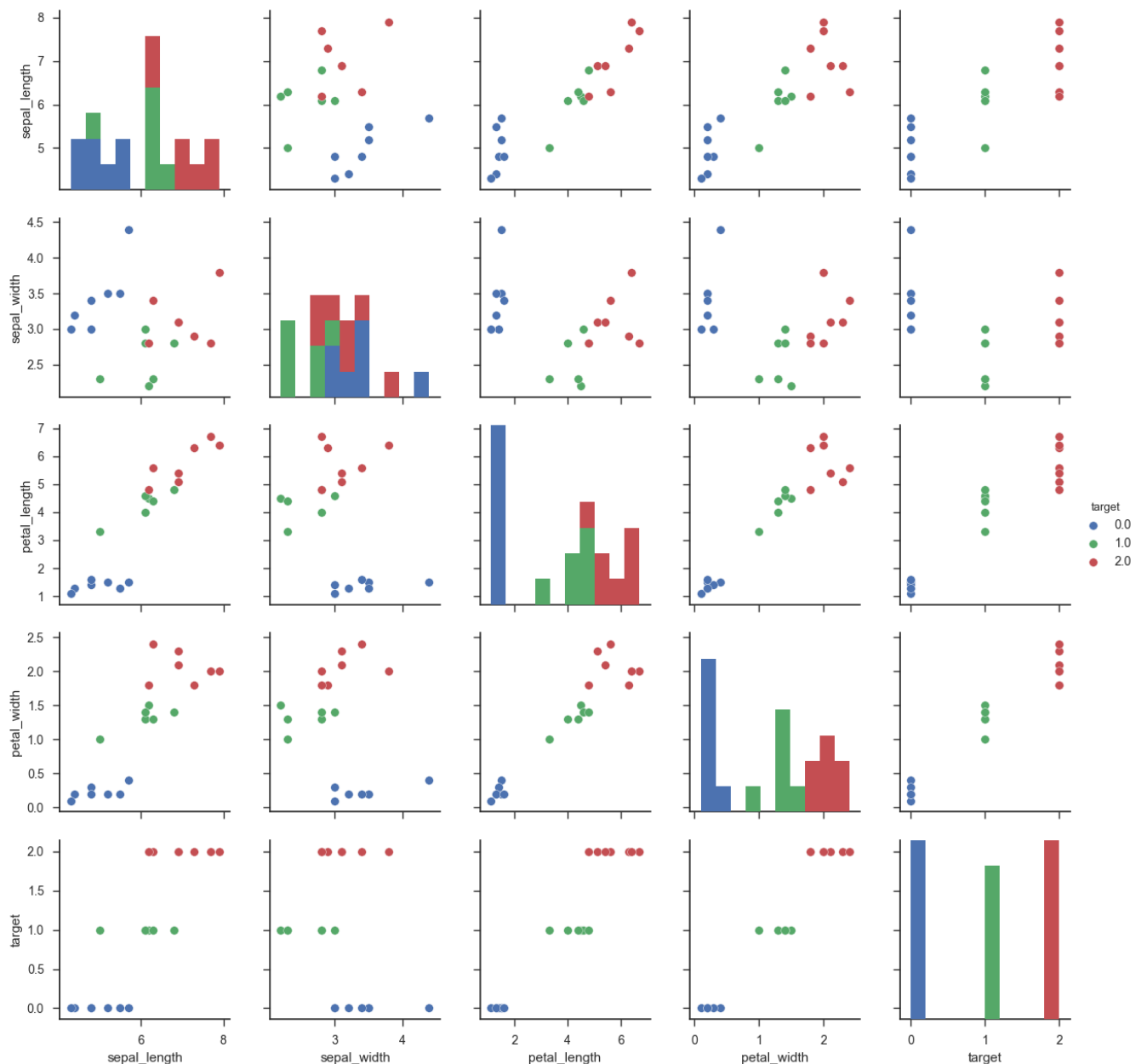
4. Random Sampling

```
1. random_sampled=iris.take(np.random.permutation(len(iris))[:20])  
2. print(random_sampled)
```

	sepal_length	sepal_width	petal_length	petal_width	target
75	6.6	3.0	4.4	1.4	1.0
72	6.3	2.5	4.9	1.5	1.0
28	5.2	3.4	1.4	0.2	0.0
103	6.3	2.9	5.6	1.8	2.0
58	6.6	2.9	4.6	1.3	1.0
10	5.4	3.7	1.5	0.2	0.0
9	4.9	3.1	1.5	0.1	0.0
7	5.0	3.4	1.5	0.2	0.0
137	6.4	3.1	5.5	1.8	2.0
39	5.1	3.4	1.5	0.2	0.0
51	6.4	3.2	4.5	1.5	1.0
131	7.9	3.8	6.4	2.0	2.0
124	6.7	3.3	5.7	2.1	2.0
52	6.9	3.1	4.9	1.5	1.0
112	6.8	3.0	5.5	2.1	2.0
53	5.5	2.3	4.0	1.3	1.0
41	4.5	2.3	1.3	0.3	0.0
50	7.0	3.2	4.7	1.4	1.0
70	5.9	3.2	4.8	1.8	1.0
44	5.1	3.8	1.9	0.4	0.0

Scatter plot on sampling dataset.

```
1. sns.set(style="ticks")
2. sns.pairplot(random_sampled,hue="target")
3. plt.savefig('sampling')
4. plt.show()
```



5. Dimensionality reduction (Principal Components Analysis - PCA)

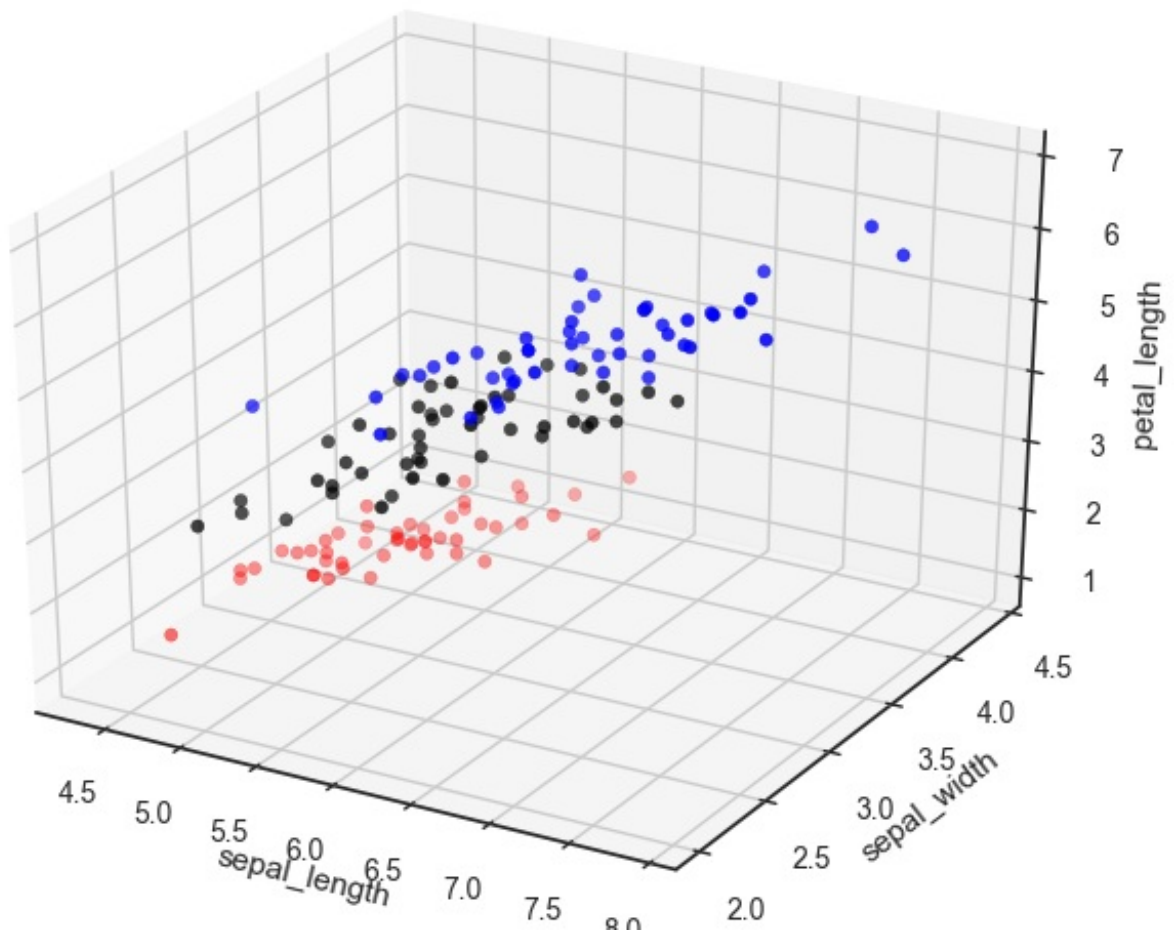
Plot 3D scatter plot for the first three features.

```
1. from mpl_toolkits.mplot3d import Axes3D
2. fig=plt.figure()
3. ax=Axes3D(fig)
4. colors=['red','k','blue']
5. x_vals=iris.sepal_length; y_vals=iris.sepal_width;
```

```

z_vals=iris.petal_length
6. ax.scatter(x_vals,y_vals,z_vals,c=iris.target.apply(lambda x: colors[int(x)]))
7. ax.set_xlabel('sepal_length')
8. ax.set_ylabel('sepal_width')
9. ax.set_zlabel('petal_length')
10. plt.show()

```



Find the suitable components for PCA.

```

1. from sklearn.decomposition import PCA
2. pca=PCA()
3. pca.fit(iris)
4. print(pca.explained_variance_ratio_)

```

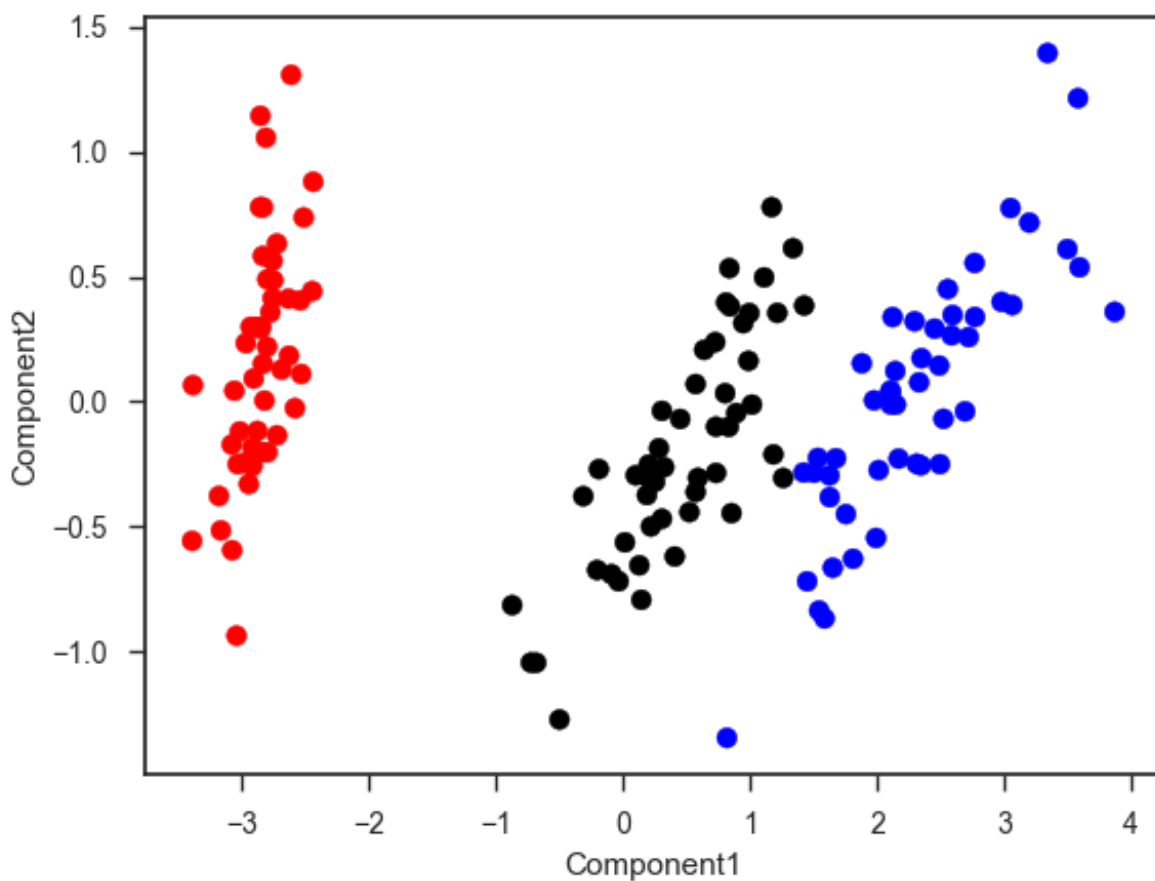
Note that only the first dimension matters, but in this example we consider the first two dimensions.

```
[ 0.92154126  0.04875355  0.01851016  0.00716384  0.00403119]
```

```
1.  pca.n_components=2
2.  iris_reduced=pca.fit_transform(iris)
```

Plot the scatter of new reduced dataset.

```
1.  fig=plt.figure()
2.  ax1=fig.add_subplot(111)
3.  x_val=iris_reduced[:,0];y_val=iris_reduced[:,1]
4.  colors=['red','k','blue']
5.  ax1.scatter(x_val,y_val,c=iris.target.apply(lambda x:colors[int(x)]))
6.  ax1.set_xlabel('Component1')
7.  ax1.set_ylabel('Component2')
```

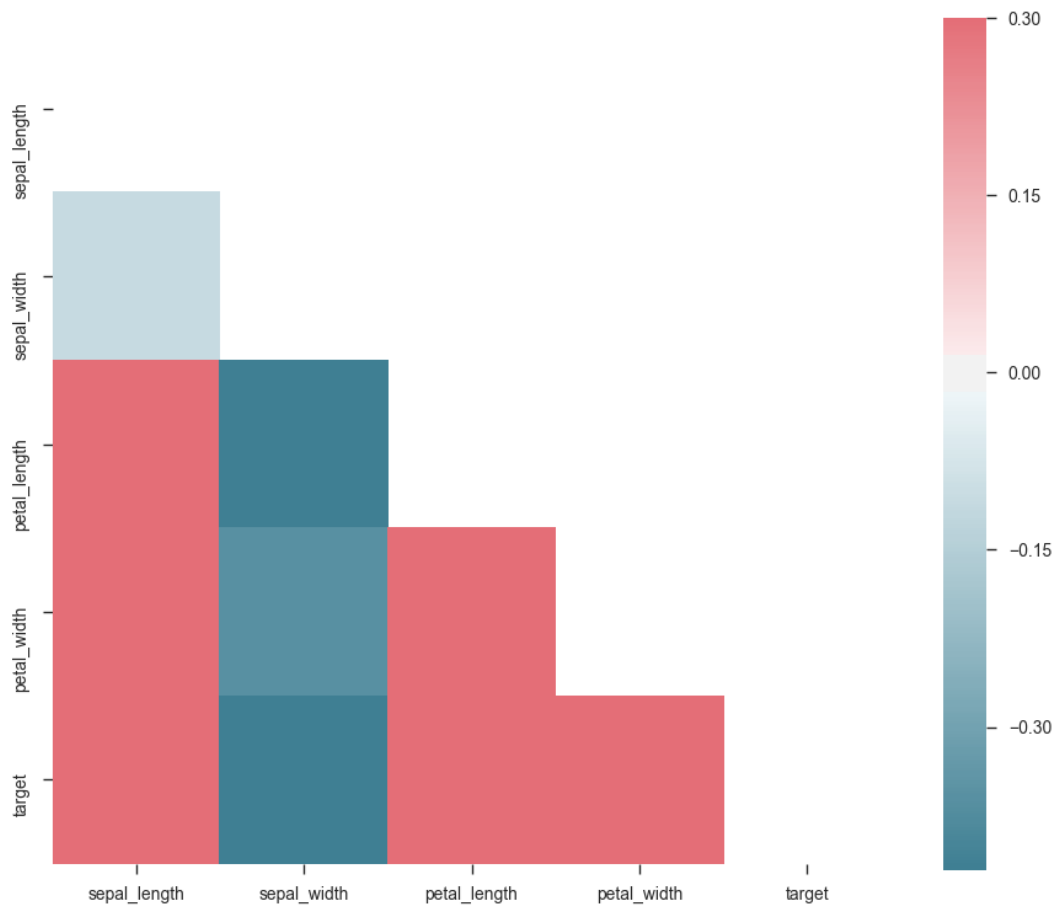


6 Correlation Matrix


```

1. correlation_matrix=iris.corr()
2. mask = np.zeros_like(correlation_matrix, dtype=np.bool)
3. mask[np.triu_indices_from(mask)] = True
4. f, ax = plt.subplots(figsize=(11, 9))
5. cmap = sns.diverging_palette(220, 10, as_cmap=True)
6. sns.heatmap(correlation_matrix, mask=mask, cmap=cmap, vmax=.3, center=
0,
7.             square=True, ax=ax)
8. plt.show()

```



To be continued.....