▼ Pre-requisites

```
#importing ibraries to use
import pandas as pd
import numpy as np

data=pd.read_excel('my_iris.xlsx')

# checking data
data.describe()
```



	Unnamed: 0	sepal depth	sepal diameter	petal depth	petal diameter	sepa!
count	150.000000	130.000000	130.000000	130.000000	100.000000	1!
mean	74.500000	5.901538	3.005385	4.115385	1.453000	
std	43.445368	0.835082	0.410013	1.621200	0.685117	
min	0.000000	4.300000	2.000000	1.100000	0.100000	
25%	37.250000	5.125000	2.800000	3.350000	1.100000	
50%	74.500000	5.850000	3.000000	4.500000	1.500000	
75%	111.750000	6.475000	3.200000	5.200000	2.000000	
max	149.000000	7.900000	4.100000	6.900000	2.500000	

Data Cleaning

▼ Dropping redundant columns

```
data=data.drop([data.columns[0]],axis=1)
data.describe()

# Till now only first column is dropped as indexes of dataframe are duplicating with i
# So dropping index column will have no effect on data.
data=data.drop([data.columns[1]],axis=1) # sepal diameter is redundant
```

data=data.drop([data.columns[2]],axis=1) # petal diameter is redundant
data.head()

	sepal depth	petal depth	sepal length	sepal width	petal length	petal width
0	NaN	NaN	10.2	-7.0	5.6	-0.8
1	4.9	1.4	9.8	-6.0	5.6	-0.8
2	4.7	NaN	9.4	-6.4	5.2	-0.8
3	4.6	1.5	9.2	-6.2	6.0	-0.8
4	NaN	NaN	10.0	-7.2	5.6	-0.8

Structuring and Standardising data

data['sepal width']=data['sepal width'].apply(lambda x: -1*x) # for sepal width data['petal width']=data['petal width'].apply(lambda x: -1*x) # for petal width data.describe()

The column of sepal width and petal width have all negative values, however a measure # This may be considered a human error and all values should be converted to positive

	sepal depth	petal depth	sepal length	sepal width	petal length	petal wi
count	130.000000	130.000000	150.000000	150.000000	150.000000	150.00
mean	5.901538	4.115385	11.686667	6.108000	15.034667	4.79
std	0.835082	1.621200	1.656132	0.867189	7.057682	3.05
min	4.300000	1.100000	8.600000	4.000000	4.000000	0.40
25%	5.125000	3.350000	10.200000	5.600000	6.400000	1.20
50%	5.850000	4.500000	11.600000	6.000000	17.400000	5.20
75%	6.475000	5.200000	12.800000	6.600000	20.400000	7.20
max	7.900000	6.900000	15.800000	8.800000	27.600000	10.00

▼ Filling missing values

for petal depth column
temp=pd.DataFrame({'original':data['petal depth'],'interpolation':data['petal depth'].
temp.describe()

	original	interpolation	mean	median
count	130.000000	149.000000	150.000000	150.000000
mean	4.115385	3.780201	4.115385	4.166667
std	1.621200	1.751021	1.508475	1.514169
min	1.100000	1.100000	1.100000	1.100000
25%	3.350000	1.600000	3.825000	3.825000
50%	4.500000	4.400000	4.350000	4.500000

for sepal depth column
temp=pd.DataFrame({'original':data['sepal depth'],'interpolation':data['sepal depth'].
temp.describe()

	original	interpolation	mean	median
count	130.000000	149.000000	150.000000	150.000000
mean	5.901538	5.830537	5.901538	5.894667
std	0.835082	0.826886	0.777018	0.777216
min	4.300000	4.300000	4.300000	4.300000
25%	5.125000	5.100000	5.400000	5.400000
50%	5.850000	5.800000	5.901538	5.850000
75%	6.475000	6.400000	6.400000	6.400000
max	7.900000	7.900000	7.900000	7.900000

data['petal depth']=data['petal depth'].fillna(data['petal depth'].median())
data['sepal depth']=data['sepal depth'].fillna(data['sepal depth'].median())

Here replacing missing values with median over mean or interpolation is preferred as # of all three approaches. It can be observed that replacing with median values create # in data as both mean and median deviate by minimum in this case. data.describe()

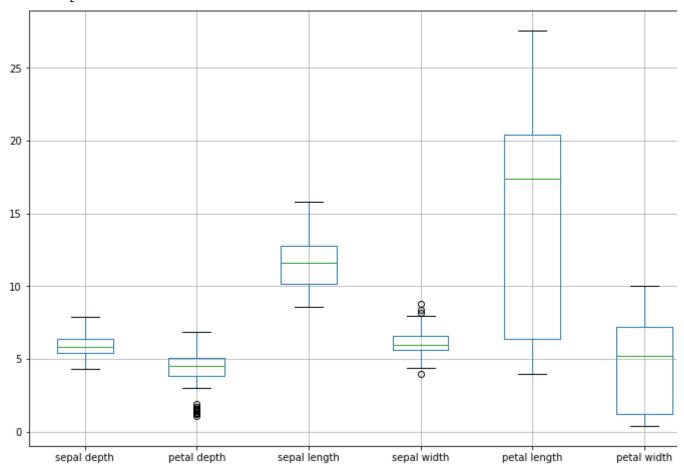
	sepal depth	petal depth	sepal length	sepal width	petal length	petal wi
count	150.000000	150.000000	150.000000	150.000000	150.000000	150.00
mean	5.894667	4.166667	11.686667	6.108000	15.034667	4.79

Outlier Detection and Removal

```
data.boxplot(figsize=(12,8))
```

Here box and whisker plot is used to visualize any outliers present in the data.

<AxesSubplot:>



```
# applying log transformation
data['sepal depth'] = np.log10(data['sepal depth'])
data['petal depth'] = np.log10(data['petal depth'])
data.describe()
```

	sepal depth	petal depth	sepal length	sepal width	petal length	petal wi
count	150.000000	150.000000	150.000000	150.000000	150.000000	150.00
mean	0.766711	0.577021	11.686667	6.108000	15.034667	4.79
std	0.057337	0.215248	1.656132	0.867189	7.057682	3.05
min	0.633468	0.041393	8.600000	4.000000	4.000000	0.40
25%	0.732394	0.582604	10.200000	5.600000	6.400000	1.20
remove_outlier(df_in, col_name): q1 = df_in[col_name].quantile(0.25)						

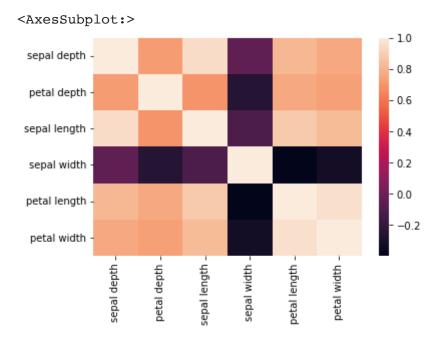
```
def remove_outlier(df_in, col_name):
    q1 = df_in[col_name].quantile(0.25)
    q3 = df_in[col_name].quantile(0.75)
    iqr = q3-q1 #Interquartile range
    fence_low = q1-1.5*iqr
    fence_high = q3+1.5*iqr
    df_out = df_in.loc[(df_in[col_name] > fence_low) & (df_in[col_name] < fence_high);
    return df_out</pre>
```

After performing log transformation or outlier removal on this data, Log tranformati # approach in this case as it does not reduce the size of data while minimizing the ou

```
data=remove_outlier(data, "sepal width")
data.boxplot(figsize=(12,8))
```

Correlation and removing correlated columns

import seaborn as sns
sns.heatmap(data.corr())

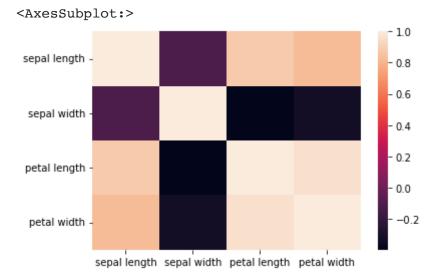


Judging by this heatmap, we can see that most of the areas in heat map are towards of # However sepal depth is very highly correlated to sepal length. In addition to that # related to petal length and width adn is also presenting outliers in data so we can

data=data.drop(['sepal depth','petal depth'],axis=1)
data.describe()

	sepal length	sepal width	petal length	petal width
count	146.000000	146.000000	146.000000	146.000000
mean	11.713699	6.073973	15.230137	4.879452
std	1.668186	0.790291	7.028468	3.041459
min	8.600000	4.400000	4.000000	0.400000
25%	10.200000	5.600000	6.400000	1.200000
50%	11.600000	6.000000	17.600000	5.200000
75%	12.800000	6.600000	20.400000	7.200000
max	15.800000	8.000000	27.600000	10.000000

here is final form of data
sns.heatmap(data.corr())



#exporting all data to an excel file for further use
data.to_excel('cleaned data.xlsx')