Iris Dataset

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0.1 ECE 657A: Data and Knowledge Modelling and Analysis

0.1.1 Assignment 1: Data Cleaning and Classification

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[5]:
```
# NumPy v1.20.3 https://numpy.org/
import numpy as np
# Pandas v1.2.4 https://pandas.pydata.org/
import pandas as pd
# Matplotlib v3.4.2 https://matplotlib.org/
import matplotlib.pyplot as plt
%matplotlib inline
# seaborn v0.11.1 https://seaborn.pydata.org/
import seaborn as sns
# scikit-learn v0.24.2 https://scikit-learn.org/
from sklearn.preprocessing import MinMaxScaler, LabelEncoder
from sklearn.model_selection import train_test_split,cross_val_score,KFold
from sklearn.neighbors import KNeighborsClassifier
from sklearn import metrics
from sklearn.metrics import confusion_matrix, classification_report,␣
↪roc_auc_score, roc_curve,auc
# SciPy v1.6.3 https://www.scipy.org/
from scipy.stats import zscore, kurtosis, skew
# Suppress warning messages for better readability
import warnings
warnings.filterwarnings('ignore')
```

Iris Dataset: A sample dataset describing the features of three different flowers.

- Features:
  - Sepal Length = Length of sepal of a particular flower in cm.
  - Sepal Width = Width of sepal of a particular flower in cm.
  - Petal Length = Length of petal of a particular flower in cm.
  - Petal Width = Width of petal of a particular flower in cm.
- Categories:
  - Iris-Setosa
  - Iris-Versicolor

  - Iris-Virginica
- Numerical columns:
  - 'sepal_length'
  - 'sepal_width'
  - 'petal_length'
  - 'petal_width'
- Categorical column:
  - 'species'

Data Retrieval and Exploration:

[6]:
```
df_iris=pd.read_csv('iris_dataset_missing.csv')
df=df_iris.copy()
df.describe()
```

[6]:

	sepal_length	sepal_width	petal_length	petal_width
count	105.000000	101.000000	97.000000	105.000000
mean	5.858909	3.059083	3.812370	1.199708
std	0.861638	0.455116	1.793489	0.787193
min	4.344007	1.946010	1.033031	-0.072203
25%	5.159145	2.768688	1.545136	0.333494
50%	5.736104	3.049459	4.276817	1.331797
75%	6.435413	3.290318	5.094427	1.817211
max	7.795561	4.409565	6.768611	2.603123

From description of dataset above, it is clear that the total number of rows and columns are 105 and 5, respectively. In which, there are 4 numerical columns and 1 categorical (target).

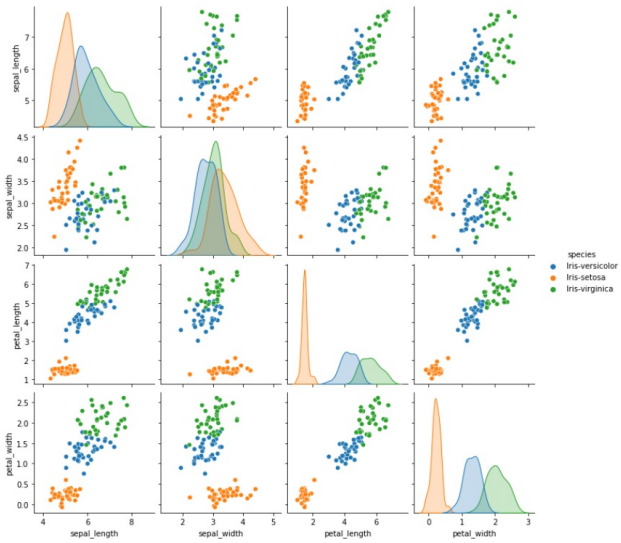
There are 35 dataset entries of each flower with their features as, **sepal_length**, **sepal_width**, **petal_length**, **petal_width**.

Although, it is visible that there are missing values in sepal_width and petal_length column. Also, there are negative values in petal_width column, which is invalid *(as length cannot be negative)*.

Pairplot to see comparison of these categories as well as their features (before any modifications):

[7]:
```
sns.pairplot(df,hue='species')
```

[7]:
```
<seaborn.axisgrid.PairGrid at 0x7fda75bc3ac0>
```



It's visible that all these three categories of flowers differ in their features dimensions. Depending on the species, the measurements of both petal and sepal have their own range and distribution. As a result, to fill out these missing values, categorical imputation will be used.

0.2 Question 1: Data Exploration

0.2.1 [CM1] Data Cleaning

[8]:
```
# Retreiving all the rows having NaN values:
df[df.isnull().any(axis=1)]
```

[8]:

	sepal_length	sepal_width	petal_length	petal_width	species
7	5.205868	NaN	1.675654	0.112269	Iris-setosa
21	6.365979	NaN	4.964905	1.817211	Iris-virginica
30	5.673096	4.409565	NaN	0.370518	Iris-setosa
32	5.847160	2.743619	NaN	0.748681	Iris-versicolor
37	6.271780	2.521065	NaN	1.896626	Iris-virginica
39	5.040516	3.466344	NaN	0.314548	Iris-setosa

```
41      4.496342     3.098270           NaN     0.242853      Iris-setosa
50      5.817283     2.633800           NaN     1.141347  Iris-versicolor
54      6.265590          NaN      4.701306     1.290187  Iris-versicolor
64      6.340344          NaN      4.302989     1.331797  Iris-versicolor
65      6.235536     3.425253           NaN     2.423053   Iris-virginica
85      5.911822     2.560512           NaN     1.766513   Iris-virginica
```

[9]:
```
# Retrieving all the rows with negative values:
df[df.values[:,:4]<0]
```

[9]:
```
    sepal_length  sepal_width  petal_length  petal_width      species
6        4.81174     3.037915      1.494268    -0.042428  Iris-setosa
67       4.86021     3.071128      1.487504    -0.072203  Iris-setosa
```

As we could see from above, there are 4 missing values from each category of flower, and two measurements in 'Iris-setosa' are negative. There are multiple ways of dealing with missing values, and comparision between two main methods is done to get the best suitable answer:

[10]:
```
# Replacing negative values with np.nan:
df.petal_width = np.where(df.petal_width<0, np.nan, df.petal_width)

# Defining  Dataframes for each category of flower:
df_versicolor=df[df.species=='Iris-versicolor']
df_setosa=df[df.species=='Iris-setosa']
df_virginica=df[df.species=='Iris-virginica']

# Handling missing values through median:
df_versicolor_median=df_versicolor.fillna(df_versicolor.median())
df_setosa_median=df_setosa.fillna(df_setosa.median())
df_virginica_median=df_virginica.fillna(df_virginica.median())
df_median= df.copy()
df_median[df_median.species=='Iris-versicolor']=df_versicolor_median
df_median[df_median.species=='Iris-setosa']=df_setosa_median
df_median[df_median.species=='Iris-virginica']=df_virginica_median

# ### Handling missing values through interpolation:
df_versicolor_interpolate=df_versicolor.fillna(df_versicolor.interpolate())
df_setosa_interpolate=df_setosa.fillna(df_setosa.interpolate())
df_virginica_interpolate=df_virginica.fillna(df_virginica.interpolate())
df_interpolate= df.copy()
df_interpolate[df_interpolate.
 ↪species=='Iris-versicolor']=df_versicolor_interpolate
df_interpolate[df_interpolate.species=='Iris-setosa']=df_setosa_interpolate
df_interpolate[df_interpolate.
 ↪species=='Iris-virginica']=df_virginica_interpolate

# Comparing the methods to get optimal result:
```

```
compare= pd.concat([df.corr(),df_median.corr(),df_interpolate.
↪corr()],keys=['original df corr','median df corr','interpolation df corr'])
compare
```

[10]:

		sepal_length	sepal_width	petal_length	petal_width
original df corr	sepal_length	1.000000	-0.031792	0.880635	0.804025
	sepal_width	-0.031792	1.000000	-0.285793	-0.275066
	petal_length	0.880635	-0.285793	1.000000	0.957425
	petal_width	0.804025	-0.275066	0.957425	1.000000
median df corr	sepal_length	1.000000	-0.042971	0.872683	0.809713
	sepal_width	-0.042971	1.000000	-0.330310	-0.275638
	petal_length	0.872683	-0.330310	1.000000	0.955780
	petal_width	0.809713	-0.275638	0.955780	1.000000
interpolation df corr	sepal_length	1.000000	-0.035287	0.870549	0.809707
	sepal_width	-0.035287	1.000000	-0.321562	-0.262398
	petal_length	0.870549	-0.321562	1.000000	0.956214
	petal_width	0.809707	-0.262398	0.956214	1.000000

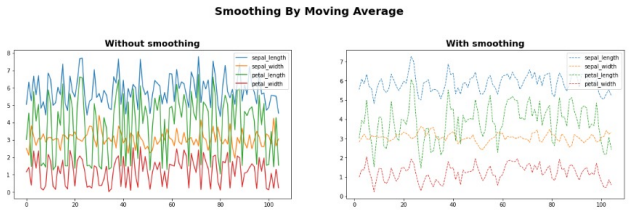
Based on the comparison above, using median() for missing values, correlation becomes strong. While using interpolate(), correlation is effected, but not as great as median(). So, we use median for missing values for further exploration.

[11]:
```
df= df_median.copy()
df_setosa= df_setosa_interpolate
df_virginica= df_virginica_interpolate
df_versicolor= df_versicolor_interpolate
```

Effect of Smoothing by Moving Average:

[12]:
```
roll=df.rolling(window=3)
smooth_iris=roll.mean()

fig, axes= plt.subplots(1,2,figsize=(20,5))
df.plot(ax=axes[0])
```

```
smooth_iris.plot(linestyle='dashed',linewidth=1,ax=axes[1])
axes[0].set_title('Without smoothing',fontsize=16,fontweight='bold')
axes[1].set_title('With smoothing',fontsize=16,fontweight='bold')
plt.suptitle('Smoothing By Moving Average',fontsize=20,fontweight='bold',y=1.1)
plt.show()
```



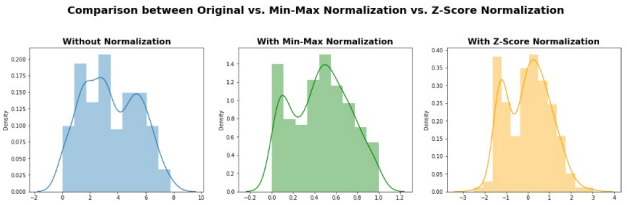
Smoothing is used to remove noise from the data, but, in this case, smoothing is not suitable. It provides inaccurate results and may remove the useful data.

0.2.2 Normalization

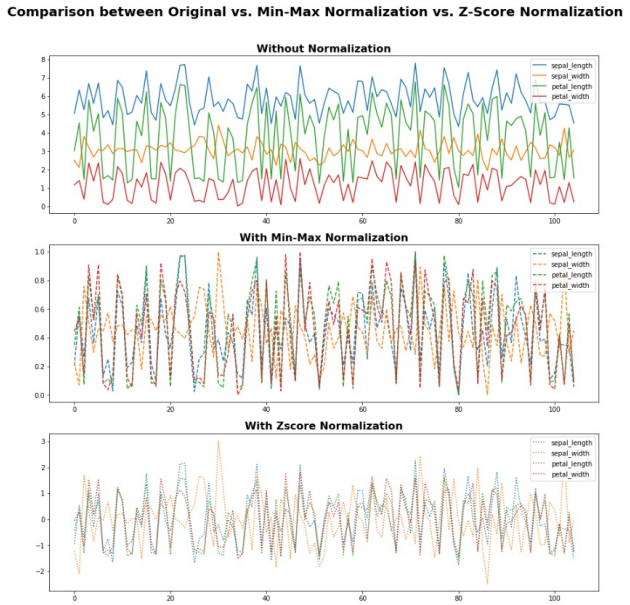
Used for rescaling the data in particular range.

[13]:
```
# Min-Max Normalization
scaler=MinMaxScaler()
minmax_norm= scaler.
 ↪fit_transform(df[['sepal_length','sepal_width','petal_length','petal_width']])
minmax_norm = pd.DataFrame(minmax_norm, columns= df.columns[:4])
minmax_norm['species']= df.species

# Z-Score Normalization
zscore_norm=␣
 ↪zscore(df[['sepal_length','sepal_width','petal_length','petal_width']])
zscore_norm = pd.DataFrame(zscore_norm, columns= df.columns[:4])

# Comparison between Original vs. Min-Max Normalization vs. Z-Score␣
 ↪Normalization
fig, axes= plt.subplots(1,3,figsize=(20,5))
sns.distplot(df.values[:,:4],ax=axes[0])
sns.distplot(minmax_norm.values[:,:4],ax=axes[1], color='green')
sns.distplot(zscore_norm.values[:,:4],ax=axes[2],color='orange')
axes[0].set_title('Without Normalization',fontsize=16,fontweight='bold')
axes[1].set_title('With Min-Max Normalization',fontsize=16,fontweight='bold')
axes[2].set_title('With Z-Score Normalization',fontsize=16,fontweight='bold')
```

```
plt.suptitle('Comparison between Original vs. Min-Max Normalization vs. Z-Score␣
↪Normalization',fontsize=20,fontweight='bold',y=1.1)
plt.show()
```



[14]:
```
fig, axes= plt.subplots(3,1,figsize=(15,15))
df.plot(ax=axes[0])
minmax_norm.plot(linestyle='dashed',ax=axes[1])
zscore_norm.plot(linestyle='dotted',ax=axes[2])
axes[0].set_title('Without Normalization',fontsize=16,fontweight='bold')
axes[1].set_title('With Min-Max Normalization',fontsize=16,fontweight='bold')
axes[2].set_title('With Zscore Normalization',fontsize=16,fontweight='bold')
plt.suptitle('Comparison between Original vs. Min-Max Normalization vs. Z-Score␣
↪Normalization',fontsize=20,fontweight='bold',y=0.95)
plt.show()
```



Based on the comparison above, we will use **Z-Score Normalization** for this dataset, as it handles outliers and provides better accuracy

[15]:
```
df.iloc[:,:4]=zscore_norm
```

0.2.3 [CM2] Data Visulalization

[16]:
```
# Pairs Plot
sns.pairplot( df, hue='species')
plt.suptitle('Comparision of Features after Data Cleaning',fontsize=20,y=1.
↪05,fontweight='bold')
```

[16]:
```
Text(0.5, 1.05, 'Comparision of Features after Data Cleaning')
```

Heart Disease Dataset

June 7, 2021

0.1 ECE 657A: Data and Knowledge Modelling and Analysis

0.1.1 Assignment 1: Data Cleaning and Classification

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[1]:
```
# NumPy v1.20.3 https://numpy.org/
import numpy as np
# Pandas v1.2.4 https://pandas.pydata.org/
import pandas as pd
# Matplotlib v3.4.2 https://matplotlib.org/
import matplotlib.pyplot as plt
%matplotlib inline
# seaborn v0.11.1 https://seaborn.pydata.org/
import seaborn as sns
# scikit-learn v0.24.2 https://scikit-learn.org/
from sklearn.impute import KNNImputer
from sklearn.preprocessing import OneHotEncoder, MinMaxScaler
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
from sklearn import metrics
from sklearn.metrics import roc_auc_score, roc_curve, classification_report
# SciPy v1.6.3 https://www.scipy.org/
from scipy.stats import zscore
from scipy.stats import kurtosis,skew
# Suppress warning messages for better readability
import warnings
warnings.filterwarnings('ignore')
```

Heart Disease Dataset: It is a sample dataset representing various features that will help in predicting the presence of heart disiase in a patient. Its aim is to find target.

- Features:
  1. age : represents age in numbers.
  2. sex : represents the gender, with 0 as female and 1 as male.
  3. cp : Chest pain type with values(0 = Asymptomatic angina, 1 = Atypical angina, 2 = Non-angina, 3 = Typical angina)
  4. trestbps : resting blood pressure(mm hg)

5. chol : serum cholestrol (mg/dl)
6. fbs : Fasting blood sugar > 120 mg/dl with values(0 = False, 1= True)
7. restecg : Resting electrocardiographic results with values(0 = Left ventricular hypertrophy, 1 = Normal, 2 = ST-T wave abnormality)
8. thalach : Maximum heart rate achieved, during thalium stress test
9. exang : represents exercise induced angina with values(0 = No, 1 = Yes)
10. oldpeak : represents ST depression induced by exercise, relative to rest
11. slope : represents slope of peak exercise ST segment with values(0 = Downsloping, 1 = Upsloping, 2 = Flat)
12. ca : represents number of major vessels in range(0,3)
13. thal : represents thalium stress test results with values(0 = NA, 1 = Fixed defect, 2 = Normal, 3 = Reversible defect)
14. target : represents the presence of heart disease with values(0 = No, 1 = Yes)

- Binary features:
  - sex
  - fbsand
  - exang
- Nominal features:
  - cp
  - restecg
  - slope
  - thal
- Ordinal features:
  - ca
- Numerical features:
  - age
  - restbps
  - chol
  - thalach
  - oldpeak

Data Retrieval and Exploration:

[2]:
```
df_heart_disease= pd.read_csv('heart_disease_missing.csv')
df=df_heart_disease.copy()
df.describe()
```

[2]:

	age	sex	cp	trestbps	chol	fbs	\
count	212.000000	212.000000	212.000000	205.000000	202.000000	212.000000	
mean	54.311321	0.688679	0.957547	131.784610	244.133256	0.132075	
std	9.145339	0.464130	1.022537	18.057222	46.444257	0.339374	
min	29.000000	0.000000	0.000000	93.944184	126.085811	0.000000	
25%	47.000000	0.000000	0.000000	119.968114	211.969594	0.000000	
50%	55.000000	1.000000	1.000000	130.010256	241.467023	0.000000	
75%	61.000000	1.000000	2.000000	139.965470	272.484222	0.000000	
max	77.000000	1.000000	3.000000	192.020200	406.932689	1.000000	

	restecg	thalach	exang	oldpeak	slope	ca	\

```
count  207.000000  208.000000  212.000000  200.000000  210.000000  212.000000
mean     0.560386  149.647978    0.344340    1.113106    1.423810    0.731132
std      0.535149   22.076206    0.476277    1.255908    0.623622    1.038762
min      0.000000   88.032613    0.000000   -0.185668    0.000000    0.000000
25%      0.000000  135.946808    0.000000    0.050778    1.000000    0.000000
50%      1.000000  151.939216    0.000000    0.726060    1.000000    0.000000
75%      1.000000  165.260092    1.000000    1.816733    2.000000    1.000000
max      2.000000  202.138041    1.000000    6.157114    2.000000    4.000000

             thal      target
count  211.000000  212.000000
mean     2.349112    0.542453
std      0.602117    0.499374
min      0.858554    0.000000
25%      1.949795    0.000000
50%      2.078759    1.000000
75%      2.970842    1.000000
max      3.277466    1.000000
```

[3]:
```
df.nunique()
```

[3]:
```
age          41
sex           2
cp            4
trestbps    205
chol        202
fbs           2
restecg       3
thalach     208
exang         2
oldpeak     200
slope         3
ca            5
thal        211
target        2
dtype: int64
```

[4]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 212 entries, 0 to 211
Data columns (total 14 columns):
 #   Column    Non-Null Count  Dtype
---  ------    --------------  -----
 0   age       212 non-null    int64
 1   sex       212 non-null    int64
 2   cp        212 non-null    int64
 3   trestbps  205 non-null    float64
```

```
 4   chol      202 non-null    float64
 5   fbs       212 non-null    int64
 6   restecg   207 non-null    float64
 7   thalach   208 non-null    float64
 8   exang     212 non-null    int64
 9   oldpeak   200 non-null    float64
 10  slope     210 non-null    float64
 11  ca        212 non-null    int64
 12  thal      211 non-null    float64
 13  target    212 non-null    int64
dtypes: float64(7), int64(7)
memory usage: 23.3 KB
```

0.2 Question 1: Data Exploration

0.2.1 1.1 [CM1] Data Cleaning

It shows that there are missing values and negative values in dataset, which needs to be handled. Data Cleaning is a process of detection and correction of inaccurate data values, such as, missing values, invalid values, outliers and noise. So, in our dataset, there are 7, 10, 5, 4, 12, 2 and 1 missing values in trestbps, chol, restecg, thalach, oldpeak, slope and thal columns, respectively. Also, there is a presence of negative values in oldpeak column and out of range value in ca column. Therefore, replaced these values with unknown ones and later performed imputation.

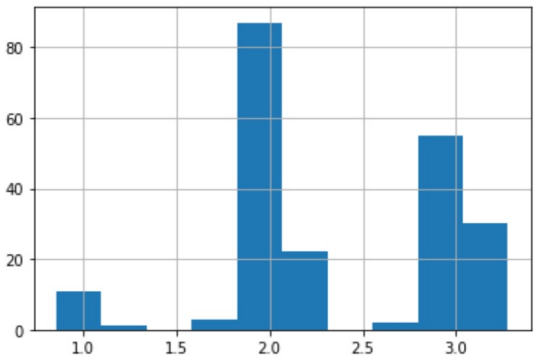
[5]:
```
# Count all the rows having NaN values:
print(f'\033[1mCount for Rows with NaN Values:\033[0m\n{df[df.isnull().
 ↪any(axis=1)].count()}\n')
# Count all the rows with negative values:
print(f'\033[1mCount for Rows with Negative Values:\033[0m\n{df[df.values[:,:
 ↪14]<0].count()}')
```

```
Count for Rows with NaN Values:
age         38
sex         38
cp          38
trestbps    31
chol        28
fbs         38
restecg     33
thalach     34
exang       38
oldpeak     26
slope       36
ca          38
thal        37
target      38
dtype: int64

Count for Rows with Negative Values:
```

```
age         38
sex         38
cp          38
trestbps    38
chol        37
fbs         38
restecg     36
thalach     37
exang       38
oldpeak     38
slope       38
ca          38
thal        37
target      38
dtype: int64
```

[6]:
```
# Replacing negative values with np.nan:
df.oldpeak = np.where(df.oldpeak<0, np.nan, df.oldpeak)
# Replacing data in 'ca' where it's greater than 3 (0,3)
df.ca = np.where(df.ca>3,np.nan,df.ca)

# Dividing the features into Binary, Nominal, Ordinal and Numeric data:
binary_features = ['sex','fbs','exang']
nominal_features= ['cp','restecg','slope','thal']
ordinal_features= ['ca']
categorical_features = ['sex','fbs','exang','cp','restecg','slope','ca','thal']
numeric_features=['age','trestbps','chol','thalach','oldpeak']
cat_ord= ['cp','restecg','slope','ca','thal']

# Feature 'thal' is categorical, but provided data represents it as continuous,
 ↪so, it will be converted into categorical form to perform further process.
df['thal'].hist()
```

[6]: <AxesSubplot:>



Here, features have been divided depending upon their behaviors, such as: - binary features are sex, fbs, exang - nominal features are ap, restecg, slope, thal - ordinal feature includes ca - numerical feature has all the continuous variables

Furthermore, looking deep into dataset, it is visible (figure above) that 'thal' column of dataset is having continuous numerical values, but, in reality, it has categorical behavior. Hence, converted it from float column to category column.

[7]:
```
df['thal']= pd.cut(df['thal'],3,labels= [1,2,3])
df['thal'].astype('Int64')
```

[7]:
```
0      2
1      3
2      2
3      2
4      3
      ..
207    1
208    2
209    3
210    2
211    2
Name: thal, Length: 212, dtype: Int64
```

There are many ways to handle missing values such as, interpolation, extrapolation or imputation, but, it varies from dataset to dataset. In heart disease dataset, the missing values are handled by three methods, in which two methods are combination of another two methods: - First method

used is simple imputation by median - Second method is a combination of interpolation for numeric values and median for categorical data - Third method is also combination of knn imputation for numeric values and median for categories

[8]:
```
# Handling missing data by median
df_median= df.copy()
df_median=df_median.fillna(df_median.median())
cat_median=df[categorical_features].copy()
cat_median=cat_median.fillna(cat_median.median())
# df_median

# Handling missing data by interpolation(numeric) and median(categorical):
df_interpolate= df[numeric_features].copy()
df_interpolate=df_interpolate.fillna(df_interpolate.interpolate())
df_interpolation= pd.concat([df_interpolate,cat_median,df.target],axis=1)
# df_interpolation

# Handling missing data by KNN Imputation(numeric) and median(categorical):
knn_imputed= df[numeric_features].copy()
kimputed= KNNImputer(n_neighbors=5)
knn_imputed= kimputed.fit_transform(knn_imputed)
knn_imputed= pd.DataFrame(knn_imputed,columns=df[numeric_features].columns)
knn_imputation=pd.concat([knn_imputed,cat_median,df.target],axis=1)
# knn_imputation

# Comparision of Missing Values handled by Median, Interpolation and KNN␣
↪Imputation:
compare = pd.concat([df.corr(),df_median.corr(),df_interpolation.
↪corr(),knn_imputation.corr()],keys=[
    'Original Dataset correlation','Median correlation','Interpolation␣
↪correlation','KNN Imputation correlation'])
compare
```

[8]:

		age	sex	cp	trestbps	\
Original Dataset correlation	age	1.000000	-0.140074	-0.084230	0.335944	
	sex	-0.140074	1.000000	-0.057939	-0.049906	
	cp	-0.084230	-0.057939	1.000000	-0.007449	
	trestbps	0.335944	-0.049906	-0.007449	1.000000	
	chol	0.185861	-0.195213	-0.061591	0.162162	
	fbs	0.050823	0.081750	0.057205	0.138907	
	restecg	-0.124819	-0.050203	0.035935	-0.106940	
	thalach	-0.382280	0.017446	0.246019	-0.100284	
	exang	0.114545	0.122773	-0.349369	0.088717	
	oldpeak	0.080801	0.115038	-0.175151	0.146234	
	slope	-0.117989	-0.057160	0.156145	-0.134180	
	ca	0.389111	0.088996	-0.238708	0.071915	
	target	-0.196967	-0.249428	0.490819	-0.118476	

```
Median correlation           age       1.000000 -0.140074 -0.084230  0.331159
                             sex      -0.140074  1.000000 -0.057939 -0.049287
                             cp       -0.084230 -0.057939  1.000000 -0.006081
                             trestbps  0.331159 -0.049287 -0.006081  1.000000
                             chol      0.182275 -0.190700 -0.059884  0.158675
                             fbs       0.050823  0.081750  0.057205  0.132736
                             restecg  -0.126079 -0.044643  0.035974 -0.110995
                             thalach  -0.379480  0.017559  0.243831 -0.097124
                             exang     0.114545  0.122773 -0.349369  0.086465
                             oldpeak   0.085931  0.103196 -0.162622  0.136891
                             slope    -0.123061 -0.054050  0.154827 -0.132938
                             ca        0.396850  0.079135 -0.242469  0.066227
                             target   -0.196967 -0.249428  0.490819 -0.114587
Interpolation correlation    age       1.000000 -0.140074 -0.084230  0.318457
                             trestbps  0.318457 -0.049125 -0.008003  1.000000
                             chol      0.163386 -0.185987 -0.046192  0.130216
                             thalach  -0.383527  0.014529  0.247382 -0.104446
                             oldpeak   0.076005  0.099281 -0.155386  0.087869
                             sex      -0.140074  1.000000 -0.057939 -0.049125
                             fbs       0.050823  0.081750  0.057205  0.154423
                             exang     0.114545  0.122773 -0.349369  0.103134
                             cp       -0.084230 -0.057939  1.000000 -0.008003
                             restecg  -0.126079 -0.044643  0.035974 -0.095158
                             slope    -0.123061 -0.054050  0.154827 -0.130164
                             ca        0.396850  0.079135 -0.242469  0.056168
                             target   -0.196967 -0.249428  0.490819 -0.107400
KNN Imputation correlation   age       1.000000 -0.140074 -0.084230  0.330554
                             trestbps  0.330554 -0.046642 -0.002554  1.000000
                             chol      0.189925 -0.200029 -0.065967  0.158039
                             thalach  -0.381539  0.020173  0.242331 -0.092370
                             oldpeak   0.103487  0.074398 -0.160099  0.153209
                             sex      -0.140074  1.000000 -0.057939 -0.046642
                             fbs       0.050823  0.081750  0.057205  0.122958
                             exang     0.114545  0.122773 -0.349369  0.079069
                             cp       -0.084230 -0.057939  1.000000 -0.002554
                             restecg  -0.126079 -0.044643  0.035974 -0.102507
                             slope    -0.123061 -0.054050  0.154827 -0.127474
                             ca        0.396850  0.079135 -0.242469  0.058892
                             target   -0.196967 -0.249428  0.490819 -0.103555

                                          chol       fbs   restecg   thalach  \
Original Dataset correlation age       0.185861  0.050823 -0.124819 -0.382280
                             sex      -0.195213  0.081750 -0.050203  0.017446
                             cp       -0.061591  0.057205  0.035935  0.246019
                             trestbps  0.162162  0.138907 -0.106940 -0.100284
                             chol      1.000000 -0.025549 -0.079196 -0.057679
                             fbs      -0.025549  1.000000 -0.110983  0.036934
```

```
                          restecg  -0.079196 -0.110983  1.000000  0.016873
                          thalach  -0.057679  0.036934  0.016873  1.000000
                          exang     0.065738  0.098474 -0.036140 -0.360246
                          oldpeak   0.079821 -0.083458 -0.096473 -0.291068
                          slope     0.028301 -0.019514  0.056843  0.463824
                          ca        0.102768  0.120978 -0.114173 -0.245041
                          target   -0.078063 -0.005276  0.087048  0.415354
Median correlation        age       0.182275  0.050823 -0.126079 -0.379480
                          sex      -0.190700  0.081750 -0.044643  0.017559
                          cp       -0.059884  0.057205  0.035974  0.243831
                          trestbps  0.158675  0.132736 -0.110995 -0.097124
                          chol      1.000000 -0.024365 -0.084286 -0.054528
                          fbs      -0.024365  1.000000 -0.104312  0.036103
                          restecg  -0.084286 -0.104312  1.000000  0.036065
                          thalach  -0.054528  0.036103  0.036065  1.000000
                          exang     0.063715  0.098474 -0.049757 -0.357632
                          oldpeak   0.070111 -0.074062 -0.092070 -0.274455
                          slope     0.030176 -0.016944  0.074378  0.462661
                          ca        0.111459  0.113701 -0.116865 -0.250813
                          target   -0.075929 -0.005276  0.095500  0.412468
Interpolation correlation age       0.163386  0.050823 -0.126079 -0.383527
                          trestbps  0.130216  0.154423 -0.095158 -0.104446
                          chol      1.000000 -0.021913 -0.062742 -0.039059
                          thalach  -0.039059  0.036279  0.042634  1.000000
                          oldpeak   0.075335 -0.045573 -0.097156 -0.247692
                          sex      -0.185987  0.081750 -0.044643  0.014529
                          fbs      -0.021913  1.000000 -0.104312  0.036279
                          exang     0.080550  0.098474 -0.049757 -0.364503
                          cp       -0.046192  0.057205  0.035974  0.247382
                          restecg  -0.062742 -0.104312  1.000000  0.042634
                          slope     0.032851 -0.016944  0.074378  0.461215
                          ca        0.111947  0.113701 -0.116865 -0.253375
                          target   -0.066440 -0.005276  0.095500  0.418747
KNN Imputation correlation age       0.189925  0.050823 -0.126079 -0.381539
                          trestbps  0.158039  0.122958 -0.102507 -0.092370
                          chol      1.000000 -0.020434 -0.095361 -0.063207
                          thalach  -0.063207  0.035412  0.036467  1.000000
                          oldpeak   0.090753 -0.079572 -0.094573 -0.287731
                          sex      -0.200029  0.081750 -0.044643  0.020173
                          fbs      -0.020434  1.000000 -0.104312  0.035412
                          exang     0.064995  0.098474 -0.049757 -0.357631
                          cp       -0.065967  0.057205  0.035974  0.242331
                          restecg  -0.095361 -0.104312  1.000000  0.036467
                          slope     0.027892 -0.016944  0.074378  0.464072
                          ca        0.122943  0.113701 -0.116865 -0.250509
                          target   -0.074931 -0.005276  0.095500  0.412829
```

		exang	oldpeak	slope	ca
Original Dataset correlation	age	0.114545	0.080801	-0.117989	0.389111
	sex	0.122773	0.115038	-0.057160	0.088996
	cp	-0.349369	-0.175151	0.156145	-0.238708
	trestbps	0.088717	0.146234	-0.134180	0.071915
	chol	0.065738	0.079821	0.028301	0.102768
	fbs	0.098474	-0.083458	-0.019514	0.120978
	restecg	-0.036140	-0.096473	0.056843	-0.114173
	thalach	-0.360246	-0.291068	0.463824	-0.245041
	exang	1.000000	0.241528	-0.314675	0.127656
	oldpeak	0.241528	1.000000	-0.612618	0.232739
	slope	-0.314675	-0.612618	1.000000	-0.130592
	ca	0.127656	0.232739	-0.130592	1.000000
	target	-0.450321	-0.410084	0.419238	-0.408445
Median correlation	age	0.114545	0.085931	-0.123061	0.396850
	sex	0.122773	0.103196	-0.054050	0.079135
	cp	-0.349369	-0.162622	0.154827	-0.242469
	trestbps	0.086465	0.136891	-0.132938	0.066227
	chol	0.063715	0.070111	0.030176	0.111459
	fbs	0.098474	-0.074062	-0.016944	0.113701
	restecg	-0.049757	-0.092070	0.074378	-0.116865
	thalach	-0.357632	-0.274455	0.462661	-0.250813
	exang	1.000000	0.235311	-0.314293	0.128679
	oldpeak	0.235311	1.000000	-0.556003	0.237332
	slope	-0.314293	-0.556003	1.000000	-0.140882
	ca	0.128679	0.237332	-0.140882	1.000000
	target	-0.450321	-0.378938	0.422970	-0.408534
Interpolation correlation	age	0.114545	0.076005	-0.123061	0.396850
	trestbps	0.103134	0.087869	-0.130164	0.056168
	chol	0.080550	0.075335	0.032851	0.111947
	thalach	-0.364503	-0.247692	0.461215	-0.253375
	oldpeak	0.223071	1.000000	-0.501431	0.221260
	sex	0.122773	0.099281	-0.054050	0.079135
	fbs	0.098474	-0.045573	-0.016944	0.113701
	exang	1.000000	0.223071	-0.314293	0.128679
	cp	-0.349369	-0.155386	0.154827	-0.242469
	restecg	-0.049757	-0.097156	0.074378	-0.116865
	slope	-0.314293	-0.501431	1.000000	-0.140882
	ca	0.128679	0.221260	-0.140882	1.000000
	target	-0.450321	-0.342418	0.422970	-0.408534
KNN Imputation correlation	age	0.114545	0.103487	-0.123061	0.396850
	trestbps	0.079069	0.153209	-0.127474	0.058892
	chol	0.064995	0.090753	0.027892	0.122943
	thalach	-0.357631	-0.287731	0.464072	-0.250509
	oldpeak	0.227819	1.000000	-0.531960	0.230220
	sex	0.122773	0.074398	-0.054050	0.079135
	fbs	0.098474	-0.079572	-0.016944	0.113701

```
                          exang     1.000000  0.227819 -0.314293  0.128679
                          cp       -0.349369 -0.160099  0.154827 -0.242469
                          restecg  -0.049757 -0.094573  0.074378 -0.116865
                          slope    -0.314293 -0.531960  1.000000 -0.140882
                          ca        0.128679  0.230220 -0.140882  1.000000
                          target   -0.450321 -0.365623  0.422970 -0.408534

                                             target
Original Dataset correlation age       -0.196967
                          sex       -0.249428
                          cp         0.490819
                          trestbps  -0.118476
                          chol      -0.078063
                          fbs       -0.005276
                          restecg    0.087048
                          thalach    0.415354
                          exang     -0.450321
                          oldpeak   -0.410084
                          slope      0.419238
                          ca        -0.408445
                          target     1.000000
Median correlation        age       -0.196967
                          sex       -0.249428
                          cp         0.490819
                          trestbps  -0.114587
                          chol      -0.075929
                          fbs       -0.005276
                          restecg    0.095500
                          thalach    0.412468
                          exang     -0.450321
                          oldpeak   -0.378938
                          slope      0.422970
                          ca        -0.408534
                          target     1.000000
Interpolation correlation age       -0.196967
                          trestbps  -0.107400
                          chol      -0.066440
                          thalach    0.418747
                          oldpeak   -0.342418
                          sex       -0.249428
                          fbs       -0.005276
                          exang     -0.450321
                          cp         0.490819
                          restecg    0.095500
                          slope      0.422970
                          ca        -0.408534
                          target     1.000000
```

```
KNN Imputation correlation   age      -0.196967
                             trestbps -0.103555
                             chol     -0.074931
                             thalach   0.412829
                             oldpeak  -0.365623
                             sex      -0.249428
                             fbs      -0.005276
                             exang    -0.450321
                             cp        0.490819
                             restecg   0.095500
                             slope     0.422970
                             ca       -0.408534
                             target    1.000000
```

By using interpolation and knn imputation correlation is affected, but also, it gives 0.5 or 0.8 values for some categorical features which is invalid. So, we combined both interpolation and knn imputation for numeric data and median for categorical data. Also, knn_imputation provides better accuracy than others (provided the maximum accuracy of data, i.e., 100%, whereas other methods, gave 88.37 or 90.0697% accuracy).

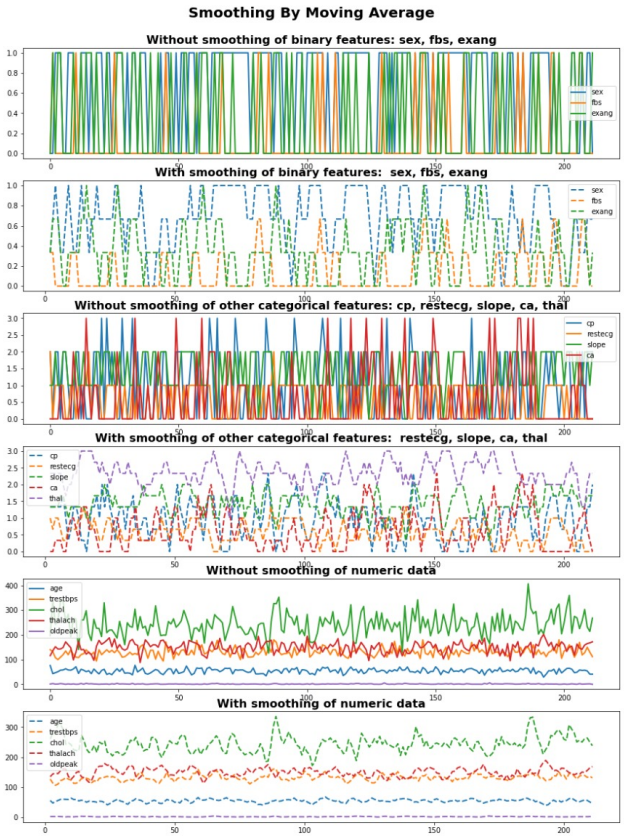
Therefore, **KNN Imputation** will be used for handling missing values.

[9]:
```
df= knn_imputation.copy()
```

Effect of Smoothing by Moving Average:

[10]:
```
roll1=df[categorical_features].rolling(window=3)
smooth_heart_cat=roll1.mean()
roll2=df[numeric_features].rolling(window=3)
smooth_heart_num=roll2.mean()

fig, axes= plt.subplots(6,1,figsize=(15,20))
df[categorical_features].iloc[:,:3].plot(linewidth=2,ax=axes[0])
smooth_heart_cat.iloc[:,:3].plot(linestyle='dashed',linewidth=2,ax=axes[1])
df[categorical_features].iloc[:,3:8].plot(linewidth=2,ax=axes[2])
smooth_heart_cat.iloc[:,3:8].plot(linestyle='dashed',linewidth=2,ax=axes[3])
df[numeric_features].plot(linewidth=2,ax=axes[4])
smooth_heart_num.plot(linestyle='dashed',linewidth=2,ax=axes[5])
axes[0].set_title('Without smoothing of binary features: sex, fbs, exang',
                  fontsize=16,fontweight='bold')
axes[1].set_title('With smoothing of binary features:  sex, fbs, exang',
                  fontsize=16,fontweight='bold')
axes[2].set_title('Without smoothing of other categorical features: cp,␣
↪restecg, slope, ca, thal',
                  fontsize=16,fontweight='bold')
axes[3].set_title('With smoothing of other categorical features:  restecg,␣
↪slope, ca, thal',
                  fontsize=16,fontweight='bold')
```

```
axes[4].set_title('Without smoothing of numeric␣
 ↪data',fontsize=16,fontweight='bold')
axes[5].set_title('With smoothing of numeric␣
 ↪data',fontsize=16,fontweight='bold')
plt.suptitle('Smoothing By Moving Average',fontsize=20,fontweight='bold',y=0.92)
plt.show()
```



In case of smoothing, smoothing by moving average has been applied on data, which results into rows with NaN values. As, it leads to data loss, so smoothing **will not be applied** for the dataset. Also, it provides invalid values for categorical data. The first two figures show the impact of smoothing on

binary and nominal data. The figure provides a clear picture of why smoothing should be avoided in categorical cases, as it provides float data entries for categorical data. Compared to the third figure, in terms of effect of smoothing on numeric data, it resulted in number of windows minus one rows of NaN values. So, it is cut out from the application.

0.2.2 Normalization

[11]:
```
# OneHotEncoding on nominal and ordinal features:
onehot= OneHotEncoder(handle_unknown='ignore',sparse=False)
cat_encoded=onehot.fit_transform(df[cat_ord])
cat_encoded= pd.
 ↪DataFrame(cat_encoded,columns=['cp=0','cp=1','cp=2','cp=3','restecg=0','restecg=1','restecg
cat_encoded
```

[11]:

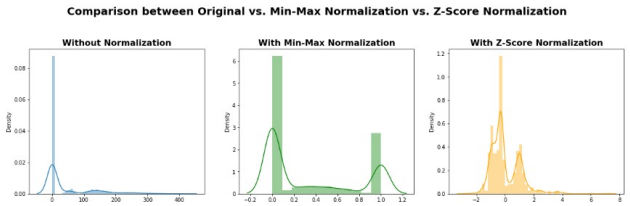
	cp=0	cp=1	cp=2	cp=3	restecg=0	restecg=1	restecg=2	slope=0	\
0	0.0	0.0	1.0	0.0	0.0	0.0	1.0	0.0	
1	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	
2	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0	
3	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0	
4	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0	
..	…	…	…	…	…	…	…	…	
207	0.0	0.0	1.0	0.0	1.0	0.0	0.0	0.0	
208	1.0	0.0	0.0	0.0	1.0	0.0	0.0	0.0	
209	0.0	0.0	1.0	0.0	1.0	0.0	0.0	0.0	
210	0.0	0.0	1.0	0.0	1.0	0.0	0.0	0.0	
211	0.0	0.0	1.0	0.0	1.0	0.0	0.0	0.0	

	slope=1	slope=2	ca=0	ca=1	ca=2	ca=3	thal=0	thal=1	thal=2	thal=3
0	1.0	0.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
1	1.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0
2	0.0	1.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
3	1.0	0.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
4	1.0	0.0	0.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0
..	…	…	…	…	…	…	…	…	…	
207	1.0	0.0	0.0	1.0	0.0	0.0	1.0	0.0	0.0	0.0
208	0.0	1.0	0.0	1.0	0.0	0.0	0.0	1.0	0.0	0.0
209	0.0	1.0	1.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0
210	1.0	0.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0
211	0.0	1.0	1.0	0.0	0.0	0.0	0.0	1.0	0.0	0.0

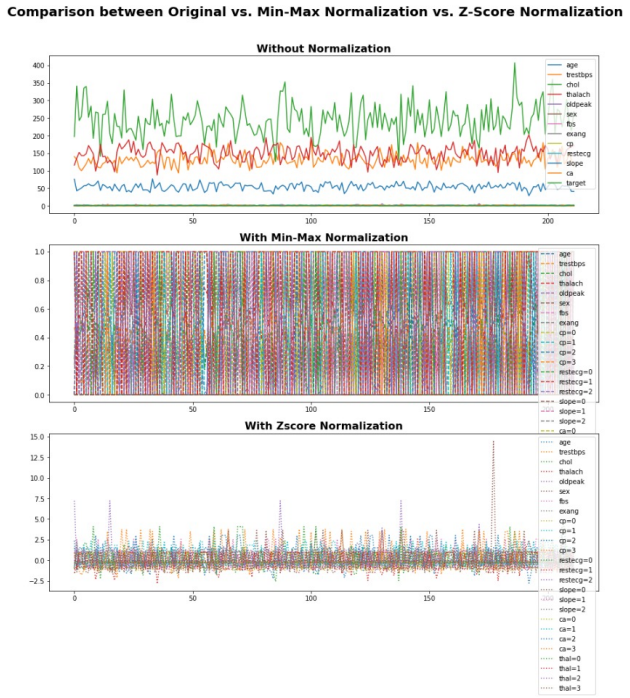
[212 rows x 18 columns]

[12]:
```
# Combining the data after OneHotEncoding
df_encoded= pd.
 ↪concat([df[numeric_features],df[binary_features],cat_encoded],axis=1)

# Min-Max Normalization:
```

```
scaler=MinMaxScaler()
minmax_norm= scaler.fit_transform(df_encoded)
minmax_norm = pd.DataFrame(minmax_norm, columns= df_encoded.columns)

# Z-Score Normalization:
zscore_norm= zscore(df_encoded)
zscore_norm = pd.DataFrame(zscore_norm, columns= df_encoded.columns)

# Comparison between Original vs. Min-Max Normalization vs. Z-Score
↪Normalization
fig, axes= plt.subplots(1,3,figsize=(20,5))
sns.distplot(df.values[:,:25],ax=axes[0])
sns.distplot(minmax_norm.values[:,:25],ax=axes[1], color='green')
sns.distplot(zscore_norm.values[:,:25],ax=axes[2], color='orange')
axes[0].set_title('Without Normalization',fontsize=16,fontweight='bold')
axes[1].set_title('With Min-Max Normalization',fontsize=16,fontweight='bold')
axes[2].set_title('With Z-Score Normalization',fontsize=16,fontweight='bold')
plt.suptitle('Comparison between Original vs. Min-Max Normalization vs. Z-Score
↪Normalization',fontsize=20,fontweight='bold',y=1.1)
plt.show()
```



[13]:
```
fig, axes= plt.subplots(3,1,figsize=(15,15))
df.plot(ax=axes[0])
minmax_norm.plot(linestyle='dashed',ax=axes[1])
zscore_norm.plot(linestyle='dotted',ax=axes[2])
axes[0].set_title('Without Normalization',fontsize=16,fontweight='bold')
axes[1].set_title('With Min-Max Normalization',fontsize=16,fontweight='bold')
axes[2].set_title('With Zscore Normalization',fontsize=16,fontweight='bold')
plt.suptitle('Comparison between Original vs. Min-Max Normalization vs. Z-Score
↪Normalization',fontsize=20,fontweight='bold',y=0.95)
plt.show()
```



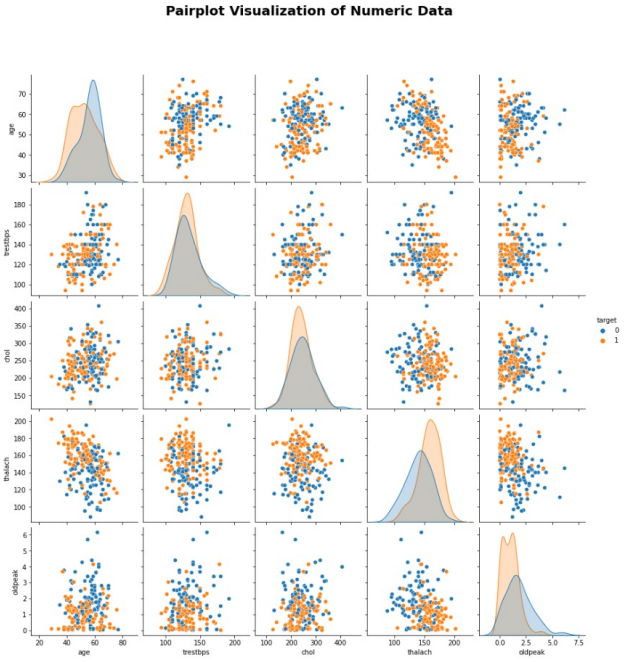
Two types of methods are performed, namely, min-max and z-score normalization. In which, min-max provided less accurate model than z-score. Also, z-score handles outliers. Thus, the best approach to normalize the data is z-score. Apart from it, it is quite visible from the graph that original data has skewness and many outliers, and, min-max normalization provides totally different distribution of data. However, z-score transformed the data really great and has less outliers. Lastly, min-max normalization tries to shrink the date into range (0, 1) whereas, z-score defines the range in which mean and standard deviation of variable is maintained and not disturbed.

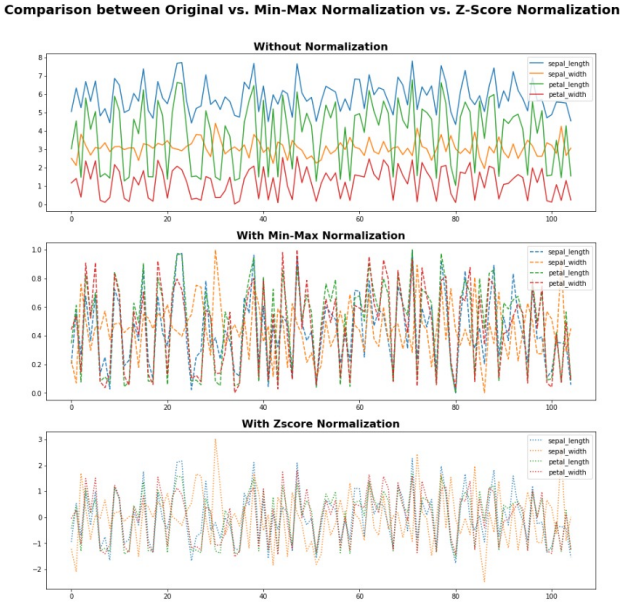
As a result, **Z-Score** will be used in model implementation.

[14]:
```
norm_df=zscore_norm
norm_df['target']=df.target
```

0.2.3 1.2 [CM2] Data Visulalization

[15]:
```
# Pairs Plot of Numeric Data
num=pd.concat([df[numeric_features],df.target],axis=1)
sns.pairplot(num,hue='target')
plt.suptitle('Pairplot Visualization of Numeric␣
↪Data',fontsize=20,fontweight='bold',y=1.1)
plt.show()
```





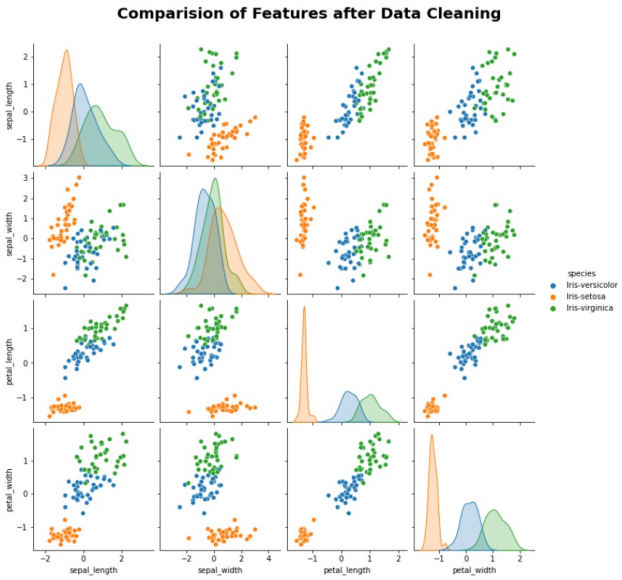
Based on the comparison above, we will use **Z-Score Normalization** for this dataset, as it handles outliers and provides better accuracy

[15]:
```
df.iloc[:,:4]=zscore_norm
```

0.2.3 [CM2] Data Visulalization

[16]:
```
# Pairs Plot
sns.pairplot( df, hue='species')
plt.suptitle('Comparision of Features after Data Cleaning',fontsize=20,y=1.
↪05,fontweight='bold')
```

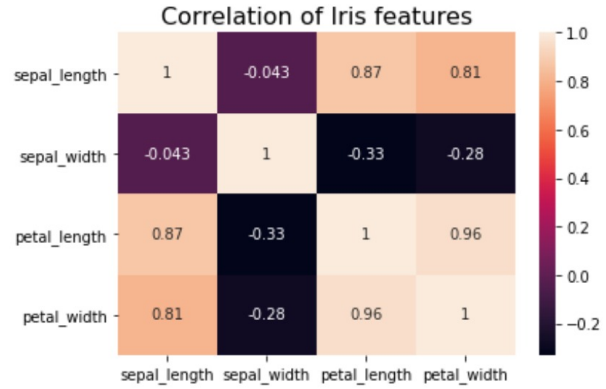
[16]:
```
Text(0.5, 1.05, 'Comparision of Features after Data Cleaning')
```

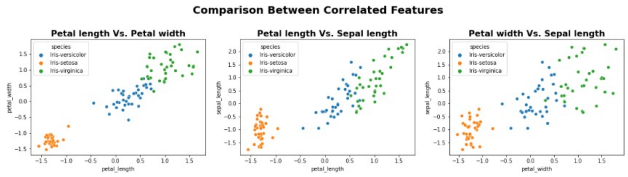


Correlation Coefficient of All 3 Species: Based on the plots above, it is quite clear that in general, petal_length and petal_width *(0.96)* > petal_length and sepal_length *(0.87)* > petal_width and sepal_length *(0.81)* has strong positive correlations.

[17]:
```
# Correlation Coefficient Heatmap
correlation=df.corr()
sns.heatmap(correlation,annot=True)
plt.title('Correlation of Iris features',fontsize=16)

# Comparison between Correlated Features
fig, axes= plt.subplots(1,3,figsize=(20,4))
sns.scatterplot(df.petal_length,df.petal_width,hue= df.species,ax=axes[0])
sns.scatterplot(df.petal_length,df.sepal_length,hue= df.species,ax=axes[1])
sns.scatterplot(df.petal_width,df.sepal_length,hue= df.species,ax=axes[2])
axes[0].set_title('Petal length Vs. Petal width',fontsize=16,fontweight='bold')
```

```
axes[1].set_title('Petal length Vs. Sepal length',fontsize=16,fontweight='bold')
axes[2].set_title('Petal width Vs. Sepal length',fontsize=16,fontweight='bold')
plt.suptitle('Comparison Between Correlated␣
 ↪Features',fontsize=20,fontweight='bold',y=1.1)
plt.show()
```

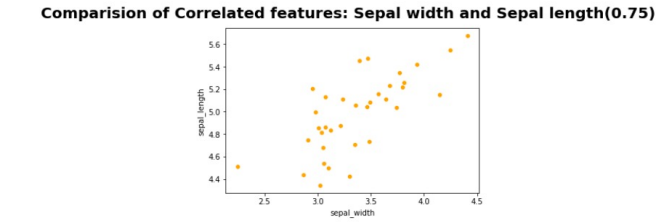




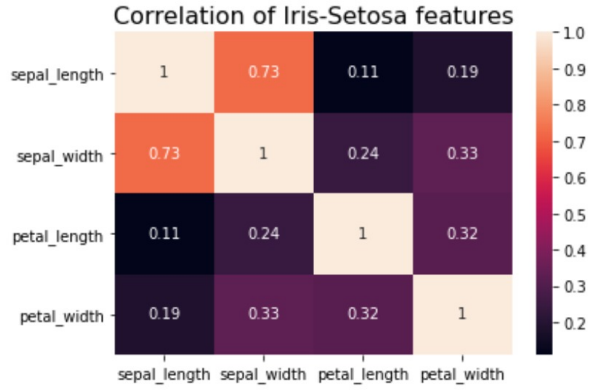
Correlation of Features on Iris-Setosa: This species has only one feature that is positively correlated, i.e., sepal_width and sepal_length (0.75).

[18]:
```
# Scatter Plot of sepal width vs. sepal length for Iris-Setosa
sns.scatterplot(df_setosa.sepal_width,df_setosa.sepal_length,color='orange')
```

```
plt.suptitle('Comparision of Correlated features: Sepal width and Sepal␣
 ↪length(0.75)',fontsize=20,fontweight='bold')
plt.show()

# Correlation Coefficient Heatmap (Iris-Setosa)
correlation_setosa=df_setosa.corr()
sns.heatmap(correlation_setosa,annot=True)
plt.title('Correlation of Iris-Setosa features',fontsize=16)
```

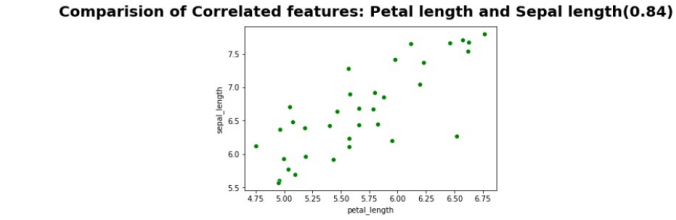


[18]: Text(0.5, 1.0, 'Correlation of Iris-Setosa features')

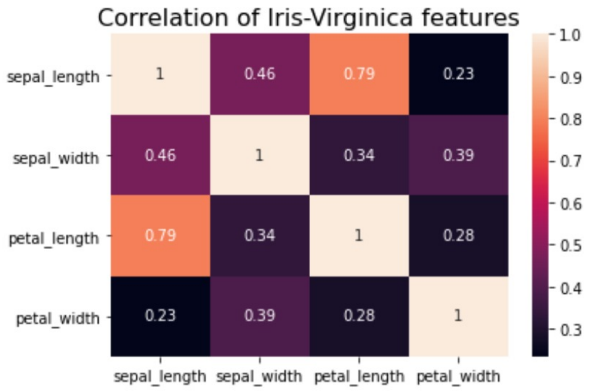


Correlation of Features on Iris-Virginica: This species has only one feature that is positively correlated, i.e., petal_length and sepal_length (0.84).

[19]:
```
# Scatter Plot of sepal width vs. sepal length for Iris-Virginica
sns.scatterplot(df_virginica.petal_length,df_virginica.sepal_length,color='g')
plt.suptitle('Comparision of Correlated features: Petal length and Sepal␣
↪length(0.84)',fontsize=20,fontweight='bold')
plt.show()

# Correlation Coefficient Heatmap (Iris-Virginica)
correlation_virginica=df_virginica.corr()
sns.heatmap(correlation_virginica,annot=True)
plt.title('Correlation of Iris-Virginica features',fontsize=16)
```

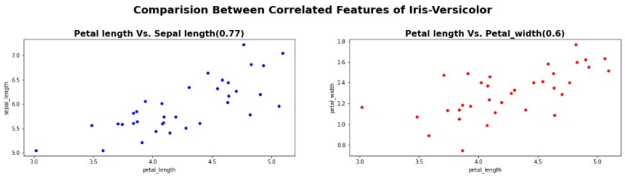


[19]: `Text(0.5, 1.0, 'Correlation of Iris-Virginica features')`

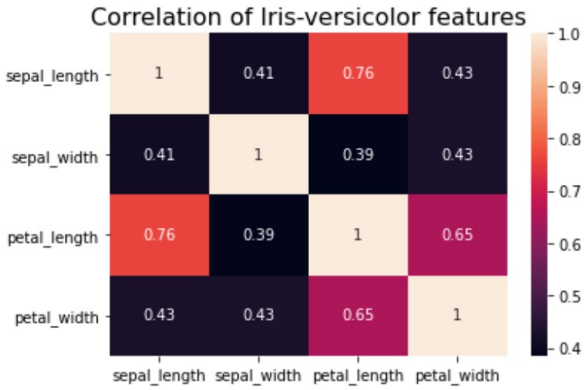


Correlation of Features on Iris-Versicolor: This species has two positively correlations, i.e., petal_length and sepal_length (0.77), and the other one is petal_width and petal_length (0.6).

[20]:
```
# Scatter Plots of petal_length vs. sepal_length and petal_width vs.␣
↪petal_length for Iris-Versicolor
fig, axes= plt.subplots(1,2,figsize=(20,4))
sns.scatterplot(df_versicolor.petal_length,df_versicolor.
↪sepal_length,color='b',ax=axes[0])
sns.scatterplot(df_versicolor.petal_length,df_versicolor.
↪petal_width,color='r',ax=axes[1])
axes[0].set_title('Petal length Vs. Sepal length(0.
↪77)',fontsize=16,fontweight='bold')
axes[1].set_title('Petal length Vs. Petal_width(0.
↪6)',fontsize=16,fontweight='bold')
plt.suptitle('Comparision Between Correlated Features of␣
↪Iris-Versicolor',fontsize=20,fontweight='bold',y=1.1)
plt.show()

# Correlation Coefficient Heatmap (Iris-Versicolor)
correlation_versicolor=df_versicolor.corr()
sns.heatmap(correlation_versicolor,annot=True)
plt.title('Correlation of Iris-versicolor features',fontsize=16)
```



[20]: Text(0.5, 1.0, 'Correlation of Iris-versicolor features')



0.2.4 [CM3]

Correlation Coefficients

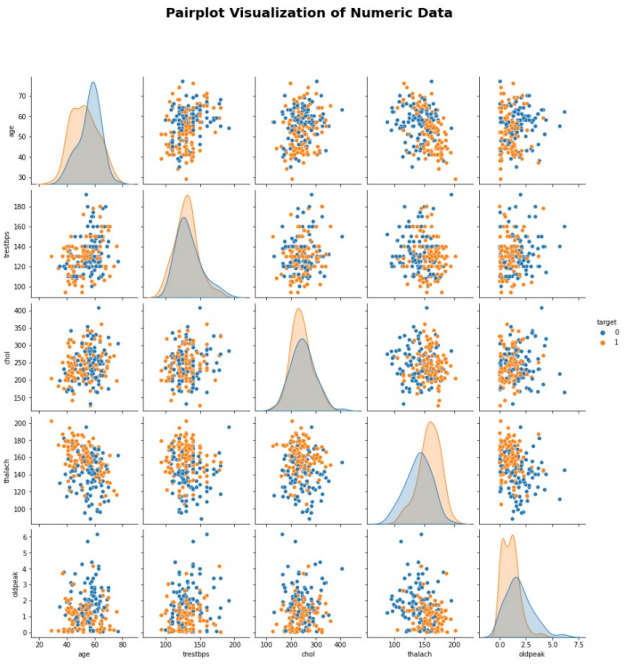
[21]:
```
# Correlation Coefficients for All Pairs of Features
correlation=df.corr()
sns.heatmap(correlation,annot=True)
plt.title('Correlation of Iris features',fontsize=16)
```

[21]: Text(0.5, 1.0, 'Correlation of Iris features')

[14]:
```
norm_df=zscore_norm
norm_df['target']=df.target
```

0.2.3 1.2 [CM2] Data Visulalization

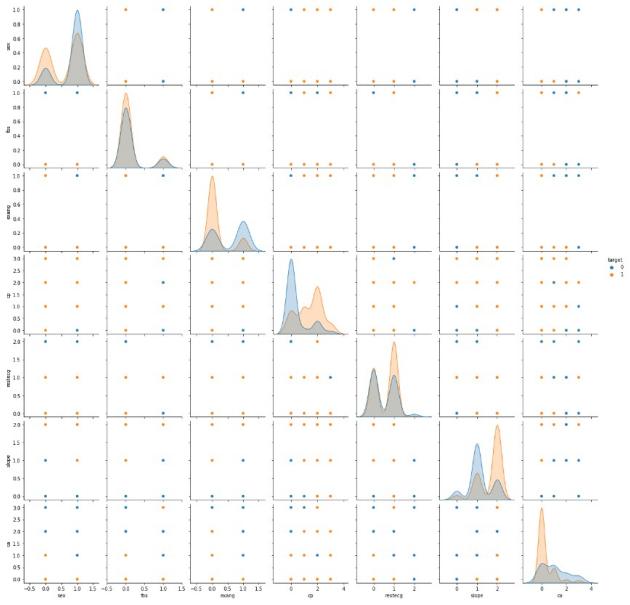
[15]:
```
# Pairs Plot of Numeric Data
num=pd.concat([df[numeric_features],df.target],axis=1)
sns.pairplot(num,hue='target')
plt.suptitle('Pairplot Visualization of Numeric␣
↪Data',fontsize=20,fontweight='bold',y=1.1)
plt.show()
```



It shows good correlation of **age** with **heart rate (thalach)** and **blood pressure(trestbps)**.

[16]:
```
# Pairplot Visualization of Categorical Data:
cat=pd.concat([df[categorical_features],df.target],axis=1)
sns.pairplot(cat,hue='target')
plt.suptitle('Pairplot Visualization of Categorical␣
 ↪Data',fontsize=30,fontweight='bold',y=1.1)
plt.show()
```

Pairplot Visualization of Categorical Data

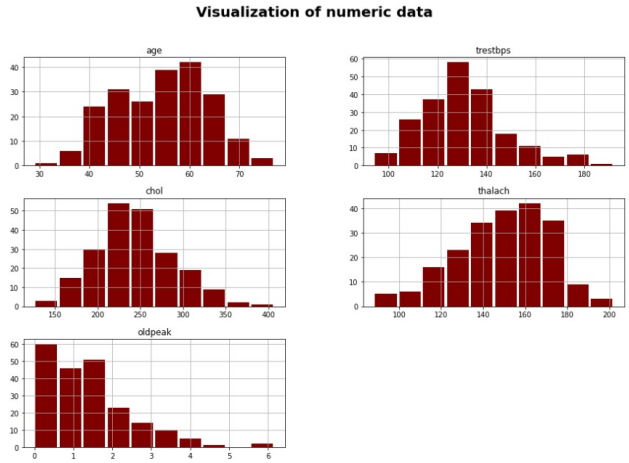


Pairs plot of numeric entities in dataset has been used to know the dependency of one numeric variable over another: 1. Age numeric factor shows a slight good correlation with trestbps (Blood

Pressure), thalach (Heart Rate) and chol (Cholestrol) with correlation values as 0.33, -38 and 0.19, respectively. So, age has positive correlation with trestbps and chol, which means, as one variable increases, then the other too, depending upon their correlation. And, age has negative correlation with heart rate, thalach, which means as age increases heart rate decreases. Furthermore, in bivariate visualization, the effect of age is shown with respect to thalach, trestbps and chol features and also, it displays the chances of one, having heart disease, relative to about features. Hence, age is one of the important factor. 2. Other considerable factors are exang and cp, as their correlation with predicting the heart disease risk is better, compared to other features. The correlation of exang with target is negative (-0.45), meaning heart disease risk will be lower in the having exang induce angina. On the other hand, chest pain (cp) has positive correlation with target, defining that, with the increase in chest pain, the heart disease chance will also rise. 3. In case of categorical data, pairplot confirms that there is no strong correlation between any of these features. Therefore, **age** and **sex** will be considered two important features.

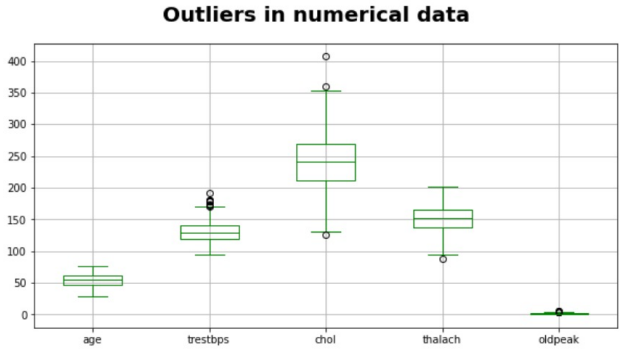
Univariate Visualization

[17]:
```
# Visualization of Numeric Data:
df[numeric_features].hist(figsize=(15,10),color=['maroon'],rwidth=0.9)
plt.suptitle('Visualization of numeric data',fontsize=20,fontweight='bold')
plt.show()
```



It represents the distribution of different numerical features of data, either normally or skewed.

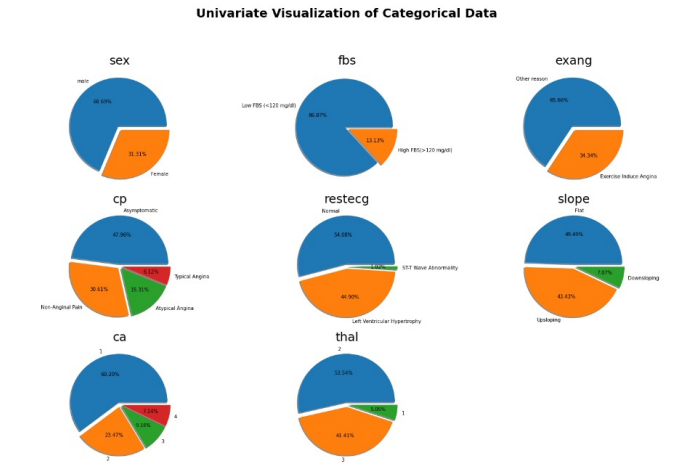
[18]:
```
# Outliers in Numerical Data:
df[numeric_features].boxplot(figsize=(10,5),color='green')
plt.suptitle('Outliers in numerical data',fontsize=20,fontweight='bold')
plt.show()
```



Here, it depicts the presence of outliers in numeric data. Although, it should be removed, but removing it may not always lead to correct results. So, by using Z-Score normalization, this problem will be minimized. In numeric values, the figure represents their distribution and skewness, which also tells about presence of outliers in skewed data. Observation from univariate numeric plotting is as: 1. Age and chol has slightly normal distribution, with a few outliers. 2. Oldpeak is skewed and has many outliers. 3. Thalach and trestbps is not skewed but, it is also not exactly normally distributed, so it contains few outliers as well. 4. From the outliers diagram, it becomes crystal clear that oldpeak has maximum number of outliers, whereas , others have less number of outliers in data, which will definitely be handled further.

[19]:
```
# Visualization of Categorical Data:
cat_val_names= {'sex':{0:'Female',1:'male'},
                'cp':{0:'Asymptomatic',1:'Atypical Angina',2:'Non-Anginal␣
↪Pain',3:'Typical Angina'},
               'fbs':{0: 'Low FBS (<120 mg/dl)',1: 'High FBS(>120 mg/dl)'},
               'restecg':{0:'Left Ventricular Hypertrophy',1:'Normal',2:'ST-T␣
↪Wave Abnormality'},
               'exang':{0:'Other reason',1:'Exercise Induce Angina'},
               'slope':{0:'Downsloping',1:'Upsloping',2:'Flat'},
               'ca':{0:1,1:2,2:3,3:4},
                'thal':{1:1,2:2,3:3}
```

```
            }
fig= plt.figure(figsize=(20,12))
for i in range(len(list(df[categorical_features].columns))):
    labels=list(df[categorical_features][categorical_features[i]].
 ↪value_counts().reset_index()['index'])
    new_labels= [cat_val_names[categorical_features[i]][j] for j in labels]
    ex= tuple( 0.05 for m in range(len(labels)))

    ax= plt.subplot(3,3,i+1)
    size= [k for k in list(df[categorical_features][categorical_features[i]].
                           value_counts().
 ↪reset_index()[categorical_features[i]])]
    percent = [int((1/sum(size))*100) for l in size]

    ax.pie(percent,labels=new_labels,explode=ex,shadow=True,autopct='%0.2f%%')
    plt.title(categorical_features[i], fontsize= 25)
plt.tight_layout()
plt.suptitle('Univariate Visualization of Categorical␣
 ↪Data',fontsize=25,fontweight='bold',y=1.1)
plt.show()
```

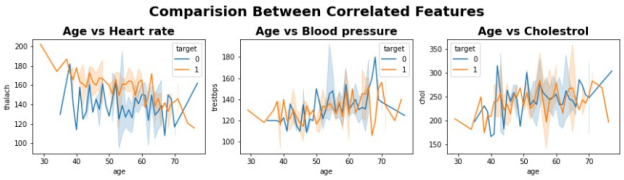


All these columns represent the proportion of different categories of features, with respect to heart disease data. In categorical values, the percentage represents their proportion of their presence in particular data variable. Observations are as follows: 1. 68.69% represents the male data in sex column and the rest 31.31% represents the female data in same. 2. There are 13.13% data entries having sugar level or high fbs >120 mg/dl. 3. 34.34% of sample data has exercise induce angina. 4. The most common type of pain found with maximum percentage is Asymptomatic chest pain with 47.96% and least found is Typical angina chest pain with 6.12% of the whole. 5. In restecg, maximum (54.08%) of the data have normal results and only 1. 02% suffers from ST-T wave abnormality. 6. Almost for half of the data, the slope is flat. 7. In ca, around 60.20% of data, has 1 major vessel and 7.14% has maximum (4) major vessels. 8. In thal, 53.54% (more than half of data variable) provides normal result and about only 5% shows fixed defects.

Bivariate Visualization The chosen features showing great impact are: **age** (w.r.t. **thalach,trestbps,chol**), **cp, exang**, and **sex**.

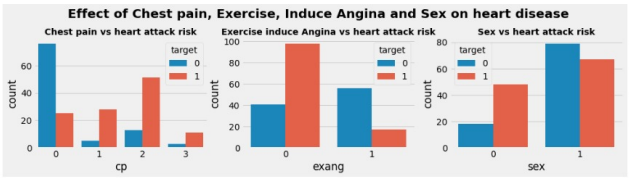
Risk of Heart attack with increase Heart rate (thalach), cholestrol (chol) and Blood Pressure (trestbps), relative to Age.

[20]:
```
# Risk of heart attack with increase Heart rate (thalach), cholestrol (chol)␣
↪and Blood Pressure (trestbps), relative to Age:
fig, axes= plt.subplots(1,3,figsize=(15,3))
sns.lineplot(df.age,df.thalach,hue= df.target,ax=axes[0])
sns.lineplot(df.age,df.trestbps,hue= df.target,ax=axes[1])
sns.lineplot(df.age,df.chol,hue= df.target,ax=axes[2])
axes[0].set_title('Age vs Heart rate',fontsize=16,fontweight='bold')
axes[1].set_title('Age vs Blood pressure',fontsize=16,fontweight='bold')
axes[2].set_title('Age vs Cholestrol',fontsize=16,fontweight='bold')
plt.suptitle('Comparision Between Correlated␣
↪Features',fontsize=20,fontweight='bold',y=1.1)
plt.show()
plt.style.use('fivethirtyeight')
```



It shows that as cholestrol increases, risk of heart disease will increase as well. Also, as blood pressure and age increases, heart risk increases as well. However, as heart rate decreases, chances of heart disease increments.

[21]:
```
# Comparision of correlated features in heart_disease dataset:
corr_features=df.corr()

# Plot
fig, axes= plt.subplots(1,3,figsize=(15,3))
sns.countplot(data=df,x='cp',hue=df.target,ax=axes[0])
sns.countplot(data=df,x=df.exang,hue=df.target,ax=axes[1])
sns.countplot(data=df,x=df.sex,hue=df.target,ax=axes[2])
axes[0].set_title('Chest pain vs heart attack␣
 ↪risk',fontsize=14,fontweight='bold')
axes[1].set_title('Exercise induce Angina vs heart attack␣
 ↪risk',fontsize=14,fontweight='bold')
axes[2].set_title('Sex vs heart attack risk',fontsize=14,fontweight='bold')
plt.suptitle('Effect of Chest pain, Exercise, Induce Angina and Sex on heart␣
 ↪disease',fontsize=20,fontweight='bold',y=1.1)
plt.show()
```

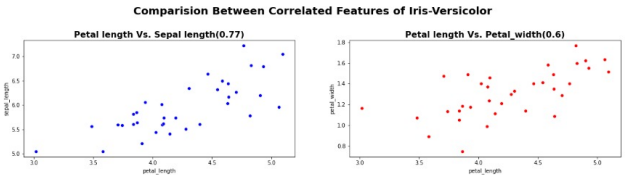


Few observations: 1. It shows with increase in age, blood pressure (trestbps) will increase as well as the risk of heart disease. 2. With increase in age, cholesterol (chol) will rise and so does the risk. 3. As age increments, the heart rate (thalach) decreases and risk increases. 4. In countplot, it is visible that, chest pain and other reasons than exercise indices angina will increase the chances of heart disease. 5. More male patients are found to have risk of heart disease, comparing to female.

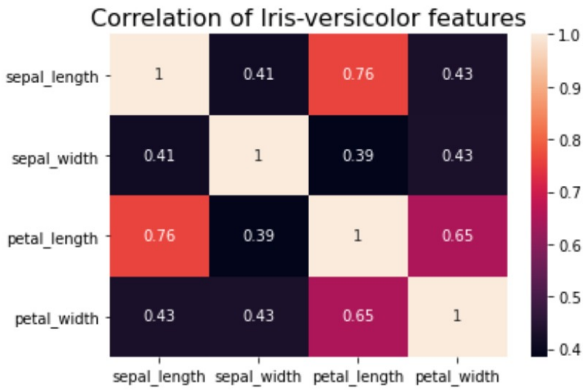
0.2.4 1.3 [CM3]

Correlation Coefficients

[22]:
```
# Correlation between features
plt.figure(figsize=(20,10))
sns.heatmap(df.corr(),annot=True)
plt.title('Correlation between features',fontsize=16)
plt.show()

# Correlation between normalized features:
plt.figure(figsize=(20,10))
sns.heatmap(norm_df.corr(),annot=True)
plt.title('Correlation between normalized features',fontsize=16)
```



[20]: Text(0.5, 1.0, 'Correlation of Iris-versicolor features')

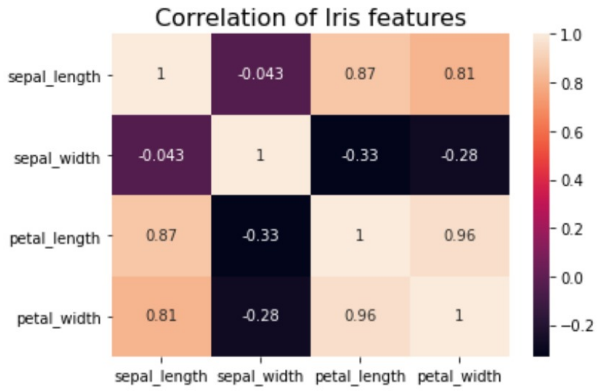


0.2.4 [CM3]

Correlation Coefficients

[21]:
```
# Correlation Coeffficients for All Pairs of Features
correlation=df.corr()
sns.heatmap(correlation,annot=True)
plt.title('Correlation of Iris features',fontsize=16)
```

[21]: Text(0.5, 1.0, 'Correlation of Iris features')



In Iris dataset, petal_length and petal_width has very strong correlation (0.96), there is another good correlation between sepal_length and petal_length (0.87), and the correlation between sepal_length and petal_width is also strong (0.81).

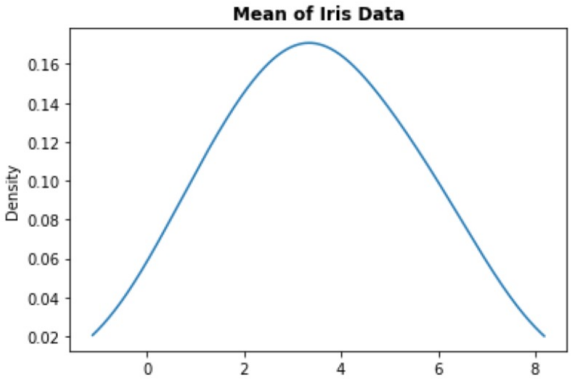
All these correlations are positive which means, they have linear and positive relationship as one increases another increments as well. Also, the correlation between different categories of flower, indicates a linear relationship on the data.

Mean, Variance, Skew and Kurtosis of Iris Dataset

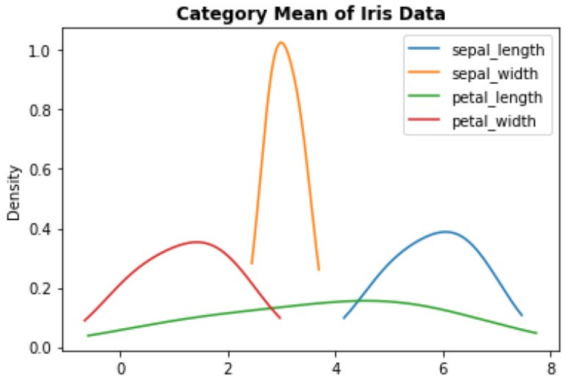
[22]:
```
# Calculation using cleaned data before normalization
# Mean
mean=df_median.mean()
print(f'\033[1mMean:\033[0m\n{mean}\n')
mean.plot(kind='density')
plt.title("Mean of Iris Data",fontweight='bold')
plt.show()
# Category Mean
cat_mean=df_median.groupby('species').mean()
print(f'\033[1mCateogry Mean:\033[0m\n{cat_mean}\n')
cat_mean.plot(kind='density')
plt.title("Category Mean of Iris Data",fontweight='bold')
plt.show()

# Variance
variance=df_median.var()
```

```
print(f'\033[1mVariance:\033[0m\n{variance}\n')
variance.plot(kind='density')
plt.title("Variance of Iris Data",fontweight='bold')
plt.show()
# Category Variance
cat_variance=df_median.groupby('species').var()
print(f'\033[1mCategory Variance:\033[0m\n{cat_variance}\n')
cat_variance.plot(kind='density')
plt.title("Variance of Iris Data",fontweight='bold')
plt.show()

# Skew
skew=df_median.skew()
print(f'\033[1mSkew:\033[0m\n{skew}\n')
skew.plot(kind='density')
plt.title("Skewness of Iris Data",fontweight='bold')
plt.show()
# Category Skew
cat_skew=df.groupby('species').skew()
print(f'\033[1mCategory Skew:\033[0m\n{cat_skew}\n')
cat_skew.plot(kind='density')
plt.title("Categroy Skew of Iris Data",fontweight='bold')
plt.show()

# Kurtosis
kurtosis=df_median.kurtosis()
print(f'\033[1mKurtosis:\033[0m\n{kurtosis}\n')
kurtosis.plot(kind='density')
plt.title("Kurtosis of Iris Data",fontweight='bold')
plt.show()
# Category Kurtosis
cat_kurtosis=pd.concat([df_setosa.kurtosis(),df_versicolor.
 ↪kurtosis(),df_virginica.
 ↪kurtosis()],axis=1,keys=['iris_setosa','iris_versicolor','iris_virginica'])
print(f'\033[1mCategory Kurtosis:\033[0m\n{cat_kurtosis}\n')
cat_kurtosis.plot(kind='density')
plt.title("Category Kurtosis of Iris Data",fontweight='bold')
plt.show()
# print(f'\033[1mKurtosis:\033[0m\n{kurtosis}\n\n\033[1mCateogry Kurtosis:
 ↪\033[0m\n{cat_kurtosis}\n')

# Summary
summary=pd.
 ↪concat([mean,variance,skew,kurtosis],axis=1,keys=['Mean','Variance','Skew','Kurtosis'])
print(f'\033[1mSummarized View on Mean, Variance, Skew and Kurtosis of Iris␣
 ↪Data:\033[0m\n{summary}')
```

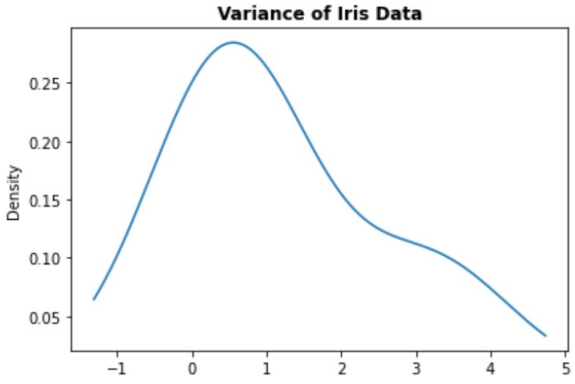
```
Mean:
sepal_length    5.858909
sepal_width     3.055949
petal_length    3.806484
petal_width     1.205093
dtype: float64
```




```
Cateogry Mean:
                sepal_length  sepal_width  petal_length  petal_width
species
Iris-setosa         4.987384     3.382670      1.485063     0.245424
Iris-versicolor     5.948732     2.758477      4.282742     1.308528
Iris-virginica      6.640611     3.026700      5.651647     2.061326
```

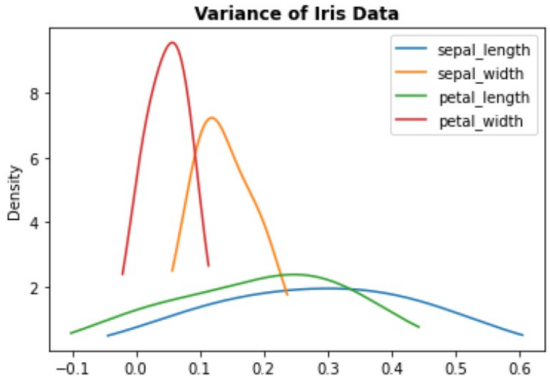



```
Variance:
sepal_length    0.742420
sepal_width     0.201898
petal_length    3.222815
petal_width     0.607509
dtype: float64
```

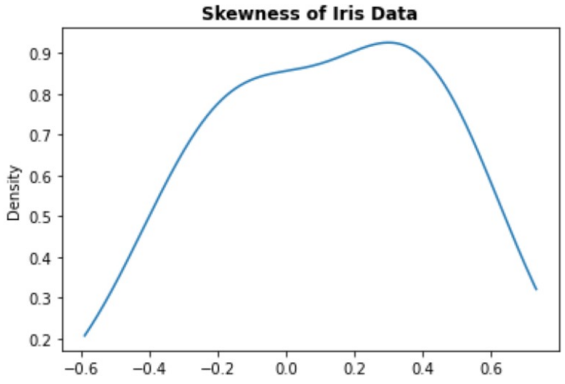


Category Variance:

species	sepal_length	sepal_width	petal_length	petal_width
Iris-setosa	0.118106	0.191651	0.034140	0.012412
Iris-versicolor	0.290830	0.101611	0.231756	0.052308
Iris-virginica	0.442762	0.122449	0.306374	0.079779

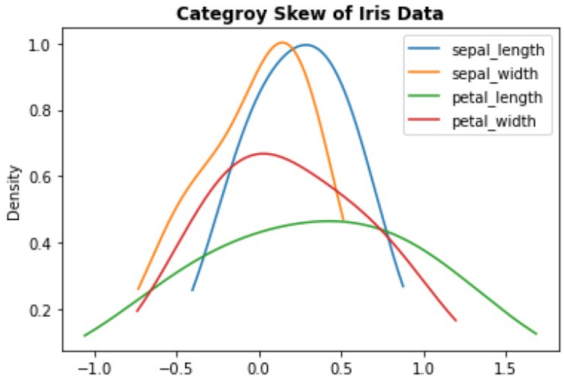



```
Skew:
sepal_length    0.401506
sepal_width     0.384402
petal_length   -0.258324
petal_width    -0.054162
dtype: float64
```

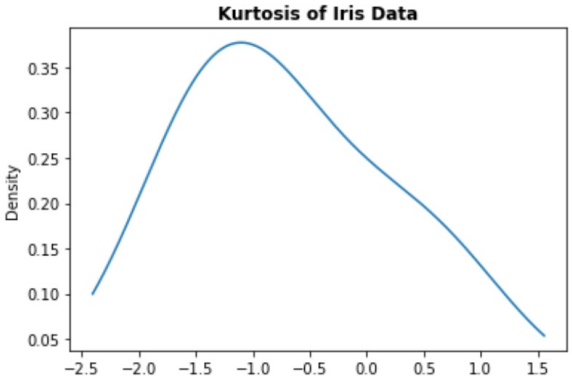


Category Skew:

species	sepal_length	sepal_width	petal_length	petal_width
Iris-setosa	-0.083972	0.200944	0.999313	0.712254
Iris-versicolor	0.556421	-0.421734	-0.372987	-0.255765
Iris-virginica	0.261658	0.158813	0.371726	0.096649

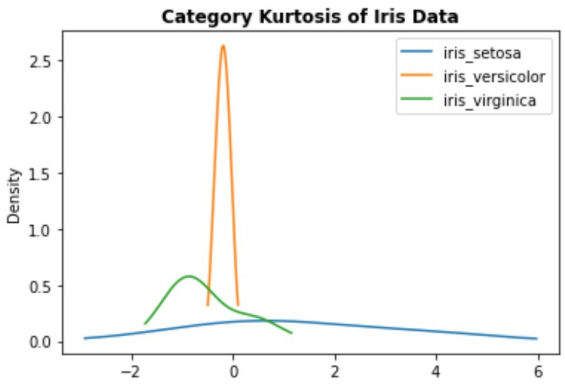



```
Kurtosis:
sepal_length   -0.544820
sepal_width     0.566680
petal_length   -1.413848
petal_width    -1.330676
dtype: float64
```



Category Kurtosis:

	iris_setosa	iris_versicolor	iris_virginica
sepal_length	-0.689305	-0.162358	-1.004403
sepal_width	0.539820	-0.044218	0.434558
petal_length	3.756036	-0.342191	-0.938679
petal_width	1.444841	-0.219342	-0.685965



Summarized View on Mean, Variance, Skew and Kurtosis of Iris Data:

	Mean	Variance	Skew	Kurtosis
sepal_length	5.858909	0.742420	0.401506	-0.544820
sepal_width	3.055949	0.201898	0.384402	0.566680
petal_length	3.806484	3.222815	-0.258324	-1.413848
petal_width	1.205093	0.607509	-0.054162	-1.330676

Discussion By looking at mean, it represents symmetrical plot, which means data is normally distributed. Also, depicting by categories, flash a light on how different categories of flowers have features on different dimension ranges. It tells that sepal_length is greatest in cm and petal_length is short. Whereas, sepal_width and petal_length are almost of same length in cm.

In variance, the plot shows how spread out the data is. In category plot, it shows that the data in sepal_width and petal_width, the data is less spead out as comparison to sepal_length and petal_length.

As for skew, the data is not skewed to great extent, which means, it has less or no outliers. Even, if we look at the category wise plot, the slowness is not that effected. As, observed by mean it is a symmetrical data, which results in less skewness.

Kurtosis defines the peak sharpness in frequency distribution, so, kurtosis of iris data is not high, but if we look at categorical plot, Iris_setosa has the highest kurtosis among others.

0.3 Question 2: KNN

0.3.1 2.1 Dividing Data

[23]:
```
# Define features and target for the training
features= zscore_norm
target= df.species
# labelEncoder() is used for multiclass data
target= LabelEncoder().fit_transform(target)

# Question 2.1 Dividing data using train_test_split()
x_train, x_test, y_train, y_test = train_test_split(features,target,test_size=0.
↪2,random_state=98)
```

0.3.2 2.2 [CM4] Training and Testing

[24]:
```
knn= KNeighborsClassifier()
knn.fit(x_train,y_train)
predictions= knn.predict(x_test)
original_accuracy=metrics.accuracy_score(y_test,predictions)
print(f"Accuracy of the model is {original_accuracy} using classifier's default␣
↪parameters.")
```

```
Accuracy of the model is 1.0 using classifier's default parameters.
```

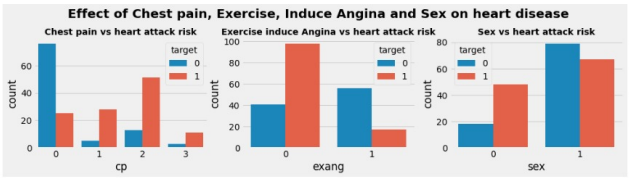
0.3.3 2.3 5-Fold Cross Validation

[25]:
```
kf_scores = []
kf = KFold()
kf_knn= KNeighborsClassifier()

for train_index, test_index in kf.split(features):
    features_train, features_test = features.iloc[train_index], features.
↪iloc[test_index]
    target_train, target_test = target[train_index], target[test_index]
    kf_knn.fit(features_train,target_train)
    kf_scores.append(metrics.accuracy_score(target_test,knn.
↪predict(features_test)))

# Output results
print(f'The accuracy scores for the 5-fold cross validation is:␣
↪{kf_scores}\nThe variance of the scores is: {pd.DataFrame({"accuracy":
↪kf_scores}).var().accuracy}')
```

```
The accuracy scores for the 5-fold cross validation is: [1.0, 1.0,
0.9523809523809523, 0.9047619047619048, 1.0]
The variance of the scores is: 0.0018140589569161
```

[CM5] Accuracy vs. k Plot The variance for the k-fold cross validation is **0.001814** with detailed scores listed above.

[21]:
```
# Comparision of correlated features in heart_disease dataset:
corr_features=df.corr()

# Plot
fig, axes= plt.subplots(1,3,figsize=(15,3))
sns.countplot(data=df,x='cp',hue=df.target,ax=axes[0])
sns.countplot(data=df,x=df.exang,hue=df.target,ax=axes[1])
sns.countplot(data=df,x=df.sex,hue=df.target,ax=axes[2])
axes[0].set_title('Chest pain vs heart attack␣
 ↪risk',fontsize=14,fontweight='bold')
axes[1].set_title('Exercise induce Angina vs heart attack␣
 ↪risk',fontsize=14,fontweight='bold')
axes[2].set_title('Sex vs heart attack risk',fontsize=14,fontweight='bold')
plt.suptitle('Effect of Chest pain, Exercise, Induce Angina and Sex on heart␣
 ↪disease',fontsize=20,fontweight='bold',y=1.1)
plt.show()
```



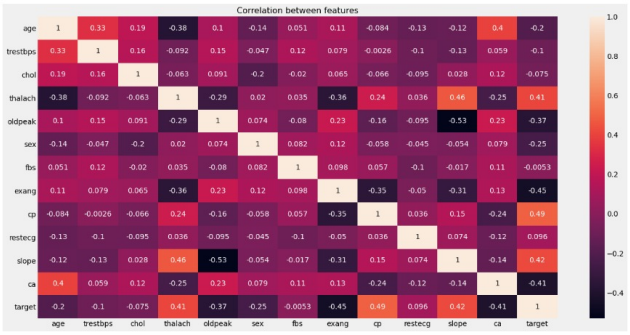
Few observations: 1. It shows with increase in age, blood pressure (trestbps) will increase as well as the risk of heart disease. 2. With increase in age, cholesterol (chol) will rise and so does the risk. 3. As age increments, the heart rate (thalach) decreases and risk increases. 4. In countplot, it is visible that, chest pain and other reasons than exercise indices angina will increase the chances of heart disease. 5. More male patients are found to have risk of heart disease, comparing to female.

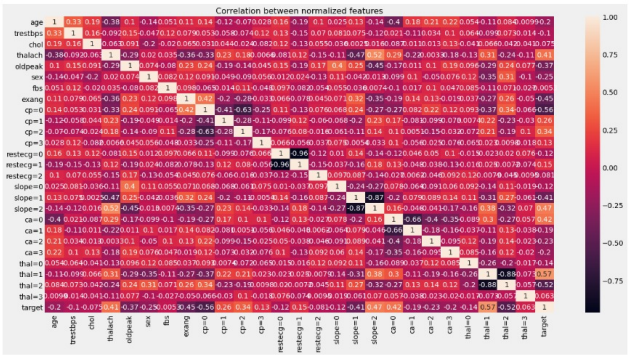
0.2.4 1.3 [CM3]

Correlation Coefficients

[22]:
```
# Correlation between features
plt.figure(figsize=(20,10))
sns.heatmap(df.corr(),annot=True)
plt.title('Correlation between features',fontsize=16)
plt.show()

# Correlation between normalized features:
plt.figure(figsize=(20,10))
sns.heatmap(norm_df.corr(),annot=True)
plt.title('Correlation between normalized features',fontsize=16)
```

```
plt.show()
```





Correlation describes the dependency of variable on each other. There are few columns, namely, thalach, exang, cp, slope and ca, which are having better and strong correlation with target variable, having correlation values as 0.41, -0.45, 0.49, 0.42 and -0.41 respectively. Therefore, thalach, co and slope are positively correlated wherever as, exang and ca has negative coorelation.

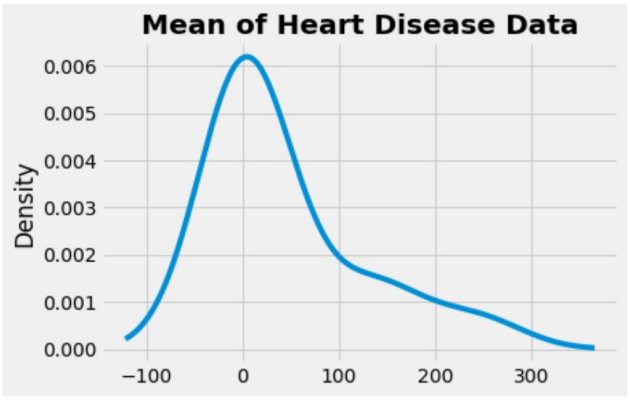
Mean, Variance, Skew and Kurtosis of Heart Disease Dataset

[23]:
```
# Mean
mean=df.mean()
print(f'\033[1mMean:\033[0m\n{mean}\n')
mean.plot(kind='density')
plt.title("Mean of Heart Disease Data",fontweight='bold')
plt.show()
# Normalized Mean
norm_mean=norm_df.mean()
print(f'\033[1mNormalized Mean:\033[0m\n{norm_mean}\n')
norm_mean.plot(kind='density')
plt.title("Normalized Mean of Heart Disease Data",fontweight='bold')
plt.show()

# Variance
variance=df.var()
print(f'\033[1mVariance:\033[0m\n{variance}\n')
variance.plot(kind='density')
plt.title("Variance of Heart Disease Data",fontweight='bold')
plt.show()
# Normalized Variance
norm_variance=norm_df.var()
print(f'\033[1mNormalized Variance:\033[0m\n{norm_variance}\n')
norm_variance.plot(kind='density')
plt.title("Normalized Variance of Heart Disease Data",fontweight='bold')
plt.show()

# Skew
skew=df.skew()
print(f'\033[1mSkew:\033[0m\n{skew}\n')
skew.plot(kind='density')
plt.title("Skew of Heart Disease Data",fontweight='bold')
plt.show()
# Normalized Skew
norm_skew=norm_df.skew()
print(f'\033[1mNormalized Skew:\033[0m\n{norm_skew}\n')
norm_skew.plot(kind='density')
plt.title("Normalized Skew of Heart Disease Data",fontweight='bold')
plt.show()

# Kurtosis
kurtosis=df.kurtosis()
print(f'\033[1mKurtosis:\033[0m\n{kurtosis}\n')
kurtosis.plot(kind='density')
plt.title("Kurtosis of Heart Disease Data",fontweight='bold')
plt.show()
# Normalized Kurtosis
```

```
norm_kurtosis=norm_df.kurtosis()
print(f'\033[1mNormalized Kurtosis:\033[0m\n{norm_kurtosis}\n')
norm_kurtosis.plot(kind='density')
plt.title("Normalized Kurtosis of Heart Disease Data",fontweight='bold')
plt.show()

# Summary
summary= pd.
 ↪concat([mean,variance,skew,kurtosis],axis=1,keys=['Mean','Variance','Skew','Kurtosis'])
print(f'\033[1m\nSummarized View on Mean, Variance, Skew and Kurtosis of Heart␣
 ↪Disease Data:\033[0m')
summary
```

Mean:

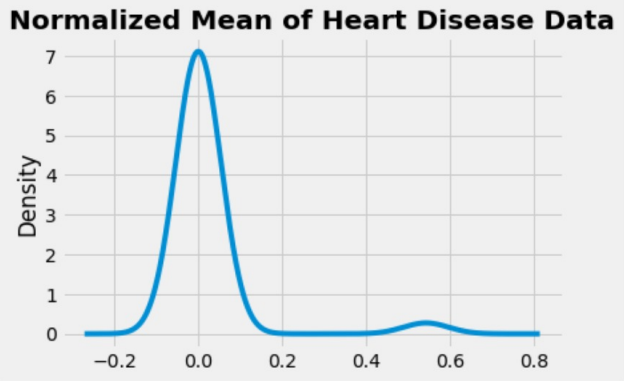
```
age          54.311321
trestbps    131.584079
chol        243.566875
thalach     149.728989
oldpeak       1.370551
sex           0.688679
fbs           0.132075
exang         0.344340
cp            0.957547
restecg       0.570755
slope         1.419811
ca            0.655660
target        0.542453
dtype: float64
```



Normalized Mean:

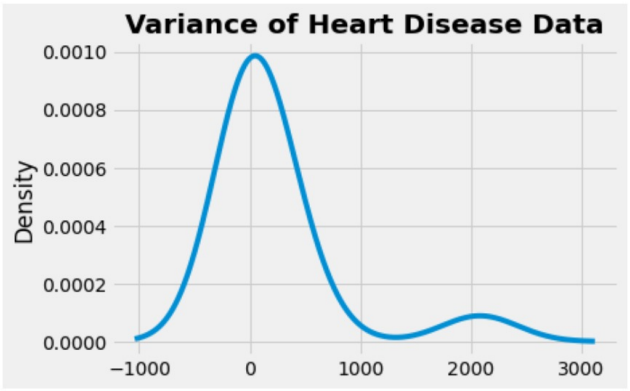
age	4.608473e-17
trestbps	-9.803479e-16
chol	-5.362587e-16
thalach	1.298751e-16
oldpeak	7.541138e-17
sex	1.047380e-17
fbs	0.000000e+00
exang	3.770569e-17
cp=0	8.379042e-18
cp=1	2.513713e-17
cp=2	6.284281e-17
cp=3	1.256856e-16
restecg=0	-3.351617e-17
restecg=1	8.379042e-18
restecg=2	-6.703233e-17
slope=0	4.189521e-17
slope=1	-1.571070e-17
slope=2	-2.723189e-17
ca=0	5.027425e-17
ca=1	-2.304236e-17
ca=2	2.304236e-17
ca=3	5.027425e-17
thal=0	2.513713e-17
thal=1	4.608473e-17

```
thal=2      -1.791020e-16
thal=3       2.094760e-17
target       5.424528e-01
dtype: float64
```



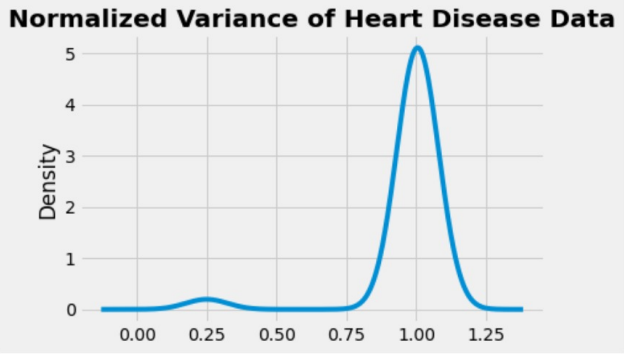
Variance:

```
age           83.637217
trestbps     317.750965
chol        2081.640550
thalach      478.645304
oldpeak        1.228762
sex            0.215416
fbs            0.115175
exang          0.226840
cp             1.045583
restecg        0.284070
slope          0.386904
ca             0.880868
target         0.249374
dtype: float64
```



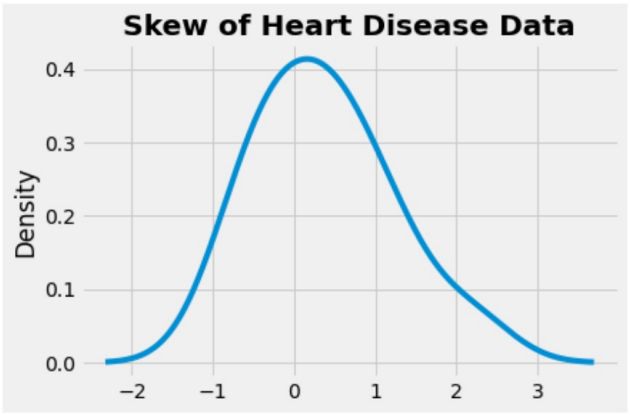

```
Normalized Variance:
age          1.004739
trestbps     1.004739
chol         1.004739
thalach      1.004739
oldpeak      1.004739
sex          1.004739
fbs          1.004739
exang        1.004739
cp=0         1.004739
cp=1         1.004739
cp=2         1.004739
cp=3         1.004739
restecg=0    1.004739
restecg=1    1.004739
restecg=2    1.004739
slope=0      1.004739
slope=1      1.004739
slope=2      1.004739
ca=0         1.004739
ca=1         1.004739
ca=2         1.004739
ca=3         1.004739
thal=0       1.004739
thal=1       1.004739
```

```
thal=2       1.004739
thal=3       1.004739
target       0.249374
dtype: float64
```



Skew:

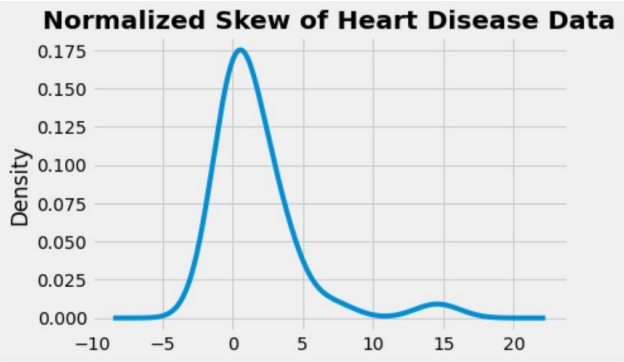
```
age         -0.106027
trestbps     0.704102
chol         0.364810
thalach     -0.408051
oldpeak      1.213051
sex         -0.820789
fbs          2.188903
exang        0.659880
cp           0.461438
restecg      0.093288
slope       -0.586510
ca           1.294338
target      -0.171644
dtype: float64
```



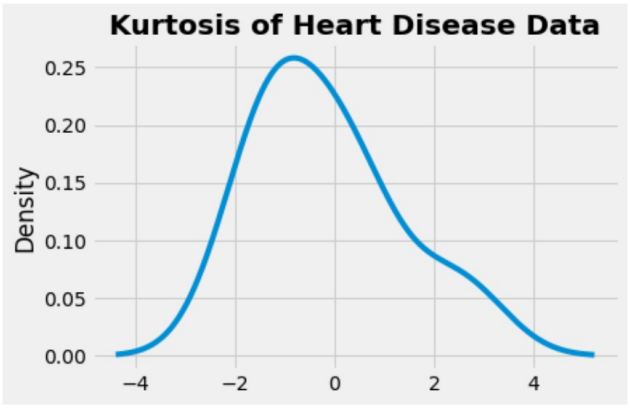
Normalized Skew:

age	-0.106027
trestbps	0.704102
chol	0.364810
thalach	-0.408051
oldpeak	1.213051
sex	-0.820789
fbs	2.188903
exang	0.659880
cp=0	0.095119
cp=1	1.913195
cp=2	0.869257
cp=3	3.519744
restecg=0	0.210164
restecg=1	-0.133309
restecg=2	7.122925
slope=0	3.371961
slope=1	0.248913
slope=2	0.038012
ca=0	-0.387004
ca=1	1.284703
ca=2	2.703413
ca=3	3.237236
thal=0	3.864934

```
thal=1       -0.114199
thal=2        0.366994
thal=3       14.560220
target       -0.171644
dtype: float64
```

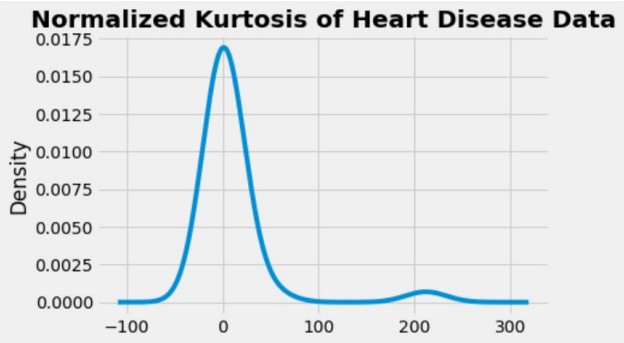



```
Kurtosis:
age         -0.561563
trestbps     0.703382
chol         0.351762
thalach     -0.160319
oldpeak      2.108134
sex         -1.339028
fbs          2.817791
exang       -1.579550
cp          -1.240674
restecg     -1.193589
slope       -0.579659
ca           0.575571
target      -1.989397
dtype: float64
```




```
Normalized Kurtosis:
age           -0.561563
trestbps       0.703382
chol           0.351762
thalach       -0.160319
oldpeak        2.108134
sex           -1.339028
fbs            2.817791
exang         -1.579550
cp=0          -2.010005
cp=1           1.676038
cp=2          -1.256334
cp=3          10.487451
restecg=0     -1.974549
restecg=1     -2.001198
restecg=2     49.200143
slope=0        9.459272
slope=1       -1.956591
slope=2       -2.017680
ca=0          -1.867940
ca=1          -0.352957
ca=2           5.358912
ca=3           8.560368
thal=0        13.060847
```

```
thal=1        -2.005973
thal=2        -1.883171
thal=3       212.000000
target        -1.989397
dtype: float64
```



Summarized View on Mean, Variance, Skew and Kurtosis of Heart Disease Data:

[23]:

	Mean	Variance	Skew	Kurtosis
age	54.311321	83.637217	-0.106027	-0.561563
trestbps	131.584079	317.750965	0.704102	0.703382
chol	243.566875	2081.640550	0.364810	0.351762
thalach	149.728989	478.645304	-0.408051	-0.160319
oldpeak	1.370551	1.228762	1.213051	2.108134
sex	0.688679	0.215416	-0.820789	-1.339028
fbs	0.132075	0.115175	2.188903	2.817791
exang	0.344340	0.226840	0.659880	-1.579550
cp	0.957547	1.045583	0.461438	-1.240674
restecg	0.570755	0.284070	0.093288	-1.193589
slope	1.419811	0.386904	-0.586510	-0.579659
ca	0.655660	0.880868	1.294338	0.575571
target	0.542453	0.249374	-0.171644	-1.989397

Mean

It represents the average of data and also defines the nature of data as symmetrical and assymetrical. If mean is close to medean, it represents less outliers. If mean and median difference is more, it

represents the asymmetrical nature of data which could leads to more numbers of outliers.

Variance
It is a variability measure. It determines the degree of spread, the more spread the data is, the more is the variance.

Skew
Despite the skewness of data, positively skewed or negatively. In general it shows whether the data is symmetrical. Also, if it is asymmetrical, the position of outliers can be determined with skewness. Left/negative skewed means there is tail and presence of outliers on the left side of asymmetrical data, and right/positive skewed means there is tail and presence of outliers on the right side of asymmetrical data.

Kurtosis
It tells the tail heaviness of distribution, such as heavy tailed or lightly tailed. High kurtosis means Heavy tailed that is more, outliers and low kutosis means less outliers.

0.3 Question 2: KNN

0.3.1 2.1 Dividing Data

For Train_Test_Validate, 20% of data will be used for testing whereas, 80% for training purposes, in which 10% will be further used for validation.

[24]:
```
# Define features and target for the training
features= zscore_norm
target= df.target

# Dividing data using train_test_split()
x_train, x_test, y_train, y_test = train_test_split(features,target,test_size=0.
↪2,random_state=98)
x_train_new, x_val, y_train_new, y_val =␣
↪train_test_split(x_train,y_train,test_size=0.1,random_state=98)
```

0.3.2 2.2 [CM4] Training and Testing

[25]:
```
knn= KNeighborsClassifier()
knn.fit(x_train,y_train)
predictions=knn.predict(x_test)
original_acc=metrics.accuracy_score(y_test,predictions)
print(f"Accuracy of the model is {original_acc} using classifier's default␣
↪parameters.")
```

```
Accuracy of the model is 0.9069767441860465 using classifier's default
parameters.
```

0.3.3 2.3 Parameter Tuning

[CM5] Accuracy vs. k Plot

0.3.1 2.1 Dividing Data

[23]:
```
# Define features and target for the training
features= zscore_norm
target= df.species
# labelEncoder() is used for multiclass data
target= LabelEncoder().fit_transform(target)

# Question 2.1 Dividing data using train_test_split()
x_train, x_test, y_train, y_test = train_test_split(features,target,test_size=0.
↪2,random_state=98)
```

0.3.2 2.2 [CM4] Training and Testing

[24]:
```
knn= KNeighborsClassifier()
knn.fit(x_train,y_train)
predictions= knn.predict(x_test)
original_accuracy=metrics.accuracy_score(y_test,predictions)
print(f"Accuracy of the model is {original_accuracy} using classifier's default␣
↪parameters.")
```

```
Accuracy of the model is 1.0 using classifier's default parameters.
```

0.3.3 2.3 5-Fold Cross Validation

[25]:
```
kf_scores = []
kf = KFold()
kf_knn= KNeighborsClassifier()

for train_index, test_index in kf.split(features):
    features_train, features_test = features.iloc[train_index], features.
↪iloc[test_index]
    target_train, target_test = target[train_index], target[test_index]
    kf_knn.fit(features_train,target_train)
    kf_scores.append(metrics.accuracy_score(target_test,knn.
↪predict(features_test)))

# Output results
print(f'The accuracy scores for the 5-fold cross validation is:␣
↪{kf_scores}\nThe variance of the scores is: {pd.DataFrame({"accuracy":
↪kf_scores}).var().accuracy}')
```

```
The accuracy scores for the 5-fold cross validation is: [1.0, 1.0,
0.9523809523809523, 0.9047619047619048, 1.0]
The variance of the scores is: 0.0018140589569161
```

[CM5] Accuracy vs. k Plot The variance for the k-fold cross validation is **0.001814** with detailed scores listed above.

represents the asymmetrical nature of data which could leads to more numbers of outliers.

Variance
It is a variability measure. It determines the degree of spread, the more spread the data is, the more is the variance.

Skew
Despite the skewness of data, positively skewed or negatively. In general it shows whether the data is symmetrical. Also, if it is asymmetrical, the position of outliers can be determined with skewness. Left/negative skewed means there is tail and presence of outliers on the left side of asymmetrical data, and right/positive skewed means there is tail and presence of outliers on the right side of asymmetrical data.

Kurtosis
It tells the tail heaviness of distribution, such as heavy tailed or lightly tailed. High kurtosis means Heavy tailed that is more, outliers and low kutosis means less outliers.

0.3 Question 2: KNN

0.3.1 2.1 Dividing Data

For Train_Test_Validate, 20% of data will be used for testing whereas, 80% for training purposes, in which 10% will be further used for validation.

[24]:
```
# Define features and target for the training
features= zscore_norm
target= df.target

# Dividing data using train_test_split()
x_train, x_test, y_train, y_test = train_test_split(features,target,test_size=0.
↪2,random_state=98)
x_train_new, x_val, y_train_new, y_val =␣
↪train_test_split(x_train,y_train,test_size=0.1,random_state=98)
```

0.3.2 2.2 [CM4] Training and Testing

[25]:
```
knn= KNeighborsClassifier()
knn.fit(x_train,y_train)
predictions=knn.predict(x_test)
original_acc=metrics.accuracy_score(y_test,predictions)
print(f"Accuracy of the model is {original_acc} using classifier's default␣
↪parameters.")
```

```
Accuracy of the model is 0.9069767441860465 using classifier's default
parameters.
```

0.3.3 2.3 Parameter Tuning

[CM5] Accuracy vs. k Plot

0.3.1 2.1 Dividing Data

[23]:
```
# Define features and target for the training
features= zscore_norm
target= df.species
# labelEncoder() is used for multiclass data
target= LabelEncoder().fit_transform(target)

# Question 2.1 Dividing data using train_test_split()
x_train, x_test, y_train, y_test = train_test_split(features,target,test_size=0.
↪2,random_state=98)
```

0.3.2 2.2 [CM4] Training and Testing

[24]:
```
knn= KNeighborsClassifier()
knn.fit(x_train,y_train)
predictions= knn.predict(x_test)
original_accuracy=metrics.accuracy_score(y_test,predictions)
print(f"Accuracy of the model is {original_accuracy} using classifier's default␣
↪parameters.")
```

```
Accuracy of the model is 1.0 using classifier's default parameters.
```

0.3.3 2.3 5-Fold Cross Validation

[25]:
```
kf_scores = []
kf = KFold()
kf_knn= KNeighborsClassifier()

for train_index, test_index in kf.split(features):
    features_train, features_test = features.iloc[train_index], features.
↪iloc[test_index]
    target_train, target_test = target[train_index], target[test_index]
    kf_knn.fit(features_train,target_train)
    kf_scores.append(metrics.accuracy_score(target_test,knn.
↪predict(features_test)))

# Output results
print(f'The accuracy scores for the 5-fold cross validation is:␣
↪{kf_scores}\nThe variance of the scores is: {pd.DataFrame({"accuracy":
↪kf_scores}).var().accuracy}')
```

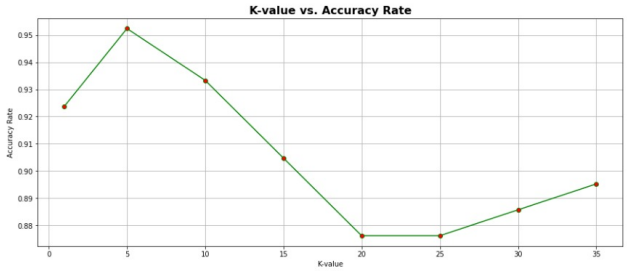
```
The accuracy scores for the 5-fold cross validation is: [1.0, 1.0,
0.9523809523809523, 0.9047619047619048, 1.0]
The variance of the scores is: 0.0018140589569161
```

[CM5] Accuracy vs. k Plot The variance for the k-fold cross validation is **0.001814** with detailed scores listed above.

[26]:
```
scores=[]
scores_with_iterations=[]
r=[1,5,10,15,20,25,30,35]
for i in r:
    knn= KNeighborsClassifier(n_neighbors=i)
    score= cross_val_score(knn,features,target,cv=5)
    scores.append(score.mean())
    scores_with_iterations.append(score)

plt.figure(figsize=(15,6))
plt.plot(r,scores,marker='o',markerfacecolor='r',color='g')
plt.xlabel("K-value")
plt.ylabel("Accuracy Rate")
plt.title("K-value vs. Accuracy Rate", fontsize=16, fontweight='bold')
plt.grid()

scores = pd.
 ↪DataFrame(scores,index=["k=1","k=5","k=10","k=15","k=20","k=25","k=30","k=35"],columns=["Ac
 ↪Rate"])
scores
```

[26]:

	Accuracy Rate
k=1	0.923810
k=5	0.952381
k=10	0.933333
k=15	0.904762
k=20	0.876190
k=25	0.876190
k=30	0.885714
k=35	0.895238



Variations of k Parameter:

[27]:
```
scores_with_iterations=pd.
↪DataFrame(scores_with_iterations,index=["k=1","k=5","k=10","k=15","k=20","k=25","k=30","k=3
↪iteration",
                                "2 iteration","3 iteration","4 iteration","5␣
↪iteration"])
scores_with_iterations
```

[27]:

	1 iteration	2 iteration	3 iteration	4 iteration	5 iteration
k=1	0.857143	0.952381	0.952381	0.904762	0.952381
k=5	0.952381	0.952381	0.952381	0.952381	0.952381
k=10	0.952381	0.904762	0.904762	0.952381	0.952381
k=15	0.952381	0.857143	0.809524	0.952381	0.952381
k=20	0.952381	0.857143	0.809524	0.904762	0.857143
k=25	0.952381	0.857143	0.809524	0.904762	0.857143
k=30	1.000000	0.857143	0.809524	0.904762	0.857143
k=35	1.000000	0.857143	0.809524	0.952381	0.857143

Accuracy with best k parameter

[28]:
```
knn= KNeighborsClassifier(n_neighbors=5)
knn.fit(x_train,y_train)
predictions= knn.predict(x_test)
k_accuracy=metrics.accuracy_score(y_test,predictions)
k_accuracy
```

[28]: 1.0

Discussion

- K-fold Validation Scores: 1.0, 1.0, 0.9523809523809523, 0.9047619047619048, 1.0
- Scores Variance: 0.0018140589569161

K-fold cross validation, in this data splits into k number of folds and iteration is performed on each one of it. It is like using all the data for training and testing. It allows to train the model on multiple train_test_splits. Therefore, it is more suitable for smaller datasets like this Iris dataset.

On the other hand, test_validate_test allows to train the model on a single train_test_split, depending upon the given sample ratio of dataset. So it is preferred on a larger dataset.

Although, k-fold cross validation method improves the performance over train_validate_test but again, it depends upon the nature of data to be applied upon.

In given dataset also, k-fold validation provided more accurate results with respect to actual test set. But, in train_validate_test, the accuracy of validation set and actual model differs.

[CM6] Evaluation of KNN model:

Confusion matrix is used for determining performance of classification model

represents the asymmetrical nature of data which could leads to more numbers of outliers.

Variance
It is a variability measure. It determines the degree of spread, the more spread the data is, the more is the variance.

Skew
Despite the skewness of data, positively skewed or negatively. In general it shows whether the data is symmetrical. Also, if it is asymmetrical, the position of outliers can be determined with skewness. Left/negative skewed means there is tail and presence of outliers on the left side of asymmetrical data, and right/positive skewed means there is tail and presence of outliers on the right side of asymmetrical data.

Kurtosis
It tells the tail heaviness of distribution, such as heavy tailed or lightly tailed. High kurtosis means Heavy tailed that is more, outliers and low kutosis means less outliers.

0.3 Question 2: KNN

0.3.1 2.1 Dividing Data

For Train_Test_Validate, 20% of data will be used for testing whereas, 80% for training purposes, in which 10% will be further used for validation.

[24]:
```
# Define features and target for the training
features= zscore_norm
target= df.target

# Dividing data using train_test_split()
x_train, x_test, y_train, y_test = train_test_split(features,target,test_size=0.
↪2,random_state=98)
x_train_new, x_val, y_train_new, y_val =␣
↪train_test_split(x_train,y_train,test_size=0.1,random_state=98)
```

0.3.2 2.2 [CM4] Training and Testing

[25]:
```
knn= KNeighborsClassifier()
knn.fit(x_train,y_train)
predictions=knn.predict(x_test)
original_acc=metrics.accuracy_score(y_test,predictions)
print(f"Accuracy of the model is {original_acc} using classifier's default␣
↪parameters.")
```

```
Accuracy of the model is 0.9069767441860465 using classifier's default
parameters.
```

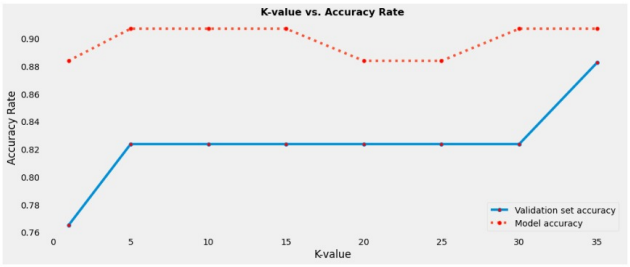
0.3.3 2.3 Parameter Tuning

[CM5] Accuracy vs. k Plot

[26]:
```
accuracy1=[]
r=[1,5,10,15,20,25,30,35]
for i in r:
    knn= KNeighborsClassifier(n_neighbors=i)
    knn.fit(x_train_new,y_train_new)
    accuracy1.append(metrics.accuracy_score(y_val,knn.predict(x_val)))
accuracy2=[]
for j in r:
    knn= KNeighborsClassifier(n_neighbors=j)
    knn.fit(x_train,y_train)
    accuracy2.append(metrics.accuracy_score(y_test,knn.predict(x_test)))

plt.figure(figsize=(15,6))
plt.plot(r,accuracy1,marker='o',markerfacecolor='r')
plt.plot(r,accuracy2,marker='o',markerfacecolor='r',linestyle='dotted')
plt.xlabel("K-value")
plt.ylabel("Accuracy Rate")
plt.title("K-value vs. Accuracy Rate", fontsize=16, fontweight='bold')
plt.legend(['Validation set accuracy','Model accuracy'])
plt.grid()
k_accurate_val=pd.
 ↪DataFrame(accuracy1,index=["k=1","k=5","k=10","k=15","k=20","k=25","k=30","k=35"],columns=[
 ↪rate"])
k_accurate_test=pd.
 ↪DataFrame(accuracy2,index=["k=1","k=5","k=10","k=15","k=20","k=25","k=30","k=35"],columns=[
 ↪rate"])

k_accurate=pd.concat([k_accurate_test,k_accurate_val],axis=1,keys=['␣
 ↪Model(k)','Validation set(k)'])
k_accurate
```

[26]:

	Model(k)	Validation set(k)
	accuracy rate	accuracy rate
k=1	0.883721	0.764706
k=5	0.906977	0.823529
k=10	0.906977	0.823529
k=15	0.906977	0.823529
k=20	0.883721	0.823529
k=25	0.883721	0.823529
k=30	0.906977	0.823529
k=35	0.906977	0.882353



Above shows the different outputs and difference between validation and testing set as well as their performances. After parameter tuning, it turned out that n_neighbors or k = 5, provides the best accuracy. Also, the given plot describes about the nature of validation set and test set. Given validation set, the maximum accuracy achieved is 0.8824 at k = 35 and 0.8235 at k = 5, whereas the test set provides maximum accuracy of 0.9070 at k = 5. So, accuracy is effected depending upon the sample of data provided. Also, parameter tuning helps in determining the accuracy rate, with change in k value.

In addition, in k-fold cross validation, the training data is split into k splits and performing iterations on each split. Thus, it provides models with the ability to train on multiple train test split, rather than single train test split. So, **k-fold cross validation** is better than simple train validate test split, it improves the performance of model better comparing to simple split methods.

[CM6] Evaluation of KNN model:

AUC and f-score:

[27]:
```
ra_score1=roc_auc_score(y_test,knn.predict(x_test))
fpr1, tpr1, thresholds1= roc_curve(y_test,knn.predict_proba(x_test)[:,1])
# ROC Plot
plt.figure()
plt.plot(fpr1, tpr1, label=" AUC : %0.2f"% ra_score1)
plt.plot((0,1),'r--')
plt.xlabel("False Positive")
plt.ylabel("True Positive")
plt.title('ROC Score',fontweight='bold',fontsize=16)
plt.show()
# AUC
auc= metrics.auc(fpr1,tpr1)
# f-score
f1score= metrics.f1_score(y_test,predictions,average='macro')
# Output
print(f'The AUC for the model is {auc}, and f-score is {f1score}.\n')
```

Variations of k Parameter:

[27]:
```
scores_with_iterations=pd.
↪DataFrame(scores_with_iterations,index=["k=1","k=5","k=10","k=15","k=20","k=25","k=30","k=3
↪iteration",
                                "2 iteration","3 iteration","4 iteration","5␣
↪iteration"])
scores_with_iterations
```

[27]:

	1 iteration	2 iteration	3 iteration	4 iteration	5 iteration
k=1	0.857143	0.952381	0.952381	0.904762	0.952381
k=5	0.952381	0.952381	0.952381	0.952381	0.952381
k=10	0.952381	0.904762	0.904762	0.952381	0.952381
k=15	0.952381	0.857143	0.809524	0.952381	0.952381
k=20	0.952381	0.857143	0.809524	0.904762	0.857143
k=25	0.952381	0.857143	0.809524	0.904762	0.857143
k=30	1.000000	0.857143	0.809524	0.904762	0.857143
k=35	1.000000	0.857143	0.809524	0.952381	0.857143

Accuracy with best k parameter

[28]:
```
knn= KNeighborsClassifier(n_neighbors=5)
knn.fit(x_train,y_train)
predictions= knn.predict(x_test)
k_accuracy=metrics.accuracy_score(y_test,predictions)
k_accuracy
```

[28]: 1.0

Discussion

- K-fold Validation Scores: 1.0, 1.0, 0.9523809523809523, 0.9047619047619048, 1.0
- Scores Variance: 0.0018140589569161

K-fold cross validation, in this data splits into k number of folds and iteration is performed on each one of it. It is like using all the data for training and testing. It allows to train the model on multiple train_test_splits. Therefore, it is more suitable for smaller datasets like this Iris dataset.

On the other hand, test_validate_test allows to train the model on a single train_test_split, depending upon the given sample ratio of dataset. So it is preferred on a larger dataset.

Although, k-fold cross validation method improves the performance over train_validate_test but again, it depends upon the nature of data to be applied upon.

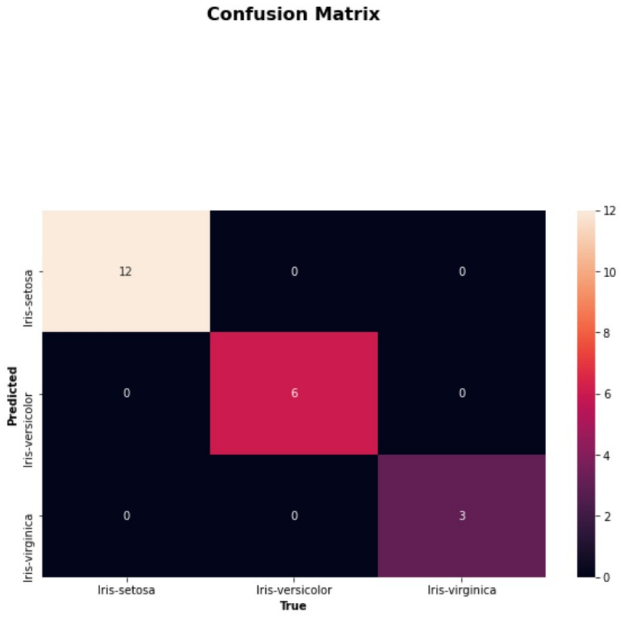
In given dataset also, k-fold validation provided more accurate results with respect to actual test set. But, in train_validate_test, the accuracy of validation set and actual model differs.

[CM6] Evaluation of KNN model:

Confusion matrix is used for determining performance of classification model

[29]:
```
cm= confusion_matrix(y_test,predictions)
cm=pd.DataFrame(cm, index= ['Iris-setosa','Iris-versicolor','Iris-virginica'],
                columns=['Iris-setosa','Iris-versicolor','Iris-virginica'])
cm

plt.figure(figsize=(10,6))
sns.heatmap(cm,annot=True)
plt.xlabel('True',fontweight='bold')
plt.ylabel('Predicted',fontweight='bold')
plt.title('Confusion Matrix', fontsize=16,fontweight='bold', y= 1.5)
```

[29]: Text(0.5, 1.5, 'Confusion Matrix')



Classification report is used to determine the precision, recall and f1-score

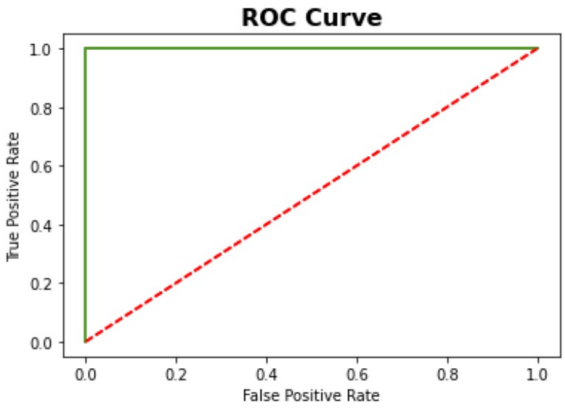
[30]:
```
cr=classification_report(y_test,predictions,output_dict=True)
cr= pd.DataFrame(cr)
cr
```

[30]:

	0	1	2	accuracy	macro avg	weighted avg
precision	1.0	1.0	1.0	1.0	1.0	1.0
recall	1.0	1.0	1.0	1.0	1.0	1.0
f1-score	1.0	1.0	1.0	1.0	1.0	1.0
support	12.0	6.0	3.0	1.0	21.0	21.0

AUC and f-score:

[31]:
```
fpr={}
tpr={}
roc_auc={}
thresh={}
for i in range(3):
    fpr[i], tpr[i], thresh[i] = roc_curve(y_test,knn.predict_proba(x_test)[:
 ↪,i],pos_label=i)
    roc_auc[i]=auc(fpr[i],tpr[i])
# ROC Plot
plt.figure()
for i in range(3):
    plt.plot(fpr[i], tpr[i], label=" AUC : %0.2f"% roc_auc[i])
    plt.plot((0,1),'r--')
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title('ROC Curve',fontweight='bold',fontsize=16)
plt.show()
# AUC
auc=roc_auc_score(y_test,knn.
 ↪predict_proba(x_test),multi_class='ovr',average='macro')
# f-score
f1score= metrics.f1_score(y_test,predictions,average='macro')

# Output
print(f'The AUC for the model is {auc}, and f-score is {f1score}.')
```




```
The AUC for the model is 1.0, and f-score is 1.0.
```

Discussion

- Accuracy: correctly predicted observations to total observations.
- F-score: it is the harmonic mean of precision and recall of a model.
- Precision: the ratio of true positive observation to total positive observations.
- Recall: the ratio of true positive observation to all the observations.

F-score, precision, and recall improves with improvement in accuracy. As for AUC, it is the probability of the fit model scoring randomly drawn positives higher than the randomly drawn negatives. So, as the accuracy improves it also improves. In addition, different results of roc curve before improvement and after improvement, also shows the impact on accuracy.

Changing k leads to change in accuracy result, whether it increases or decreases, that varies from dataset to dataset. As, in KNN classification technique, k represents the number of nearest neighbor's among which model has to predict the class of input provided. In our case, the accuracy with default parameters (k=5) is already 1 i.e., 100% accurate model. Also, it can be seen in validation set graph that maximum accuracy is achieved at k =5.

The increase in doesn't always affect the accuracy, some times it stays same. Example, in our dataset, accuracies at k= 20 and k= 25 are the same, whereas, at other k values it may decrease or increase. It happens because when k value reach a certain point where data is smoothed to maximum extent, it will be the same value. It also happens, once 1 accuracy is achieved.

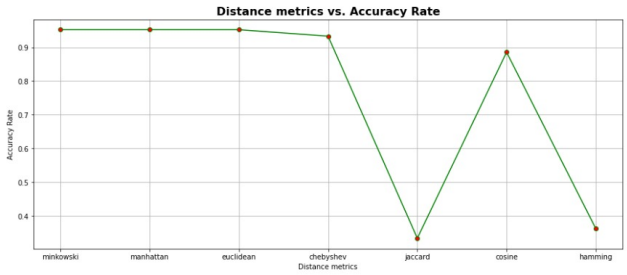
When k=1, training set is at center of area of different classes, but increasing k will smooth the

area predicting each class. Therefore, it results into area containing less number, in simple shapes and large sizes.

0.3.4 Improved Model:

2.5 Weighted KNN Effect of changing weight to 'distance' (default is 'uniform') and different distance metrics (default is 'minkowski').

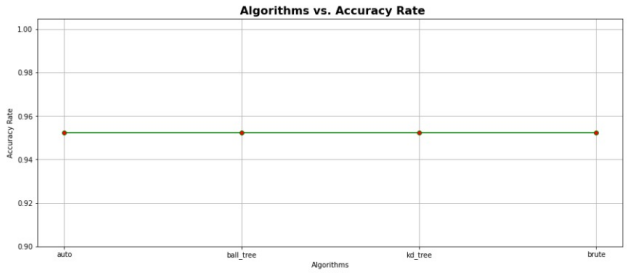
[32]:
```
w_accuracy=[]
met=␣
↪['minkowski','manhattan','euclidean','chebyshev','jaccard','cosine','hamming']
for i in met:
    knn= KNeighborsClassifier(n_neighbors=5,weights='distance',metric=i)
    score= cross_val_score(knn,features,target,cv=5)
    w_accuracy.append(score.mean())

plt.figure(figsize=(15,6))
plt.plot(met,w_accuracy,marker='o',markerfacecolor='r',color='g')
plt.xlabel("Distance metrics")
plt.ylabel("Accuracy Rate")
plt.title("Distance metrics vs. Accuracy Rate", fontsize=16, fontweight='bold')
plt.grid()
w_accuracy = pd.DataFrame(w_accuracy,index=met,columns=['accuracy rate'])
```



2.6 Different KNN Algorithms

[33]:
```
alg_accuracy=[]
alg= ['auto','ball_tree','kd_tree','brute']
for i in alg:
    knn=␣
↪KNeighborsClassifier(n_neighbors=5,weights='distance',metric='euclidean',algorithm=i)
```

```
    score= cross_val_score(knn,features,target,cv=5)
    alg_accuracy.append(score.mean())

plt.figure(figsize=(15,6))
plt.plot(alg,alg_accuracy,marker='o',markerfacecolor='r',color='g')
plt.xlabel("Algorithms")
plt.ylabel("Accuracy Rate")
plt.title(" Algorithms vs. Accuracy Rate", fontsize=16, fontweight='bold')
plt.grid()
```

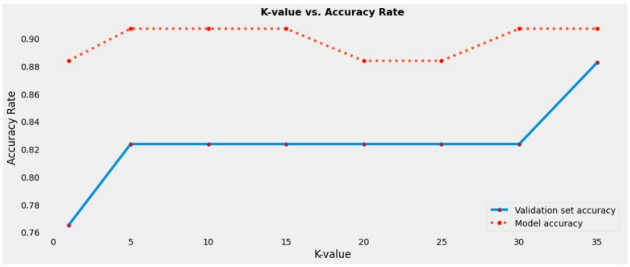


2.7 [CM7] Report on accuracy, AUC and f-score

[34]:
```
report2=pd.DataFrame({'Evaluation Report':['F-Score','AUC','Accuracy'], 'Value':
↪[f1score,auc,k_accuracy]})
report2
```

[34]:

	Evaluation Report	Value
0	F-Score	1.0
1	AUC	1.0
2	Accuracy	1.0



Above shows the different outputs and difference between validation and testing set as well as their performances. After parameter tuning, it turned out that n_neighbors or k = 5, provides the best accuracy. Also, the given plot describes about the nature of validation set and test set. Given validation set, the maximum accuracy achieved is 0.8824 at k = 35 and 0.8235 at k = 5, whereas the test set provides maximum accuracy of 0.9070 at k = 5. So, accuracy is effected depending upon the sample of data provided. Also, parameter tuning helps in determining the accuracy rate, with change in k value.

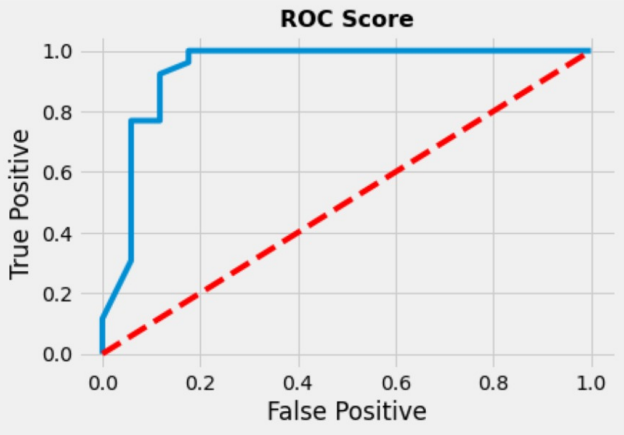
In addition, in k-fold cross validation, the training data is split into k splits and performing iterations on each split. Thus, it provides models with the ability to train on multiple train test split, rather than single train test split. So, **k-fold cross validation** is better than simple train validate test split, it improves the performance of model better comparing to simple split methods.

[CM6] Evaluation of KNN model:

AUC and f-score:

[27]:
```
ra_score1=roc_auc_score(y_test,knn.predict(x_test))
fpr1, tpr1, thresholds1= roc_curve(y_test,knn.predict_proba(x_test)[:,1])
# ROC Plot
plt.figure()
plt.plot(fpr1, tpr1, label=" AUC : %0.2f"% ra_score1)
plt.plot((0,1),'r--')
plt.xlabel("False Positive")
plt.ylabel("True Positive")
plt.title('ROC Score',fontweight='bold',fontsize=16)
plt.show()
# AUC
auc= metrics.auc(fpr1,tpr1)
# f-score
f1score= metrics.f1_score(y_test,predictions,average='macro')
# Output
print(f'The AUC for the model is {auc}, and f-score is {f1score}.\n')
```

```
# f-score and Accuracy:
cr=classification_report(y_test,predictions,output_dict=True)
cr=pd.DataFrame(cr)
cr
```




```
The AUC for the model is 0.9366515837104072, and f-score is 0.9027149321266968.
```

[27]:

	0	1	accuracy	macro avg	weighted avg
precision	0.882353	0.923077	0.906977	0.902715	0.906977
recall	0.882353	0.923077	0.906977	0.902715	0.906977
f1-score	0.882353	0.923077	0.906977	0.902715	0.906977
support	17.000000	26.000000	0.906977	43.000000	43.000000

Model Evaluation Report before Improvements:

[28]:
```
eval_report=pd.DataFrame({'Evaluation Report':['F1 Score','AUC','Accuracy'],␣
↪'Value':[f1score,auc,original_acc]})
eval_report
```

[28]:

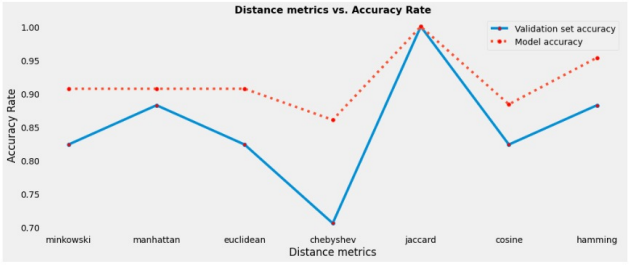
	Evaluation Report	Value
0	F1 Score	0.902715
1	AUC	0.936652

```
2          Accuracy  0.906977
```

0.3.4 Improved Model:

2.5 Weighted KNN Effect of changing weight to 'distance' (default is 'uniform') and different distance metrics (default is 'minkowski').

[29]:
```
w_accuracy1=[]
met=␣
↪['minkowski','manhattan','euclidean','chebyshev','jaccard','cosine','hamming']
for i in met:
    knn= KNeighborsClassifier(n_neighbors=5,weights='distance',metric=i)
    knn.fit(x_train_new,y_train_new)
    w_accuracy1.append(metrics.accuracy_score(y_val,knn.predict(x_val)))
w_accuracy2=[]
for j in met:
    knn= KNeighborsClassifier(n_neighbors=5,weights='distance',metric=j)
    knn.fit(x_train,y_train)
    w_accuracy2.append(metrics.accuracy_score(y_test,knn.predict(x_test)))

plt.figure(figsize=(15,6))
plt.plot(met,w_accuracy1,marker='o',markerfacecolor='r')
plt.plot(met,w_accuracy2,marker='o',markerfacecolor='r',linestyle='dotted')
plt.xlabel("Distance metrics")
plt.ylabel("Accuracy Rate")
plt.title("Distance metrics vs. Accuracy Rate", fontsize=16, fontweight='bold')
plt.legend(['Validation set accuracy','Model accuracy'])
plt.grid()
w_accurate_val=pd.
↪DataFrame(w_accuracy1,index=['minkowski','manhattan','euclidean','chebyshev','jaccard','cos
↪rate"])
w_accurate_test=pd.
↪DataFrame(w_accuracy2,index=['minkowski','manhattan','euclidean','chebyshev','jaccard','cos
↪rate"])
```



[30]:
```
w_accurate=pd.
 ↪concat([w_accurate_test,w_accurate_val],axis=1,keys=['Model(Weighted)','Validation␣
 ↪set(weighted)'])
w_accurate
```

[30]:

	Model(Weighted) accuracy rate	Validation set(weighted) accuracy rate
minkowski	0.906977	0.823529
manhattan	0.906977	0.882353
euclidean	0.906977	0.823529
chebyshev	0.860465	0.705882
jaccard	1.000000	1.000000
cosine	0.883721	0.823529
hamming	0.953488	0.882353

[31]:
```
final_knn=␣
 ↪KNeighborsClassifier(n_neighbors=5,weights='distance',metric='jaccard')
final_knn.fit(x_train,y_train)
final_predictions=final_knn.predict(x_test)
final_accuracy=metrics.accuracy_score(y_test,final_predictions)
print(f'Final accuracy is {final_accuracy} after using the jaccard metric.')
```

```
Final accuracy is 1.0 after using the jaccard metric.
```

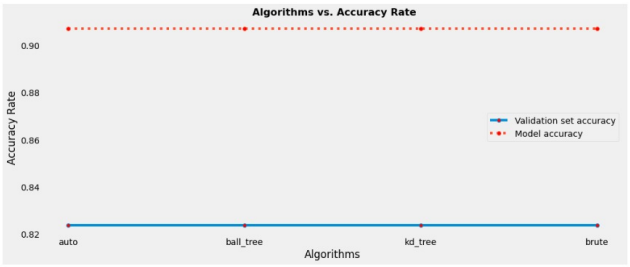
2.6 Different KNN Algorithms

[32]:
```
alg_accuracy1=[]
alg= ['auto','ball_tree','kd_tree','brute']
for i in alg:
    knn= KNeighborsClassifier(n_neighbors=5,weights='distance',algorithm=i)
    knn.fit(x_train_new,y_train_new)
    alg_accuracy1.append(metrics.accuracy_score(y_val,knn.predict(x_val)))
alg_accuracy2=[]
for j in alg:
    knn= KNeighborsClassifier(n_neighbors=5,weights='distance',algorithm=j)
    knn.fit(x_train,y_train)
    alg_accuracy2.append(metrics.accuracy_score(y_test,knn.predict(x_test)))

plt.figure(figsize=(15,6))
plt.plot(alg,alg_accuracy1,marker='o',markerfacecolor='r')
plt.plot(alg,alg_accuracy2,marker='o',markerfacecolor='r',linestyle='dotted')
plt.xlabel("Algorithms")
plt.ylabel("Accuracy Rate")
plt.title(" Algorithms vs. Accuracy Rate", fontsize=16, fontweight='bold')
plt.legend(['Validation set accuracy','Model accuracy'])
plt.grid()
```

```
alg_accurate_val=pd.
 ↪DataFrame(alg_accuracy1,index=['auto','ball_tree','kd_tree','brute'],columns=["accuracy␣
 ↪rate"])
alg_accurate_test=pd.
 ↪DataFrame(alg_accuracy2,index=['auto','ball_tree','kd_tree','brute'],columns=["accuracy␣
 ↪rate"])
alg_accurate=pd.concat([alg_accurate_test,alg_accurate_val],axis=1,keys=['␣
 ↪Model(algorithms)','Validation set(algorithms)'])
alg_accurate
```

[32]:

	Model(algorithms)	Validation set(algorithms)
	accuracy rate	accuracy rate
auto	0.906977	0.823529
ball_tree	0.906977	0.823529
kd_tree	0.906977	0.823529
brute	0.906977	0.823529



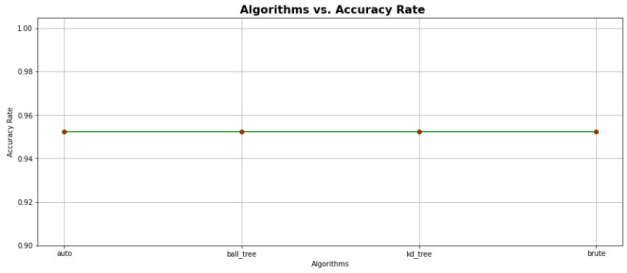
Changing algorithms doesn't effect the accuracy at all, whereas, changing weights and distance metrics did effect the accuracy, and provided the best result.

Like shown above, with **k = 5** and **distance metric = 'jaccard'**, achieved 100% accuracy.

2.7 [CM7] Report on accuracy, AUC and f-score

[33]:
```
# Final Accuracy
final_accuracy=metrics.accuracy_score(y_test,final_predictions)
# ROC Plot
ra_score2=roc_auc_score(y_test,final_predictions)
fpr2, tpr2, thresholds2= roc_curve(y_test,final_knn.predict_proba(x_test)[:,1])
plt.figure()
plt.plot(fpr2, tpr2, label=" AUC : %0.2f"% ra_score2)
```

```
    score= cross_val_score(knn,features,target,cv=5)
    alg_accuracy.append(score.mean())

plt.figure(figsize=(15,6))
plt.plot(alg,alg_accuracy,marker='o',markerfacecolor='r',color='g')
plt.xlabel("Algorithms")
plt.ylabel("Accuracy Rate")
plt.title(" Algorithms vs. Accuracy Rate", fontsize=16, fontweight='bold')
plt.grid()
```



2.7 [CM7] Report on accuracy, AUC and f-score

[34]:
```
report2=pd.DataFrame({'Evaluation Report':['F-Score','AUC','Accuracy'], 'Value':
↪[f1score,auc,k_accuracy]})
report2
```

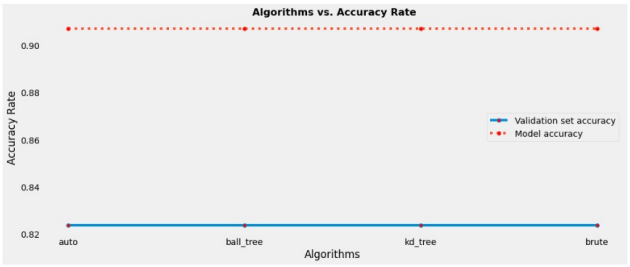
[34]:

	Evaluation Report	Value
0	F-Score	1.0
1	AUC	1.0
2	Accuracy	1.0

```
alg_accurate_val=pd.
 ↪DataFrame(alg_accuracy1,index=['auto','ball_tree','kd_tree','brute'],columns=["accuracy␣
 ↪rate"])
alg_accurate_test=pd.
 ↪DataFrame(alg_accuracy2,index=['auto','ball_tree','kd_tree','brute'],columns=["accuracy␣
 ↪rate"])
alg_accurate=pd.concat([alg_accurate_test,alg_accurate_val],axis=1,keys=['␣
 ↪Model(algorithms)','Validation set(algorithms)'])
alg_accurate
```

[32]:

	Model(algorithms)	Validation set(algorithms)
	accuracy rate	accuracy rate
auto	0.906977	0.823529
ball_tree	0.906977	0.823529
kd_tree	0.906977	0.823529
brute	0.906977	0.823529



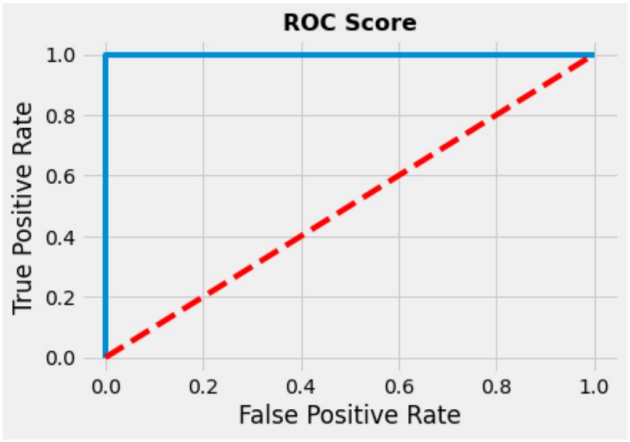
Changing algorithms doesn't effect the accuracy at all, whereas, changing weights and distance metrics did effect the accuracy, and provided the best result.

Like shown above, with **k = 5** and **distance metric = 'jaccard'**, achieved 100% accuracy.

2.7 [CM7] Report on accuracy, AUC and f-score

[33]:
```
# Final Accuracy
final_accuracy=metrics.accuracy_score(y_test,final_predictions)
# ROC Plot
ra_score2=roc_auc_score(y_test,final_predictions)
fpr2, tpr2, thresholds2= roc_curve(y_test,final_knn.predict_proba(x_test)[:,1])
plt.figure()
plt.plot(fpr2, tpr2, label=" AUC : %0.2f"% ra_score2)
```

```
plt.plot((0,1),'r--')
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title('ROC Score',fontweight='bold',fontsize=16)
plt.show()
# Final AUC
final_auc= metrics.auc(fpr2,tpr2)
# Final f-score and Accuracy
final_f1score= metrics.f1_score(y_test,final_predictions,average='macro')
# Output
print(f'\nWith updated k and distance metrics, the final accuracy is␣
↪{final_accuracy}. ROC score is {ra_score2}. AUC is {final_auc}, and f-score␣
↪is {final_f1score}.\n')

final_cr=classification_report(y_test,final_predictions,output_dict=True)
final_cr= pd.DataFrame(final_cr)
final_cr
```




```
With updated k and distance metrics, the final accuracy is 1.0. ROC score is
1.0. AUC is 1.0, and f-score is 1.0.
```

[33]:

	0	1	accuracy	macro avg	weighted avg
precision	1.0	1.0	1.0	1.0	1.0
recall	1.0	1.0	1.0	1.0	1.0
f1-score	1.0	1.0	1.0	1.0	1.0
support	17.0	26.0	1.0	43.0	43.0

Final Model Evaluation Report:

[34]:
```
final_eval=pd.DataFrame({'Evaluation Report':['F1 Score','AUC','Accuracy'],␣
↪'Value':[final_f1score,final_auc,final_accuracy]})
final_eval
```

[34]:

	Evaluation Report	Value
0	F1 Score	1.0
1	AUC	1.0
2	Accuracy	1.0

The weighted parameter tuning helps in achieving the 100% of accuracy with distance metric 'jaccard', with both validation and test set has shown maximum accuracy. However, algorithm change shows no impact on accuracy, both in validation and test set.

In conslusion (shown in the table above), the improved f1score, auc and accuracy is 1.