Assignment 1

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1 CM1

1.1 Iris data

[1]:
```
# import libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import cross_val_score
from sklearn import preprocessing
```

[2]:
```
# load iris dataset
df = pd.read_csv('iris_dataset_missing.csv')
df.head()
```

[2]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.045070	2.508203	3.018024	1.164924	Iris-versicolor
1	6.325517	2.115481	4.542052	1.413651	Iris-versicolor
2	5.257497	3.814303	1.470660	0.395348	Iris-setosa
3	6.675168	3.201700	5.785461	2.362764	Iris-virginica
4	5.595237	2.678166	4.077750	1.369266	Iris-versicolor

[3]:
```
df.describe
```

[3]:
```
<bound method NDFrame.describe of      sepal_length  sepal_width  petal_length
petal_width          species
0         5.045070     2.508203     3.018024     1.164924  Iris-versicolor
1         6.325517     2.115481     4.542052     1.413651  Iris-versicolor
2         5.257497     3.814303     1.470660     0.395348      Iris-setosa
3         6.675168     3.201700     5.785461     2.362764   Iris-virginica
4         5.595237     2.678166     4.077750     1.369266  Iris-versicolor
..             …            …            …           …              …
100       4.874848     3.217348     1.592887     0.123588      Iris-setosa
101       5.564197     2.771731     3.483588     1.074754  Iris-versicolor
102       5.548047     4.249211     1.453466     0.214527      Iris-setosa
```

```
103       5.510482     2.652867      4.276817     1.298032  Iris-versicolor
104       4.538713     3.056142      1.545136     0.241424      Iris-setosa

[105 rows x 5 columns]>
```

1.1.1 Detecting missing values in each columns & data cleaning

[4]:
```
df.isnull().sum()
```

[4]:
```
sepal_length    0
sepal_width     4
petal_length    8
petal_width     0
species         0
dtype: int64
```

[5]:
```
df.shape[0] - df.dropna().shape[0]
```

[5]:
```
12
```

1.1.2 Filling missing values and justificaiton

There are 12 rows of data contains missing value. Because the missing data is less than 15% of the total data count and it's continuous data. Therefore, it is safe to impute missing values using mean.

[6]:
```
df['sepal_width'].fillna((df['sepal_width'].mean()), inplace=True)
df['petal_length'].fillna((df['petal_length'].mean()), inplace=True)
```

[7]:
```
df.isnull().sum()
```

[7]:
```
sepal_length    0
sepal_width     0
petal_length    0
petal_width     0
species         0
dtype: int64
```

1.1.3 Z-score Normalization

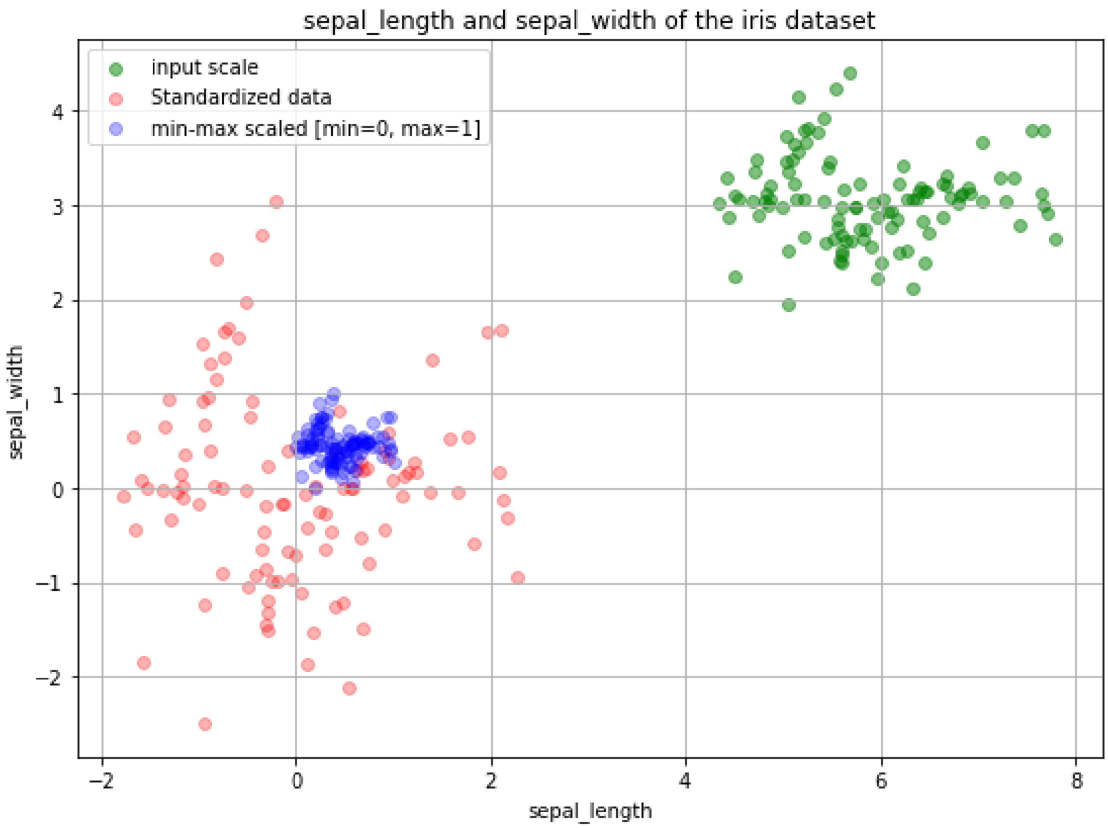
[8]:
```
from sklearn.preprocessing import StandardScaler
df_z = df.copy()
std_scaler = StandardScaler()
df_z.iloc[:,[0,1,2,3]] = std_scaler.fit_transform(df_z.iloc[:,[0,1,2,3]])
```

1.1.4 Min-Max Normalization

[9]:
```
from sklearn.preprocessing import MinMaxScaler
df_minmax= df.copy()
minmax_scaler = MinMaxScaler()
df_minmax.iloc[:,[0,1,2,3]] = minmax_scaler.fit_transform(df_minmax.iloc[:
↪,[0,1,2,3]])
```

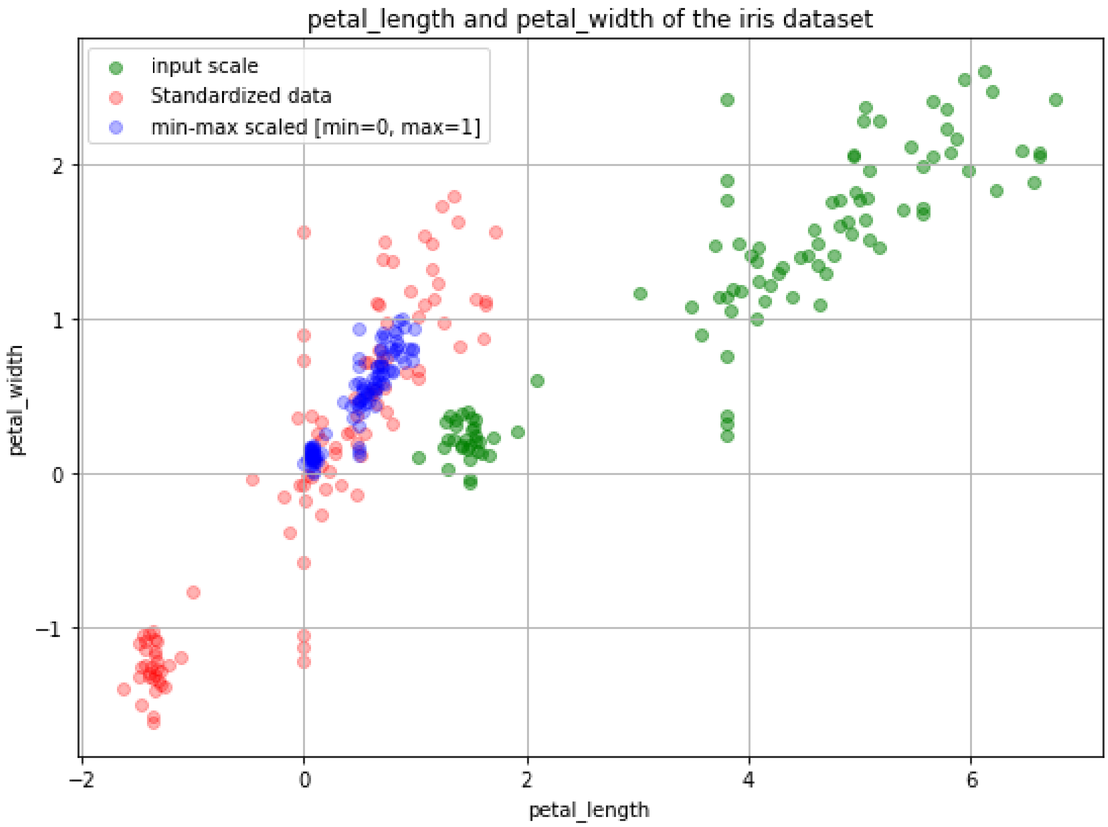
1.1.5 Compare data normailzation by ploting

[10]:
```
# matplotlib
def plot():
    plt.figure(figsize=(8,6))

    plt.scatter(df['sepal_length'], df['sepal_width'],
            color='green', label='input scale', alpha=0.5)

    plt.scatter(df_z['sepal_length'], df_z['sepal_width'], color='red',
            label='Standardized data', alpha=0.3)

    plt.scatter(df_minmax['sepal_length'], df_minmax['sepal_width'],
            color='blue', label='min-max scaled [min=0, max=1]', alpha=0.3)

    plt.title('sepal_length and sepal_width of the iris dataset')
    plt.xlabel('sepal_length')
    plt.ylabel('sepal_width')
    plt.legend(loc='upper left')
    plt.grid()

    plt.tight_layout()

plot()
plt.show()
```




```
[11]: # matplotlib
def plot():
    plt.figure(figsize=(8,6))

    plt.scatter(df['petal_length'], df['petal_width'],
            color='green', label='input scale', alpha=0.5)

    plt.scatter(df_z['petal_length'], df_z['petal_width'], color='red',
            label='Standardized data', alpha=0.3)

    plt.scatter(df_minmax['petal_length'], df_minmax['petal_width'],
            color='blue', label='min-max scaled [min=0, max=1]', alpha=0.3)

    plt.title('petal_length and petal_width of the iris dataset')
    plt.xlabel('petal_length')
    plt.ylabel('petal_width')
    plt.legend(loc='upper left')
    plt.grid()

    plt.tight_layout()
```

```
plot()
plt.show()
```



1.2 Heart disease data

[12]:
```
df_heart = pd.read_csv('heart_disease_missing.csv')
df_heart.head()
```

[12]:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	\
0	76	0	2	140.102822	197.105970	0	2.0	115.952071	0	
1	43	0	0	132.079599	341.049462	1	0.0	135.970028	1	
2	47	1	2	107.899290	242.822816	0	1.0	152.210039	0	
3	51	1	2	99.934001	NaN	0	1.0	143.049207	1	
4	57	1	0	110.103508	334.952353	0	1.0	143.099327	1	

	oldpeak	slope	ca	thal	target
0	1.284822	1.0	0	2.175904	1
1	3.110483	1.0	0	3.082071	0
2	-0.023723	2.0	0	2.020827	0
3	1.195082	1.0	0	2.100312	1

```
4  3.082052    1.0   1  2.831509       0
```

1.2.1 Detecting missing values in each columns & data cleaning

[13]:
```
df_heart.isnull().sum()
```

[13]:
```
age          0
sex          0
cp           0
trestbps     7
chol        10
fbs          0
restecg      5
thalach      4
exang        0
oldpeak     12
slope        2
ca           0
thal         1
target       0
dtype: int64
```

1.2.2 Dropping observations with missing categorial data

2 categorial data (restecg, slope) conatin missing values. Because this data set is relatively large, it's safe to ignore these observations with missing values.

[14]:
```
df_heart = df_heart.dropna(subset=['restecg', 'slope'])
```

[15]:
```
df_heart.isnull().sum()
```

[15]:
```
age          0
sex          0
cp           0
trestbps     7
chol        10
fbs          0
restecg      0
thalach      4
exang        0
oldpeak     12
slope        0
ca           0
thal         1
target       0
dtype: int64
```

1.2.3 Filling observations with missing numerical data

Now there are 5 numeric data contain missing values. Because its less than 15% of the total observation, it is safe to impute missing values using mean.

[16]:
```
df_heart['chol'].fillna((df_heart['chol'].mean()), inplace=True)
```

[17]:
```
df_heart['trestbps'].fillna((df_heart['trestbps'].mean()), inplace=True)
```

[18]:
```
df_heart['thalach'].fillna((df_heart['thalach'].mean()), inplace=True)
```

[19]:
```
df_heart['oldpeak'].fillna((df_heart['oldpeak'].mean()), inplace=True)
```

[20]:
```
df_heart['thal'].fillna((df_heart['thal'].mean()), inplace=True)
```

[21]:
```
df_heart.isnull().sum()
```

[21]:
```
age         0
sex         0
cp          0
trestbps    0
chol        0
fbs         0
restecg     0
thalach     0
exang       0
oldpeak     0
slope       0
ca          0
thal        0
target      0
dtype: int64
```

1.2.4 Min-Max Normalization

Converting numerical features into standard ranges of values. Here I chose to normalize 'age', 'trestbps', 'chol', 'thalach','oldpeak', 'thal'

[22]:
```
df_heart_minmax = df_heart.copy()
minmax_scaler = MinMaxScaler()
df_heart_minmax.iloc[:,[0,3,4,7,9,10,12]] = minmax_scaler.
 ↪fit_transform(df_heart_minmax.iloc[:,[0,3,4,7,9,10,12]])
df_heart_minmax.head()
```

[22]:
```
        age  sex  cp  trestbps      chol  fbs  restecg   thalach  exang  \
0  0.979167    0   2  0.470641  0.252879    0      2.0  0.244681      0
1  0.291667    0   0  0.388835  0.765412    1      0.0  0.420115      1
2  0.375000    1   2  0.142289  0.415661    0      1.0  0.562440      0
3  0.458333    1   2  0.061073  0.422802    0      1.0  0.482156      1
```

```
4  0.583333    1    0  0.164763  0.743703    0       1.0  0.482595      1

    oldpeak  slope  ca      thal  target
0  0.230717    0.5   0  0.544604       1
1  0.518970    0.5   0  0.919222       0
2  0.024112    1.0   0  0.480494       0
3  0.216548    0.5   0  0.513354       1
4  0.514481    0.5   1  0.815637       0
```

1.2.5 Zscore Normalization

[23]:
```python
df_heart_z = df_heart.copy()
std_scaler = StandardScaler()
df_heart_z.iloc[:,[0,3,4,7,9,10,12]]= std_scaler.fit_transform(df_heart_z.iloc[:
 ↪,[0,3,4,7,9,10,12]])
df_heart_z.head()
```

[23]:
```
        age  sex  cp  trestbps      chol  fbs  restecg   thalach  exang  \
0  2.385826    0   2  0.457921 -1.049309    0      2.0 -1.556586      0
1 -1.238722    0   0  0.007041  2.115676    1      0.0 -0.625361      1
2 -0.799383    1   2 -1.351818 -0.044101    0      1.0  0.130116      0
3 -0.360044    1   2 -1.799443  0.000000    0      1.0 -0.296041      1
4  0.298965    1   0 -1.227948  1.981615    0      1.0 -0.293709      1

    oldpeak     slope  ca      thal  target
0  0.139210 -0.657656   0 -0.285910       1
1  1.650279 -0.657656   0  1.225207       0
2 -0.943851  0.947338   0 -0.544517       0
3  0.064934 -0.657656   0 -0.411967       1
4  1.626747 -0.657656   1  0.807371       0
```

1.3 Normalization Observation

Without normalization, data shows different scales and ranges. After using Min_max normalization, all features will have the same scale(between 0 and 1). From the iris data plot, min_max scale may cause data clustering therefore it may not handle outliers well. On the other hand z_score normalization resonably scales data to same scale with certain dispersion.

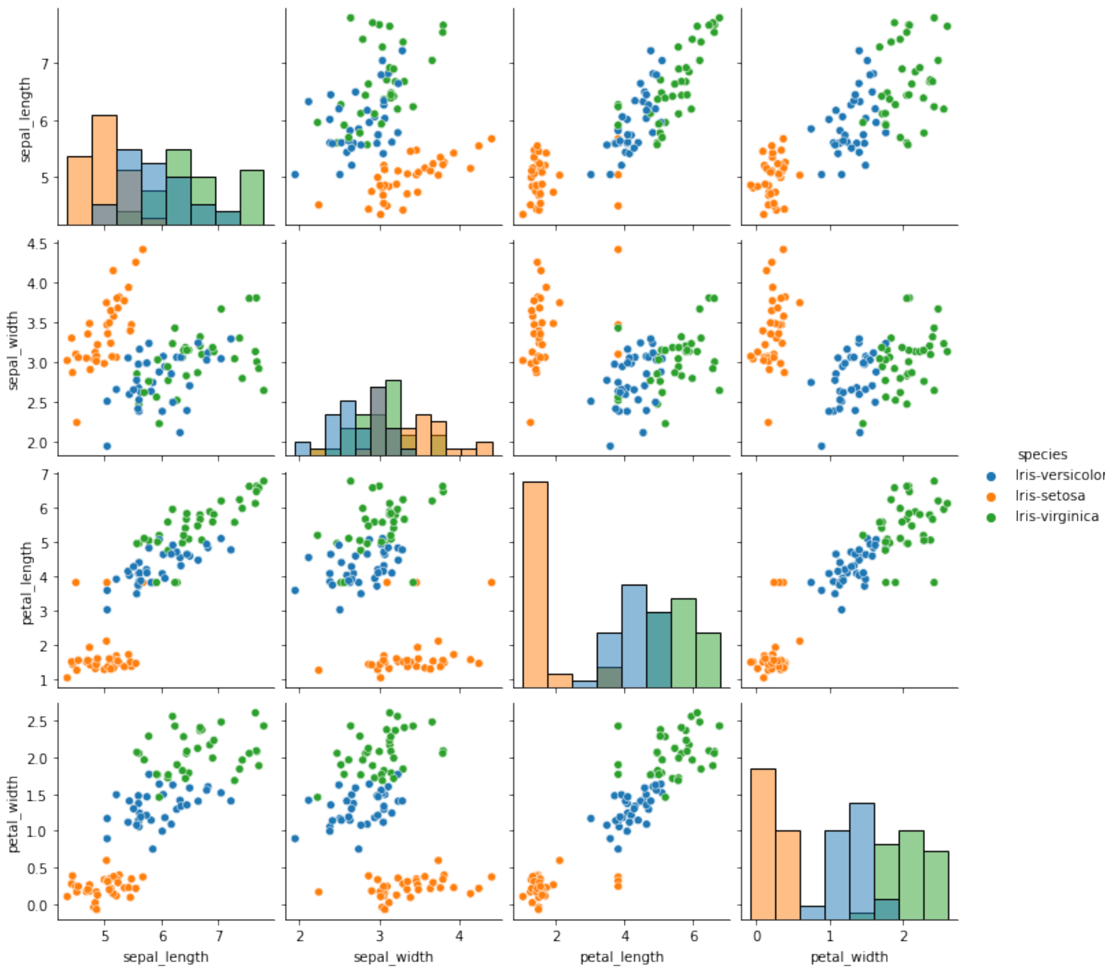
Additionaly, data normalization does not change to the shapes of pairplots from [CM2] .

2 CM2

2.1 Iris data

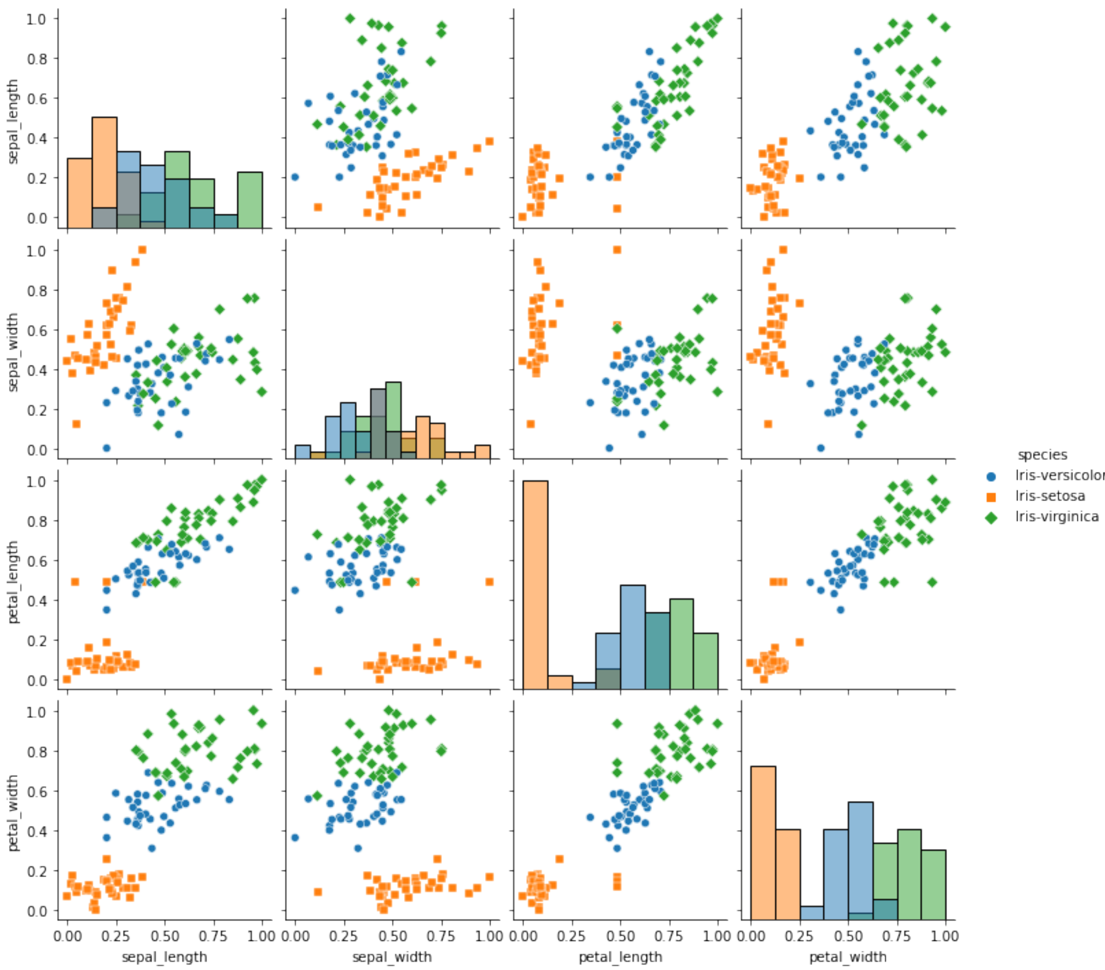
2.1.1 Pair plot using raw data

[24]:
```
g=sns.pairplot(df, hue='species',diag_kind='hist')
```



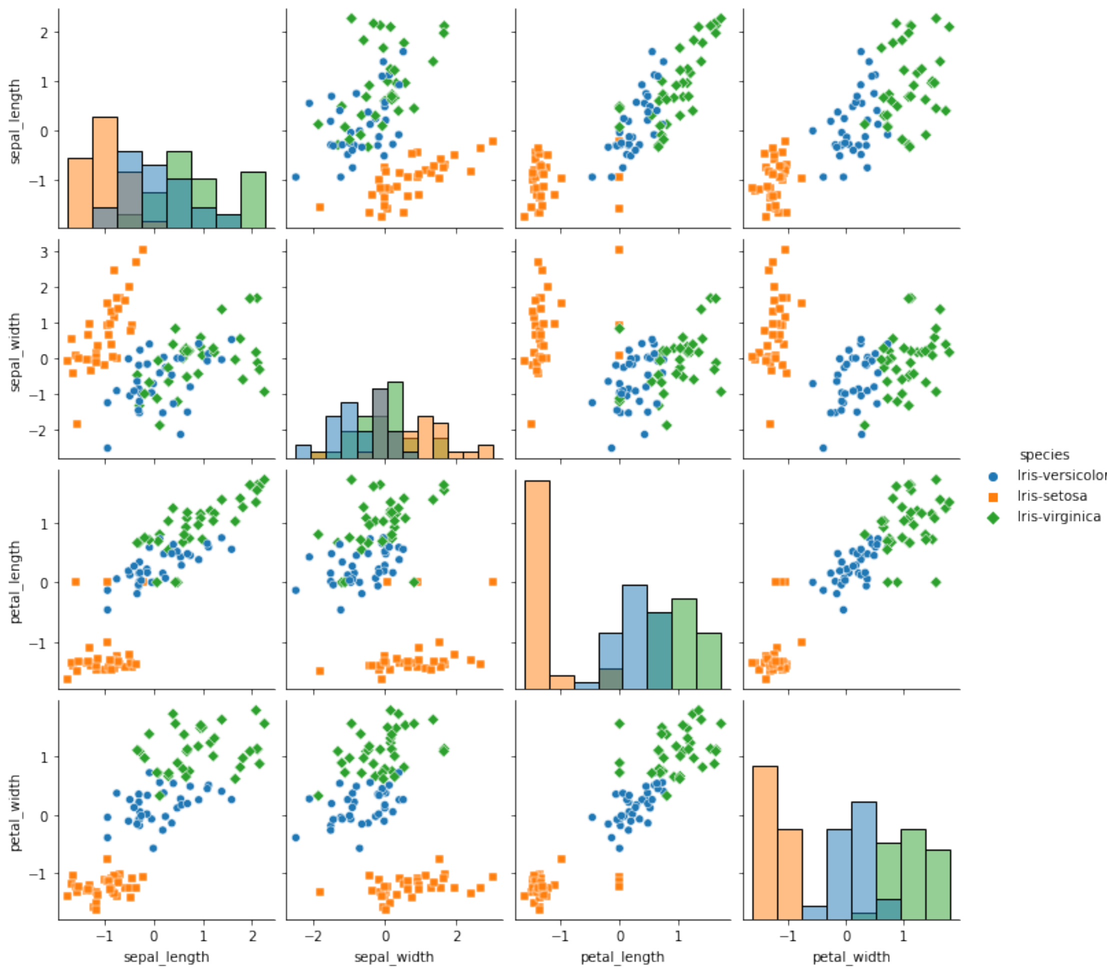
2.1.2 Pair plot using min-max normalized data

[25]:
```
g=sns.pairplot(df_minmax, hue='species',diag_kind='hist',markers=['o','s','D'])
```



2.1.3 Pair plot using z-score normalized data

[26]:
```
g=sns.pairplot(df_z, hue='species',diag_kind='hist',markers=['o','s','D'])
```

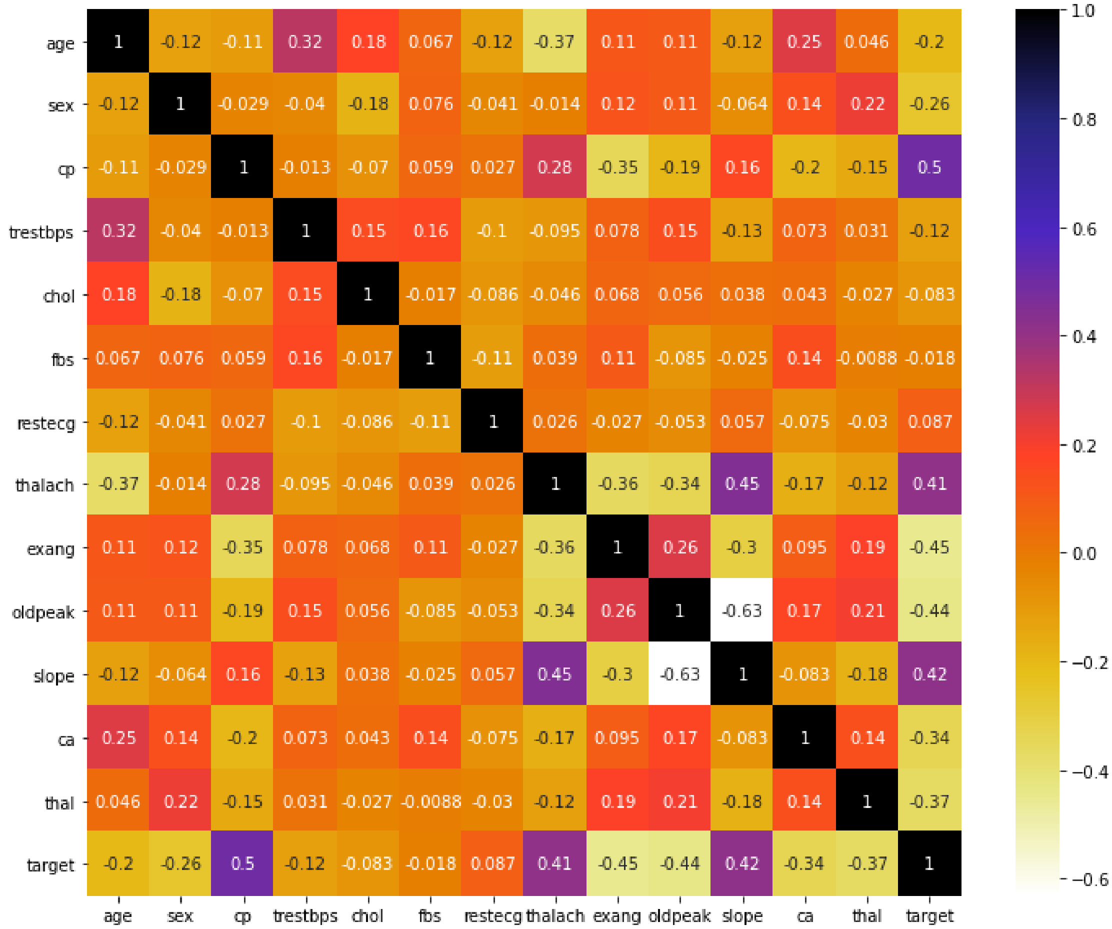


2.2 Heart disease data

2.2.1 Feature selection using pearson correlation

Features with high correlation are more linearly dependent and hence have almost the same effect on the dependent variable. So, when selecting features generally drop out features that are highly correllated(r>0.9) (https://towardsdatascience.com/feature-selection-correlation-and-p-value-da8921bfb3cf)

[27]:
```
plt.figure(figsize=(12,10))
cor = df_heart.corr()
sns.heatmap(cor,annot =True,cmap=plt.cm.CMRmap_r)
plt.show()
```



From the correlation heatmap above, cp, exang, oldpeak, slope are low to moderately corellated with target. These features are selected for the subsequent pair plots

2.2.2 Pair plot using raw data

[28]:
```
g=sns.pairplot(df_heart,
             x_vars=['cp','trestbps', 'exang', 'oldpeak', 'slope'],
             y_vars=['cp','trestbps', 'exang', 'oldpeak', 'slope'],
             hue='target')
```

2.2.3 Pair plot using z-score normalized data

```
[29]: g=sns.pairplot(df_heart_z,
                   x_vars=['cp','trestbps', 'exang', 'oldpeak', 'slope'],
                   y_vars=['cp','trestbps', 'exang', 'oldpeak', 'slope'],
                   hue='target')
```

2.2.4 Interesting pattern:

From oldpeak vs slope plot, when oldpeak<1 and slope =2, it is highly likely that a person has heart disease. Similarly, from oldpeak vs exang plot, when oldpeak<2 and exang =0, it is highly likely that a person has heart disease.

3 CM3

3.1 Iris data

3.1.1 Finding correlation r

[30]:
```
corr=df.corr()
corr
```

[30]:

	sepal_length	sepal_width	petal_length	petal_width
sepal_length	1.000000	-0.031567	0.863919	0.809915
sepal_width	-0.031567	1.000000	-0.261689	-0.264253
petal_length	0.863919	-0.261689	1.000000	0.921109
petal_width	0.809915	-0.264253	0.921109	1.000000

[31]:
```
df.head()
```

[31]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	5.045070	2.508203	3.018024	1.164924	Iris-versicolor
1	6.325517	2.115481	4.542052	1.413651	Iris-versicolor
2	5.257497	3.814303	1.470660	0.395348	Iris-setosa
3	6.675168	3.201700	5.785461	2.362764	Iris-virginica
4	5.595237	2.678166	4.077750	1.369266	Iris-versicolor

3.1.2 Observations:

From the seaborn plot above and correlation table, it is clear that petal_length and sepal_length , petal_width and sepal_length , petal_length and petal_width are strongly correlated (r>0.7). Other feature pairs are not or very weakly correlated (r<0.3).

3.1.3 Calculate mean, variance, skew and kurtosis

[32]:
```
variance= df.var()
print('Variance is:')
```

```
Variance is:
```

[33]:
```
mean =df.mean()
print('Mean is: ')
mean
```

```
Mean is:
```

[33]:
```
sepal_length    5.858909
sepal_width     3.059083
petal_length    3.812370
petal_width     1.199708
dtype: float64
```

[34]:
```
skewness = df.skew()
print('Skewness is: ')
skewness
```

```
Skewness is:
```

[34]:
```
sepal_length    0.401506
sepal_width     0.374702
petal_length   -0.265784
petal_width    -0.074751
dtype: float64
```

[35]:
```
kurt=df.kurt()
print('Kurtosis is: ')
kurt
```

```
Kurtosis is:
```

[35]:
```
sepal_length   -0.544820
sepal_width     0.649582
petal_length   -1.248929
petal_width    -1.315451
dtype: float64
```

3.2 Heart disease data

3.2.1 Finding correlation r

[36]:
```
X_heart = df_heart.iloc[:,:-1]
corr = X_heart.corr()
corr
```

[36]:
```
               age       sex        cp  trestbps      chol       fbs  \
age       1.000000 -0.121640 -0.105484  0.321295  0.178171  0.067323
sex      -0.121640  1.000000 -0.029044 -0.040403 -0.182837  0.075620
cp       -0.105484 -0.029044  1.000000 -0.013346 -0.070381  0.059283
trestbps  0.321295 -0.040403 -0.013346  1.000000  0.146390  0.159801
chol      0.178171 -0.182837 -0.070381  0.146390  1.000000 -0.017194
fbs       0.067323  0.075620  0.059283  0.159801 -0.017194  1.000000
restecg  -0.124356 -0.041339  0.027341 -0.103036 -0.086286 -0.111974
thalach  -0.373056 -0.014367  0.279063 -0.095156 -0.046239  0.038803
exang     0.111096  0.120806 -0.349594  0.077855  0.067787  0.106280
oldpeak   0.107075  0.107534 -0.191927  0.145820  0.056301 -0.084674
slope    -0.116396 -0.063791  0.159047 -0.125637  0.037975 -0.024620
ca        0.254231  0.136520 -0.195126  0.072994  0.043442  0.143594
thal      0.045731  0.220499 -0.151406  0.030510 -0.027123 -0.008814

           restecg   thalach     exang   oldpeak     slope        ca      thal
age      -0.124356 -0.373056  0.111096  0.107075 -0.116396  0.254231  0.045731
```

```
sex      -0.041339 -0.014367  0.120806  0.107534 -0.063791  0.136520  0.220499
cp        0.027341  0.279063 -0.349594 -0.191927  0.159047 -0.195126 -0.151406
trestbps -0.103036 -0.095156  0.077855  0.145820 -0.125637  0.072994  0.030510
chol     -0.086286 -0.046239  0.067787  0.056301  0.037975  0.043442 -0.027123
fbs      -0.111974  0.038803  0.106280 -0.084674 -0.024620  0.143594 -0.008814
restecg   1.000000  0.025666 -0.026598 -0.053367  0.056843 -0.075225 -0.029632
thalach   0.025666  1.000000 -0.362560 -0.335492  0.450019 -0.169422 -0.118952
exang    -0.026598 -0.362560  1.000000  0.257770 -0.303466  0.094792  0.186162
oldpeak  -0.053367 -0.335492  0.257770  1.000000 -0.630979  0.169856  0.206974
slope     0.056843  0.450019 -0.303466 -0.630979  1.000000 -0.083031 -0.177081
ca       -0.075225 -0.169422  0.094792  0.169856 -0.083031  1.000000  0.135050
thal     -0.029632 -0.118952  0.186162  0.206974 -0.177081  0.135050  1.000000
```

3.2.2 Observations:

From the correlation table, slope and thalach have a moderate positive linear relationship with r =0.45. Slope and oldpeak have a moderate to strong negative linear relationship with r= -0.63. cp and exang have a weak negative linear relationship with r =-0.34. Other feature pairs are not or very weakly correlated (r<0.3). Same criteria are used for fearture selection in CM2.

3.2.3 Calculate mean, variance, skew and kurtosis

[37]:
```python
mean =X_heart.mean()
print('Mean is: ')
mean
```

```
Mean is:
```

[37]:
```
age          54.278049
sex           0.687805
cp            0.956098
trestbps    131.954314
chol        244.828532
fbs           0.131707
restecg       0.560976
thalach     149.413011
exang         0.351220
oldpeak       1.116630
slope         1.409756
ca            0.726829
thal          2.347355
dtype: float64
```

[38]:
```python
variance= X_heart.var()
print('Variance is:')
variance
```

```
Variance is:
```

[38]:
```
age            83.299761
sex             0.215782
cp              1.042181
trestbps      318.198831
chol         2078.568287
fbs             0.114921
restecg         0.286705
thalach       464.358876
exang           0.228981
oldpeak         1.466882
slope           0.390100
ca              1.091679
thal            0.361363
dtype: float64
```

[39]:
```
skewness = X_heart.skew()
print('Skewness is: ')
skewness
```

```
Skewness is:
```

[39]:
```
age        -0.109845
sex        -0.816558
cp          0.451408
trestbps    0.702034
chol        0.321524
fbs         2.194224
restecg     0.141222
thalach    -0.379306
exang       0.627963
oldpeak     1.260606
slope      -0.567446
ca          1.400444
thal       -0.269684
dtype: float64
```

[40]:
```
kurt=X_heart.kurt()
print('Kurtosis is: ')
kurt
```

```
Kurtosis is:
```

[40]:
```
age        -0.517089
sex        -1.346465
cp         -1.261793
trestbps    0.702289
chol        0.408508
fbs         2.842256
```

```
restecg    -1.175361
thalach    -0.170362
exang      -1.621580
oldpeak     1.695990
slope      -0.595482
ca          1.063175
thal       -0.607360
dtype: float64
```

4 CM4 KNN

4.1 Iris data

[41]:
```
y=df_z.iloc[:,-1]
X=df_z.iloc[:,:-1]
# split into training and test set
from sklearn.model_selection import train_test_split
x_train,x_test,y_train,y_test = train_test_split(X,y,test_size =0.2,␣
↪random_state =98)

# Training and Predicting using default parameter
from sklearn.neighbors import KNeighborsClassifier
knn=KNeighborsClassifier()
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
```

4.1.1 Accuracy

[42]:
```
from sklearn.metrics import accuracy_score
acc= accuracy_score(y_test,y_predict)
acc
```

[42]:
```
0.9523809523809523
```

Iris: With the default parameters, accuracy obtained is 0.952

4.2 Heart disease data

[43]:
```
y_h=df_heart_z.iloc[:,-1]
X_h=df_heart_z.iloc[:,:-1]
# split into training and test set
from sklearn.model_selection import train_test_split
xh_train,xh_test,yh_train,yh_test = train_test_split(X_h,y_h,test_size =0.2,␣
↪random_state =98)

# Training and Predicting using default parameter
from sklearn.neighbors import KNeighborsClassifier
knn_h=KNeighborsClassifier()
knn_h.fit(xh_train,yh_train)
yh_predict = knn_h.predict(xh_test)
```

4.2.1 Accuracy

[44]:
```
from sklearn.metrics import accuracy_score
acc= accuracy_score(yh_test,yh_predict)
acc
```

[44]: 0.8780487804878049

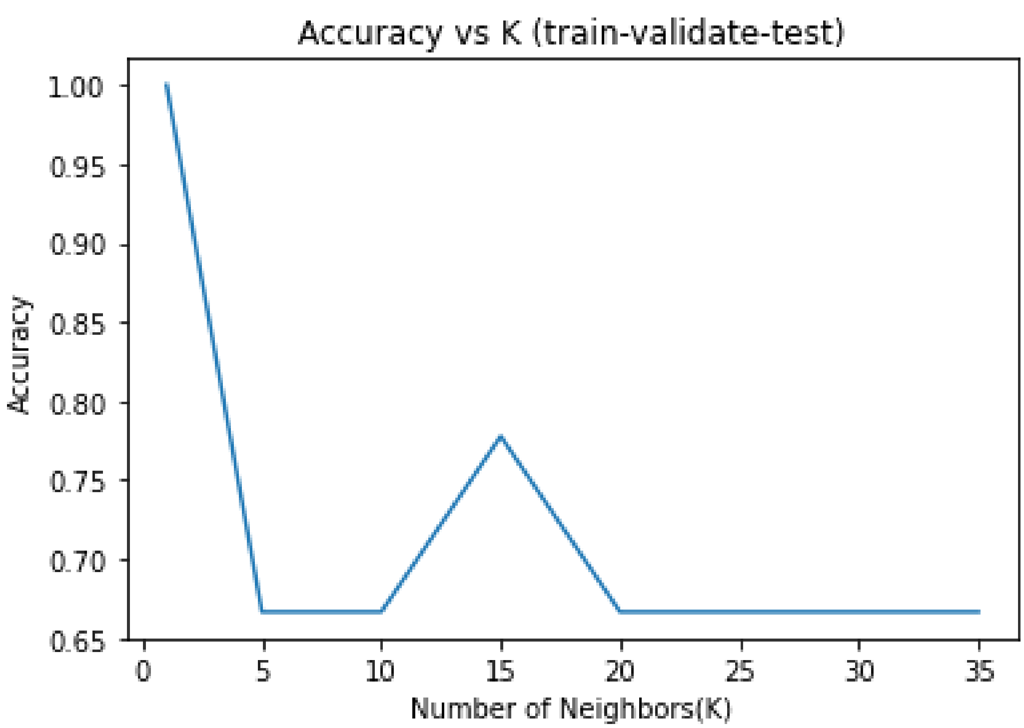
Heart disease: With the default parameters, accuracy obtained is 0.878

5 CM5 KNN Tuning

5.1 Iris data

5.1.1 Tuning K using train-validate-test

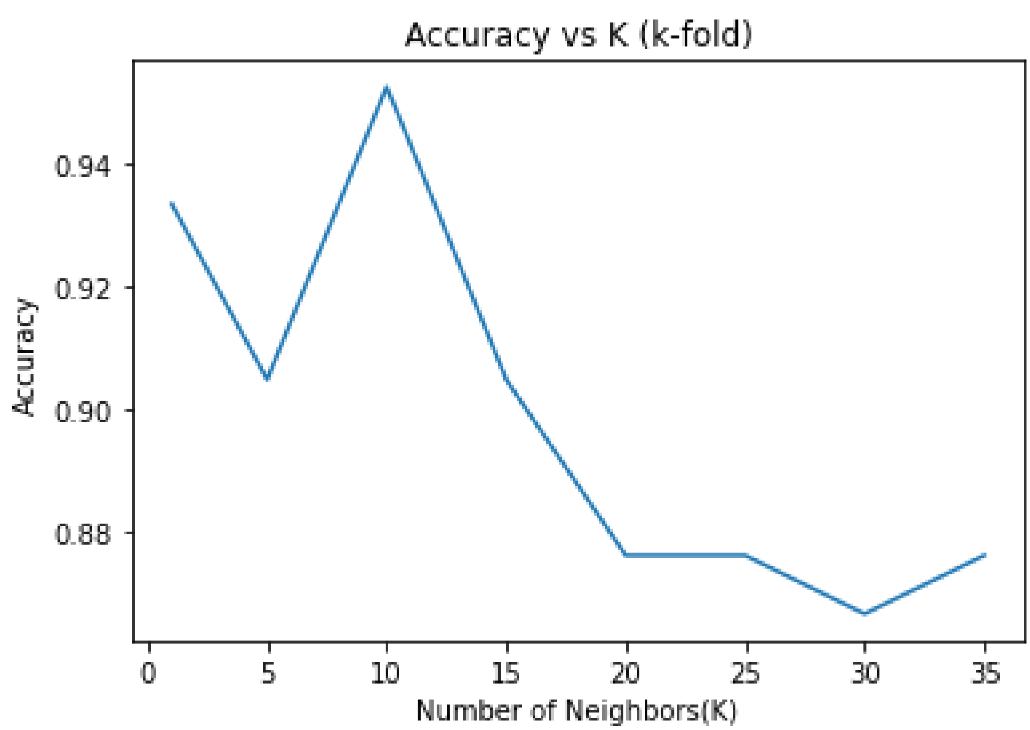
[45]:
```
# x_train,x_test,y_train,y_test = train_test_split(X,y,test_size =0.2,␣
↪random_state =98)
# further split training set into train and validation set
x_train2, x_cv, y_train2, y_cv = train_test_split(x_train,y_train,test_size = 0.
↪1,random_state=98)

k_vals= [1, 5, 10, 15, 20, 25, 30, 35]
accuracy_list=[]

for i in k_vals:
    knnmodel=KNeighborsClassifier(n_neighbors=i,).fit(x_train2,y_train2)
    y_predict = knnmodel.predict(x_cv)
    accuracy_list.append(accuracy_score(y_cv,y_predict))

# plot accuracy vs k
plt.plot(k_vals,accuracy_list)
plt.xlabel('Number of Neighbors(K)')
plt.ylabel('Accuracy')
plt.title('Accuracy vs K (train-validate-test)')
plt.show()
print(accuracy_list)
```



```
[1.0, 0.6666666666666666, 0.6666666666666666, 0.7777777777777778,
0.6666666666666666, 0.6666666666666666, 0.6666666666666666, 0.6666666666666666]
```

5.1.2 Tuning K using 5-fold cross validation method

[46]:
```
k_vals= [1, 5, 10, 15, 20, 25, 30, 35]
accuracy_list=[]
variance=[]

for i in k_vals:
    knn=KNeighborsClassifier(n_neighbors=i)
    scores = cross_val_score(knn,X,y,cv=5,scoring='accuracy')
    accuracy_list.append(scores.mean())
    variance.append(np.var(scores))

# plot Accuracy vs K 5-fold
plt.plot(k_vals,accuracy_list)
plt.xlabel('Number of Neighbors(K)')
plt.ylabel('Accuracy')
plt.title('Accuracy vs K (k-fold)')
plt.show()
```



The mean accuracies for k-fold cross validations are:

[47]:
```
print(accuracy_list)
```

```
[0.9333333333333332, 0.9047619047619048, 0.9523809523809523, 0.9047619047619049,
0.8761904761904761, 0.8761904761904761, 0.8666666666666666, 0.8761904761904761]
```

With variances of:

[48]:
```
print(variance)
```

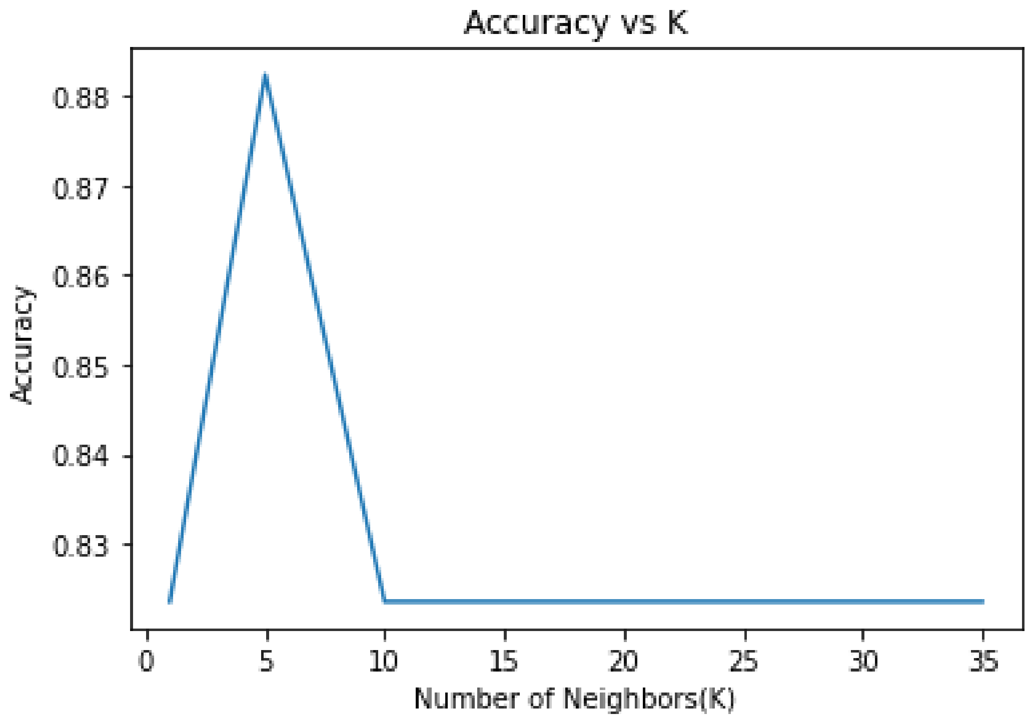
```
[0.0005442176870748286, 0.0018140589569160994, 0.0009070294784580497,
0.004535147392290249, 0.0023582766439909286, 0.0023582766439909286,
0.0030839002267573678, 0.0050793650793650785]
```

The best k in terms of classification accuracy is 10 with a corresponding accuracy of 0.9524

5.2 Heart disease data

5.2.1 Tuning K using train-validate-test

[49]:
```
# further split training set into train and validation set
xh_train2, xh_cv, yh_train2, yh_cv =␣
↪train_test_split(xh_train,yh_train,test_size = 0.1,train_size =0.
↪9,random_state=98)

k_vals=[1, 5, 10, 15, 20, 25, 30, 35]
accuracy_list2=[]

for i in k_vals:
    knnmodel=KNeighborsClassifier(n_neighbors=i).fit(xh_train2,yh_train2)
    yh_predict = knnmodel.predict(xh_cv)
    a_score = accuracy_score(yh_cv,yh_predict)
    accuracy_list2.append(a_score)

#  Accuracy vs K
plt.plot(k_vals,accuracy_list2)
plt.xlabel('Number of Neighbors(K)')
plt.ylabel('Accuracy')
plt.title('Accuracy vs K')
plt.show()

print(accuracy_list2)
```




```
[0.8235294117647058, 0.8823529411764706, 0.8235294117647058, 0.8235294117647058,
0.8235294117647058, 0.8235294117647058, 0.8235294117647058, 0.8235294117647058]
```

From the above plot, k=5 gives the highest accuracy of 0.8824 .

5.2.2 Q:Do you find any advantage to one form of validation over the other?

The cross-validation method has the ability to train on multiple train-test splits, therefore the it gives a better insight of the model performance on the entire data. The train-validate-test method however only train on one train-test splits and therefore the accuarcy is highly dependent on the random_state value.

On the other hand, because train-validate-test works like 1-fold cross validation, it's much quicker to compute than cross-validation method

6 CM6 accuracy, AUC, f-score of your best kNN classifier

6.1 Iris data

[50]:
```
# fit classifier with best k for iris data k =10
knn=KNeighborsClassifier(n_neighbors=10)
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
```

[51]:
```
accuracy_score(y_test,y_predict)
```

[51]: 0.9523809523809523

[52]:
```
from sklearn.metrics import roc_auc_score, f1_score
f1_score(y_test,y_predict,average='macro')
```

[52]: 0.9076923076923077

[53]:
```
# for multiple class classifier, need to encode the lebal and calculate predict␣
↪proba before calculate AUC

le =  preprocessing.LabelEncoder()
le.fit(y_train)
y_predict_enc = le.transform(y_predict)
y_test_enc = le.transform(y_test)
y_pred_proba =knn.predict_proba(x_test)
```

[54]:
```
roc_auc_score(y_test_enc,y_pred_proba,multi_class='ovr')
```

[54]: 0.9950617283950617

For iris data set with k=10 , the accuracy score, f-score and AUC are 0.9524, 0.9076, 0.0.9950 respectively

6.2 Heart disease data

[55]:
```
# xh_train,xh_test,yh_train,yh_test = train_test_split(X_h,y_h,test_size =0.2,␣
↪random_state =98)

knn2=KNeighborsClassifier(n_neighbors=5)
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
```

[56]:
```
accuracy_score(yh_test,yh_predict)
```

[56]: 0.8780487804878049

[57]:
```
from sklearn.metrics import roc_curve, roc_auc_score, f1_score
f1_score(yh_test,yh_predict)
```

[57]: 0.9019607843137256

[58]:
```
roc_auc_score(yh_test,yh_predict)
```

[58]: 0.8902116402116402

For heart disease data set with k=5, the accuracy score, f-score and AUC are 0.8780,0.9020,0.8902 respectively

6.2.1 Q: What was the effect of changing k? Was the accuracy always affected the same way with an increase of k? Why do you think this happened?

For iris data, the accuracy fluctuates when k is small, when k = 10, the accuracy reaches its maximum. After accuracy reaches its local maximum, the accuracy starts to decrease with increasing k values, with smaller fluctuations.

For heart disease data , increasing k in the begining shows positive effect on accuracy. After reaching maximum, accuracy decreases with increaing k. When k>10 the accuracy stays at a constant value.

This trend might happen because for low values of K, result can be subbject to the effects of outliers and noise from data and the classifier's decisions will tend to be affected by local changes more easily. On the ohter hand, large k values generates less complex classifier which could over smoothing data features and therefore lows the accuracy

source:https://stats.stackexchange.com/questions/429990/in-the-context-of-knn-why-small-k-generates-complex-models

7 CM7 the improved model

7.1 KNN with different weight and metric parameters

7.2 Iris:

7.2.1 Distance weighted KNN with minkowski metric

[59]:
```
# fit classifier with best k for iris data k =10
knn=KNeighborsClassifier(n_neighbors=10, weights='distance')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 1.0, f_score: 1.0
```

7.2.2 Distance weighted KNN with manhattan metric

[60]:
```
knn=KNeighborsClassifier(n_neighbors=10, metric='manhattan', weights='distance')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 0.9523809523809523, f_score: 0.9076923076923077
```

7.2.3 Distance weighted KNN with euclidean metric

[61]:
```
knn=KNeighborsClassifier(n_neighbors=10, metric='euclidean', weights='distance')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 1.0, f_score: 1.0
```

7.2.4 Uniform weighted KNN with minkowski metric (default parameter)

[62]:
```
knn=KNeighborsClassifier(n_neighbors=10, metric='minkowski')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 0.9523809523809523, f_score: 0.9076923076923077
```

7.2.5 Uniform weighted KNN with manhattan metric

[63]:
```
knn=KNeighborsClassifier(n_neighbors=10, metric='manhattan')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 0.9523809523809523, f_score: 0.9076923076923077
```

7.2.6 Uniform weighted KNN with euclidean metric

[64]:
```
knn=KNeighborsClassifier(n_neighbors=10, metric='euclidean')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 0.9523809523809523, f_score: 0.9076923076923077
```

Iris data: Change weights parameter to distance improves accu_score f_score to 1, 1 respectively. Changing metrics has no effect on classifer performance

7.3 Heart disease:

7.3.1 Distance weighted KNN with minkowski metric

[65]:
```
knn2=KNeighborsClassifier(n_neighbors=5,weights='distance')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.8780487804878049, f_score: 0.9019607843137256 AUC:
0.8902116402116402
```

7.3.2 Distance weighted KNN with manhattan metric

[66]:
```
knn2=KNeighborsClassifier(n_neighbors=5,weights='distance', metric='manhattan')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
```

```
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.9024390243902439, f_score: 0.923076923076923 AUC:
0.9087301587301587
```

7.3.3 Distance weighted KNN with euclidean metric

[67]:
```
knn2=KNeighborsClassifier(n_neighbors=5,weights='distance', metric='euclidean')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.8780487804878049, f_score: 0.9019607843137256 AUC:
0.8902116402116402
```

7.3.4 Uniform weighted KNN with minkowski metric (default parameter)

[68]:
```
knn2=KNeighborsClassifier(n_neighbors=5,weights='uniform', metric='minkowski')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.8780487804878049, f_score: 0.9019607843137256 AUC:
0.8902116402116402
```

7.3.5 Uniform weighted KNN with manhattan metric

[69]:
```
knn2=KNeighborsClassifier(n_neighbors=5,weights='uniform', metric='manhattan')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.9024390243902439, f_score: 0.923076923076923 AUC:
0.9087301587301587
```

7.3.6 Uniform weighted KNN with euclidean metric

[70]:
```
knn2=KNeighborsClassifier(n_neighbors=5,weights='uniform', metric='euclidean')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.8780487804878049, f_score: 0.9019607843137256 AUC:
0.8902116402116402
```

Heart disease data: Changing metric parameter to manhattan improves accu_score f_score and auc score to 0.9024, 0.9230, 0.9087 respectively. Changing weights has no effect on classifer performance

7.4 Other KNN Algorithms:

7.5 Iris:

7.5.1 KNN with ball_tree algorithm

[71]:
```
knn=KNeighborsClassifier(n_neighbors=10, algorithm='ball_tree')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 0.9523809523809523, f_score: 0.9076923076923077
```

7.5.2 KNN with kd_tree algorithm

[72]:
```
knn=KNeighborsClassifier(n_neighbors=10, algorithm='kd_tree')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 0.9523809523809523, f_score: 0.9076923076923077
```

7.5.3 KNN with brute algorithm

[73]:
```
knn=KNeighborsClassifier(n_neighbors=10, algorithm='brute')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
accuracy=accuracy_score(y_test,y_predict)
f_score=f1_score(y_test,y_predict,average='macro')
```

```
print("Accuracy score: %s, f_score: %s " % (accuracy, f_score))
```

```
Accuracy score: 0.9523809523809523, f_score: 0.9076923076923077
```

7.6 Heart Disease:

7.6.1 KNN with ball_tree algorithm

[74]:
```
knn2=KNeighborsClassifier(n_neighbors=5,algorithm='ball_tree')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.8780487804878049, f_score: 0.9019607843137256 AUC:
0.8902116402116402
```

7.6.2 KNN with kd_tree algorithm

[75]:
```
knn2=KNeighborsClassifier(n_neighbors=5,algorithm='kd_tree')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.8780487804878049, f_score: 0.9019607843137256 AUC:
0.8902116402116402
```

7.6.3 KNN with brute algorithm

[76]:
```
knn2=KNeighborsClassifier(n_neighbors=5,algorithm='brute')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.8780487804878049, f_score: 0.9019607843137256 AUC:
0.8902116402116402
```

7.6.4 Q6:

From the above calculations, different KNN algorithms have no effect on to the classifier performance. This is possible due to the limit from classifer. As stated from the online document of sklearn.neighbors.KNeighborsClassifier, "Note: fitting on sparse input will override the setting of this parameter, using brute force." Therefore with the given dataset, it's not possible evaluate the effects of different NN algorithms on to classifier performance.

source: https://scikit-learn.org/stable/modules/generated/sklearn.neighbors.KNeighborsClassifier.html

7.7 CM7 answer

7.7.1 iris

[77]:
```
# fit classifier with best k for iris data k =10 and best weights is distance
knn=KNeighborsClassifier(n_neighbors=10, weights='distance')
knn.fit(x_train,y_train)
y_predict = knn.predict(x_test)
```

[78]:
```
accuracy_score(y_test,y_predict)
```

[78]:
```
1.0
```

[79]:
```
f1_score(y_test,y_predict,average='macro')
```

[79]:
```
1.0
```

[80]:
```
# for multiple class classifier, need to encode the lebal and calculate predict␣
↪proba before calculate AUC

le =  preprocessing.LabelEncoder()
le.fit(y_train)
y_predict_enc = le.transform(y_predict)
y_test_enc = le.transform(y_test)
y_pred_proba =knn.predict_proba(x_test)
```

[81]:
```
roc_auc_score(y_test_enc,y_pred_proba,multi_class='ovr')
```

[81]:
```
1.0
```

For iris data set with k=10, weights ='distance', the accuracy score, f-score and AUC are 1,1,1 respectively

7.7.2 heart disease

[82]:
```
# fit classifer with best parameters for heart disease dataset k = 5,␣
↪metric='manhattan'
knn2=KNeighborsClassifier(n_neighbors=5, metric='manhattan')
knn2.fit(xh_train,yh_train)
yh_predict = knn2.predict(xh_test)
```

```
accuracy=accuracy_score(yh_test,yh_predict)

f_score=f1_score(yh_test,yh_predict)
auc=roc_auc_score(yh_test,yh_predict)
print("Accuracy score: %s, f_score: %s AUC: %s" % (accuracy, f_score, auc))
```

```
Accuracy score: 0.9024390243902439, f_score: 0.923076923076923 AUC:
0.9087301587301587
```

For heart disease data set with k=5, metric ='manhattan', the accuracy score, f-score and AUC are 0.9024, 0.9230, 0.9087 respectively.