final-S1G1(1)

May 17, 2020

1 Final Exam: Part B

- Section: Sec01
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- Due Date: May 7, 2020
- Purpose: Culmination of Semester Knowledge Base

1.1 Preprocessing data

[80]:
```
#--Load Libraries
import pandas as pd
import seaborn as sns
import numpy as np
import matplotlib.pyplot as plt
from scipy import stats
from sklearn.model_selection import train_test_split
from sklearn.neural_network import MLPClassifier
from sklearn import metrics
```

[81]:
```
#--Import and Preview Data Set
plants = pd.read_excel('http://barney.gonzaga.edu/~chuang/data/plants.xlsx')
plants.head()
```

[81]:

	ID	sepal_length	sepal_width	petal_length	petal_width	species
0	1	4.3	2.8	1.9	NaN	0
1	2	4.8	3.4	1.6	0.2	0
2	3	5.0	3.0	1.8	0.4	0
3	4	4.8	3.0	1.4	0.3	0
4	5	5.1	3.8	1.6	0.2	0

[82]:
```
#--Identify Missing Data
plants.isnull().sum()
```

[82]:
```
ID               0
sepal_length     1
sepal_width      5
petal_length    10
```

```
petal_width      8
species          0
dtype: int64
```

[83]:
```python
#--Identify records that have missing values
plants[plants.isnull().any(axis=1)]
```

[83]:

	ID	sepal_length	sepal_width	petal_length	petal_width	species
0	1	4.3	2.8	1.9	NaN	0
32	33	5.4	2.9	1.7	NaN	0
35	36	5.7	3.6	NaN	0.2	0
38	39	5.3	NaN	1.4	0.2	0
39	40	4.7	NaN	NaN	NaN	0
46	47	4.6	3.0	NaN	0.5	0
62	63	NaN	3.1	1.8	0.3	0
67	68	5.2	3.8	NaN	0.4	0
102	103	5.2	2.7	NaN	0.5	0
115	116	5.5	2.4	3.7	NaN	1
142	143	5.1	NaN	4.4	1.6	1
166	167	5.3	3.0	NaN	1.8	1
191	192	4.9	NaN	NaN	1.0	1
199	200	5.8	2.7	4.1	NaN	1
228	229	5.8	2.4	NaN	2.1	2
239	240	5.8	NaN	5.1	1.9	2
262	263	5.9	3.6	NaN	1.5	2
266	267	6.4	3.2	6.3	NaN	2
297	298	5.7	2.5	5.0	NaN	2
316	317	7.3	2.9	NaN	1.8	2
323	324	7.6	2.4	6.8	NaN	2

[84]:
```python
#Fill all missing data with averages grouped by species
plants['sepal_length'] = plants['sepal_length'].fillna(plants.
 ↪groupby('species')['sepal_length'].transform('mean'))
plants['sepal_width'] = plants['sepal_width'].fillna(plants.
 ↪groupby('species')['sepal_width'].transform('mean'))
plants['petal_length'] = plants['petal_length'].fillna(plants.
 ↪groupby('species')['petal_length'].transform('mean'))
plants['petal_width'] = plants['petal_width'].fillna(plants.
 ↪groupby('species')['petal_width'].transform('mean'))
plants.head()
```

[84]:

	ID	sepal_length	sepal_width	petal_length	petal_width	species
0	1	4.3	2.8	1.9	0.299057	0
1	2	4.8	3.4	1.6	0.200000	0
2	3	5.0	3.0	1.8	0.400000	0
3	4	4.8	3.0	1.4	0.300000	0
4	5	5.1	3.8	1.6	0.200000	0

[85]:
```
#-- Standardize numeric variable by adding zscore columns
plants['sepal_length_z'] = stats.zscore(plants['sepal_length'], nan_policy =␣
 ↪'omit')
plants['sepal_width_z'] = stats.zscore(plants['sepal_width'], nan_policy =␣
 ↪'omit')
plants['petal_length_z'] = stats.zscore(plants['petal_length'], nan_policy =␣
 ↪'omit')
plants['petal_width_z'] = stats.zscore(plants['petal_width'], nan_policy =␣
 ↪'omit')

plants.head()
```

[85]:
```
   ID  sepal_length  sepal_width  petal_length  petal_width  species  \
0   1           4.3          2.8           1.9     0.299057        0
1   2           4.8          3.4           1.6     0.200000        0
2   3           5.0          3.0           1.8     0.400000        0
3   4           4.8          3.0           1.4     0.300000        0
4   5           5.1          3.8           1.6     0.200000        0

   sepal_length_z  sepal_width_z  petal_length_z  petal_width_z
0       -1.679790      -0.436789       -1.034591      -1.234960
1       -1.121177       0.703984       -1.201071      -1.365184
2       -0.897731      -0.056531       -1.090085      -1.102255
3       -1.121177      -0.056531       -1.312058      -1.233719
4       -0.786009       1.464498       -1.201071      -1.365184
```

[86]:
```
#--Identify rows with zscores >3 or <-3
plants[(plants['sepal_length_z'] > 3) |
        (plants['sepal_length_z'] < -3) |
        (plants['sepal_width_z'] > 3) |
        (plants['sepal_width_z'] < -3) |
        (plants['petal_length_z'] > 3) |
        (plants['petal_length_z'] < -3) |
        (plants['petal_width_z'] > 3) |
        (plants['petal_width_z'] < -3)]
```

[86]:
```
      ID  sepal_length  sepal_width  petal_length  petal_width  species  \
106  107      4.800000     5.020648           1.8     0.200000        0
116  117      8.900000     2.600000           3.3     1.300000        1
154  155      8.975003     2.900000           4.9     1.500000        1
216  217      7.000000     4.974328           5.1     1.800000        1
261  262      9.157097     3.300000           5.2     2.400000        2
282  283      8.975003     3.800000           6.7     2.200000        2
294  295      6.700000     2.700000           5.0     4.052461        2

     sepal_length_z  sepal_width_z  petal_length_z  petal_width_z
106       -1.121177       3.785301       -1.090085      -1.365184
116        3.459455      -0.817046       -0.257685       0.080925
```

```
154        3.543250   -0.246660      0.630209      0.343854
216        1.336723    3.697233      0.741195      0.738247
261        3.746691    0.513855      0.796688      1.527034
282        3.543250    1.464498      1.629088      1.264105
294        1.001555   -0.626917      0.685702      3.699432
```

[87]:
```
#--Drop rows that conatin outliers
plants = plants.drop(plants[(plants['sepal_length_z'] > 3) |
        (plants['sepal_length_z'] < -3) |
        (plants['sepal_width_z'] > 3) |
        (plants['sepal_width_z'] < -3) |
        (plants['petal_length_z'] > 3) |
        (plants['petal_length_z'] < -3) |
        (plants['petal_width_z'] > 3) |
        (plants['petal_width_z'] < -3)].index)
plants.shape
```

[87]:
```
(319, 10)
```

[88]:
```
#Find duplicate records
plants[plants.duplicated(subset=plants.columns.difference(['ID']))]
```

[88]:
```
    ID  sepal_length  sepal_width  petal_length  petal_width  species  \
54  55           4.9          3.1           1.5          0.1        0
91  92           4.9          3.1           1.5          0.1        0

    sepal_length_z  sepal_width_z  petal_length_z  petal_width_z
54       -1.009454       0.133597       -1.256565      -1.496648
91       -1.009454       0.133597       -1.256565      -1.496648
```

[89]:
```
#Drop those records
plants.drop_duplicates(subset=plants.columns.difference(['ID']), inplace = True)
plants.shape
```

[89]:
```
(317, 10)
```

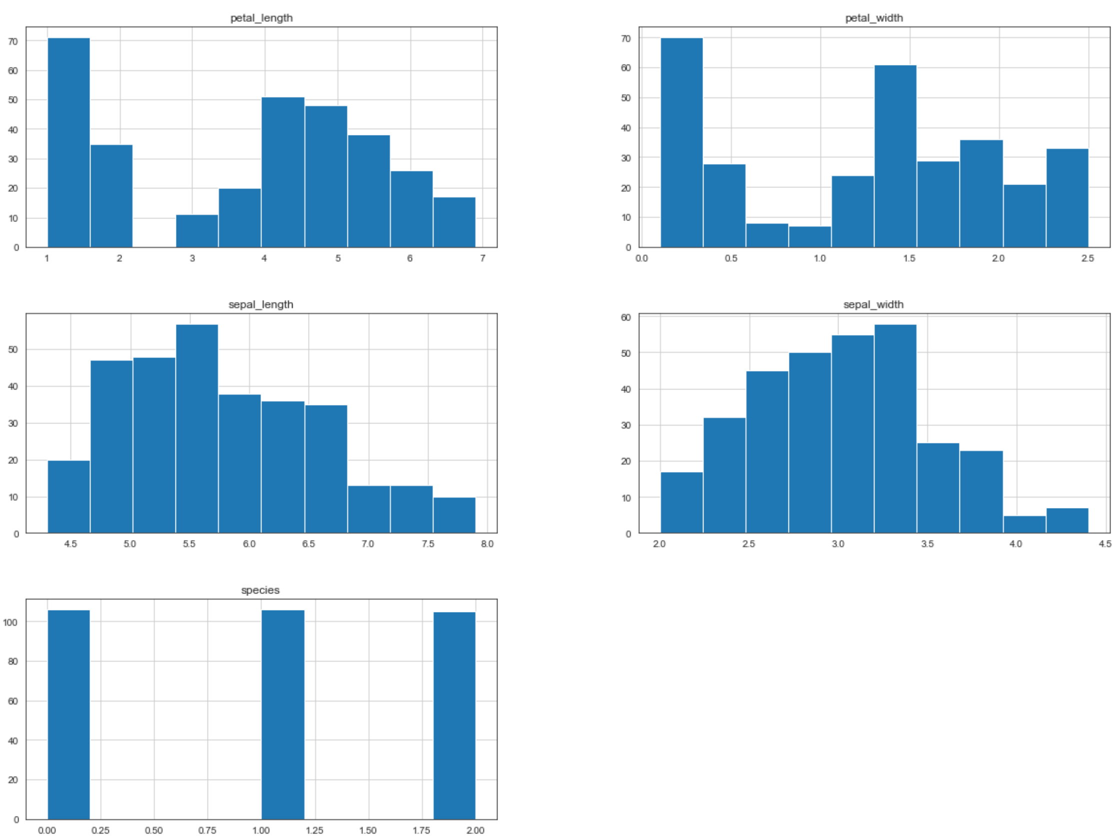
[90]:
```
#--Add Species Name Column to Data Set
def Species(x):
    if x == 0:
        return "setosa"
    elif x == 1:
        return "versicolor"
    else:
        return "virginica"

plants['SpeciesName'] = plants['species'].apply(Species)
plants.head()
```

[90]:
```
   ID  sepal_length  sepal_width  petal_length  petal_width  species  \
0   1           4.3          2.8           1.9     0.299057        0
1   2           4.8          3.4           1.6     0.200000        0
```

```
2   3           5.0           3.0           1.8       0.400000         0
3   4           4.8           3.0           1.4       0.300000         0
4   5           5.1           3.8           1.6       0.200000         0

   sepal_length_z  sepal_width_z  petal_length_z  petal_width_z SpeciesName
0       -1.679790      -0.436789       -1.034591      -1.234960      setosa
1       -1.121177       0.703984       -1.201071      -1.365184      setosa
2       -0.897731      -0.056531       -1.090085      -1.102255      setosa
3       -1.121177      -0.056531       -1.312058      -1.233719      setosa
4       -0.786009       1.464498       -1.201071      -1.365184      setosa
```

1.2 Explore Dataset

[91]:
```
#--Histogram of Each Variable (Z score variables not needed because they are␣
↪the same distribution as normal variables)
plants[['petal_length','petal_width','sepal_length','sepal_width','species']].
↪hist(bins=10,figsize=(20,15))
plt.show()
```



[92]:
```python
#--Correlation Chart (Z score variables not needed because they are the same␣
↪distribution as normal variables)
plants[['petal_length','petal_width','sepal_length','sepal_width','species']].
↪corr().style.background_gradient("Greens")
```

[92]: <pandas.io.formats.style.Styler at 0x12b50af60>

1.3 Clustering

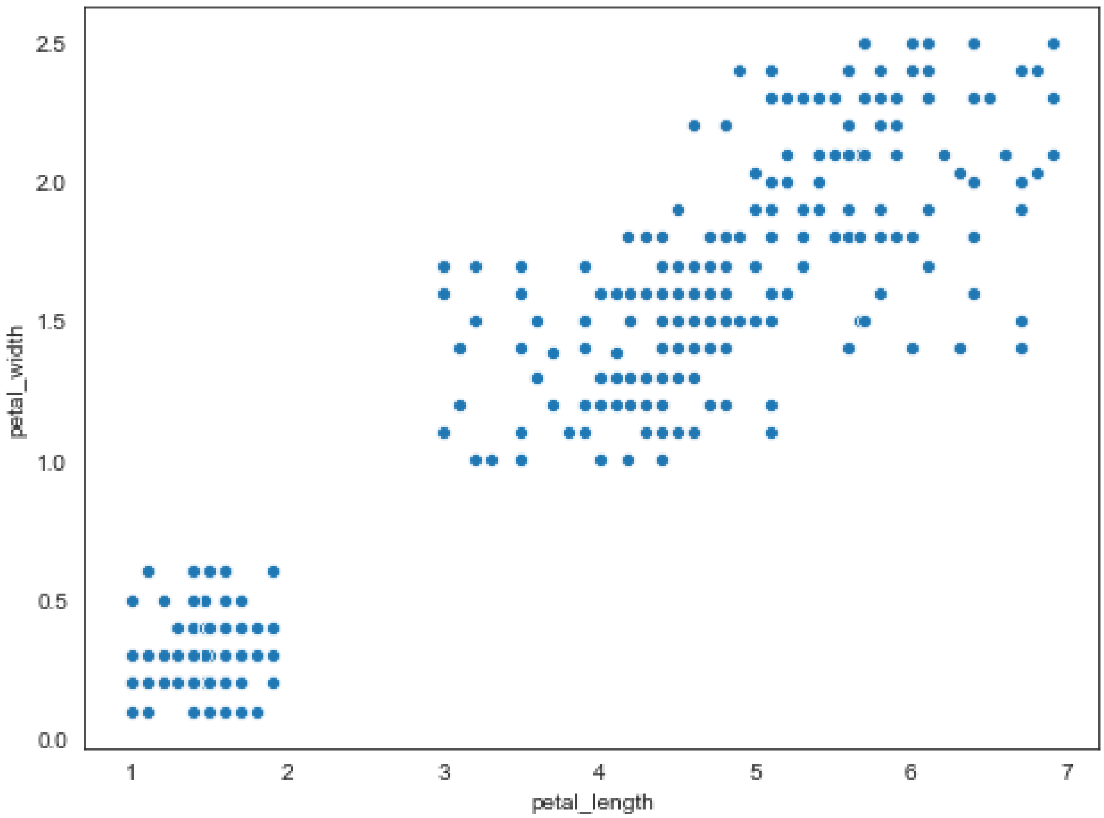
[93]:
```python
#Choose variabes to cluster and justify choice
# We chose to select the two variables with the strongest correlation to␣
↪species, petal_length and petal_width

X = plants[['petal_length', 'petal_width']]
X.head()
```

[93]:

	petal_length	petal_width
0	1.9	0.299057
1	1.6	0.200000
2	1.8	0.400000
3	1.4	0.300000
4	1.6	0.200000

[94]:
```python
#Plot the distribution of sepal_length and petal_length
plt.figure(figsize=(8,6))
sns.scatterplot(X['petal_length'], X['petal_width'])
```

[94]: <matplotlib.axes._subplots.AxesSubplot at 0x12b632048>



[95]:
```
#Save means and standard deviations
#Used to standardize data of new plants for prediction
plants_mean = X.mean()
plants_std = X.std()
print(plants_mean)
print()
print(plants_std)
```

```
petal_length    3.760817
petal_width     1.230537
dtype: float64

petal_length    1.804528
petal_width     0.742804
dtype: float64
```

[96]:
```
#Standardize the data
z_score = stats.zscore(X)
X_z = pd.DataFrame(z_score, columns = ['petal_length_z', 'petal_width_z'])
X_z.tail()
```

[96]:
```
     petal_length_z  petal_width_z
312        1.686861       1.576880
313        0.687793       0.363339
314        1.686861       1.085716
315        0.965312       0.767852
316        0.743297       1.576880
```

[97]:
```python
#Fit a model with the data
#Create three clusters
from sklearn.cluster import KMeans

kmeans_plants = KMeans(n_clusters = 3).fit(X_z)
```

[98]:
```python
#Obtain the labels
cluster = kmeans_plants.labels_
cluster
```

[98]:
```
array([1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
       1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
       2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 0, 0, 0, 0, 0, 2, 0, 0,
       0, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 0, 0, 0, 0, 0, 0, 0,
       2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 2, 2, 0, 2, 2, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 0, 0, 0, 2, 0, 0, 0, 0, 0,
       0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2, 0, 0, 0,
       0, 0, 0, 0, 0, 2, 0, 0, 0], dtype=int32)
```

[99]:
```python
#Obtain the centroids
cluster_center = kmeans_plants.cluster_centers_
cluster_center
```

[99]:
```
array([[ 1.11418969,  1.12703719],
       [-1.27561714, -1.24966339],
       [ 0.27487366,  0.24182267]])
```

[100]:
```python
X_z.tail()
```

[100]:
```
     petal_length_z  petal_width_z
312        1.686861       1.576880
313        0.687793       0.363339
314        1.686861       1.085716
315        0.965312       0.767852
316        0.743297       1.576880
```

[101]:
```
#Merge original data, rescaled data and add column to label the results of␣
↪clustering
clt = pd.DataFrame(cluster, columns=['cluster'])
plants_cluster = X.merge(X_z, on = X.index)
plants_cluster = pd.concat([plants_cluster, clt], axis = 1, sort = True)
plants_cluster = plants_cluster.rename(columns={'key_0': 'ID'})
plants_cluster.tail()
```

[101]:

	ID	petal_length	petal_width	petal_length_z	petal_width_z	cluster
312	321	6.8	2.400000	1.686861	1.576880	0
313	322	5.0	1.500000	0.687793	0.363339	2
314	323	6.8	2.035738	1.686861	1.085716	0
315	324	5.5	1.800000	0.965312	0.767852	0
316	325	5.1	2.400000	0.743297	1.576880	0

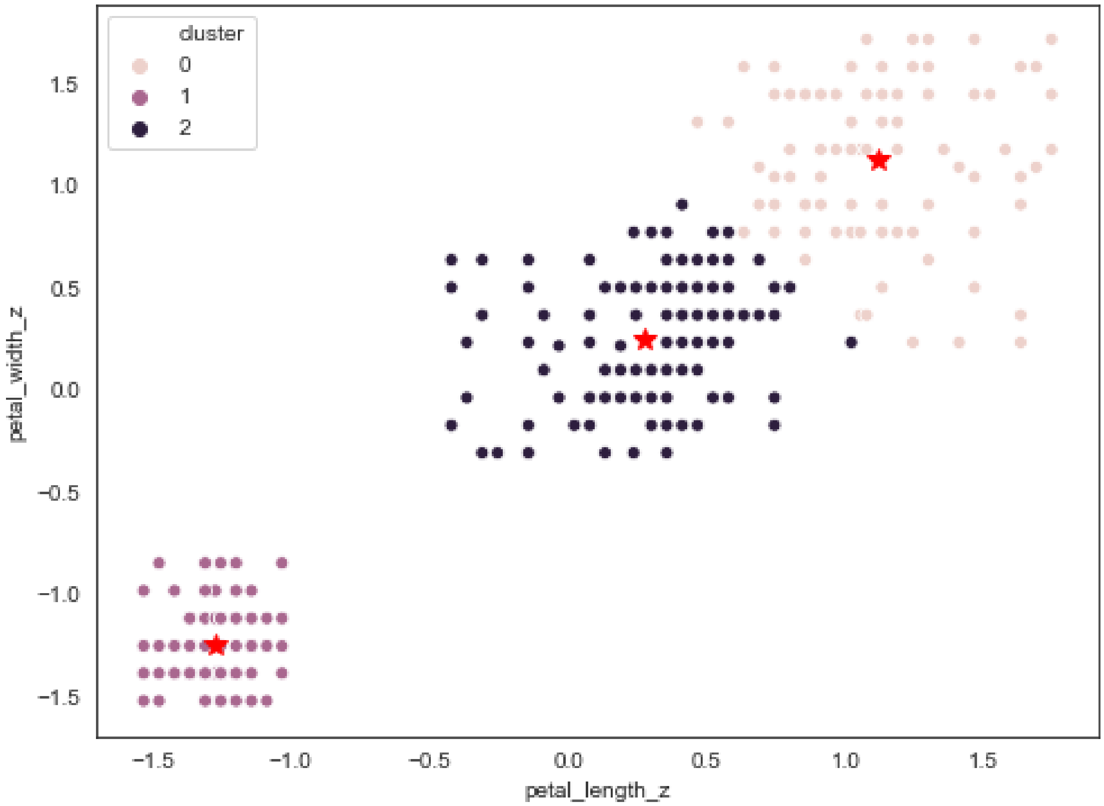
[102]:
```
#Preview the new dataset
plants_cluster.head()
```

[102]:

	ID	petal_length	petal_width	petal_length_z	petal_width_z	cluster
0	0	1.9	0.299057	-1.032823	-1.255988	1
1	1	1.6	0.200000	-1.199335	-1.389553	1
2	2	1.8	0.400000	-1.088327	-1.119878	1
3	3	1.4	0.300000	-1.310342	-1.254716	1
4	4	1.6	0.200000	-1.199335	-1.389553	1

[103]:
```
#Plot clusters
plt.figure(figsize=(8,6))
sns.scatterplot(plants_cluster['petal_length_z'],
                plants_cluster['petal_width_z'],
                hue=plants_cluster['cluster'])

#Plot centroids of the clusters
plt.plot(cluster_center[:,0],
         cluster_center[:,1],
         'r*',
         markersize=10)
# Centroids marked with stars
```

[103]:
```
[<matplotlib.lines.Line2D at 0x12ba565f8>]
```



[104]:
```
#Predict plants
#Suppose we have 5 plants and they have the following measurements
#The data is saved in a list, each element of which has two values: width and␣
 ↪length
plant_list = [[4.5, 2.3],
             [2.92, 1.5],
              [1.2, 0.3],
              [1.2, 0.5],
              [4.9, 2]]
#Convert the list to a dataframe
newplant = pd.DataFrame(plant_list,columns=['petal_length','petal_width'])
newplant
```

[104]:

	petal_length	petal_width
0	4.50	2.3
1	2.92	1.5
2	1.20	0.3
3	1.20	0.5
4	4.90	2.0

[105]:
```
#Standardize the measurements of new plants
newplant_z = (newplant-plants_mean)/plants_std
```

```
newplant_z = newplant_z.rename(columns={'petal_length': 'petal_length_z',␣
↪'petal_width': 'petal_width_z'})
newplant_z
```

[105]:

	petal_length_z	petal_width_z
0	0.409627	1.439765
1	-0.465948	0.362765
2	-1.419106	-1.252735
3	-1.419106	-0.983485
4	0.631291	1.035890

[106]:
```
#Prediction
preds = kmeans_plants.predict(newplant_z)
preds
```

[106]:
```
array([0, 2, 1, 1, 0], dtype=int32)
```

[107]:
```
#Interpretations
#The first plant belongs to the cluster of high petal_length and petal_width
#The second plant belongs to the cluster of medium petal_length and petal_width
#The thrid plant belongs to the cluster of low petal_length and petal_width
#The fourth plant belongs to the cluster of low petal_length and petal_width
#The fifth plant belongs to the cluster of high petal_length and petal_width

# Combine original data, standardized data and predicted clusters
combined_newplant = pd.concat([newplant, newplant_z, pd.DataFrame(preds,␣
↪columns=['cluster'])], axis = 1)
combined_newplant
```

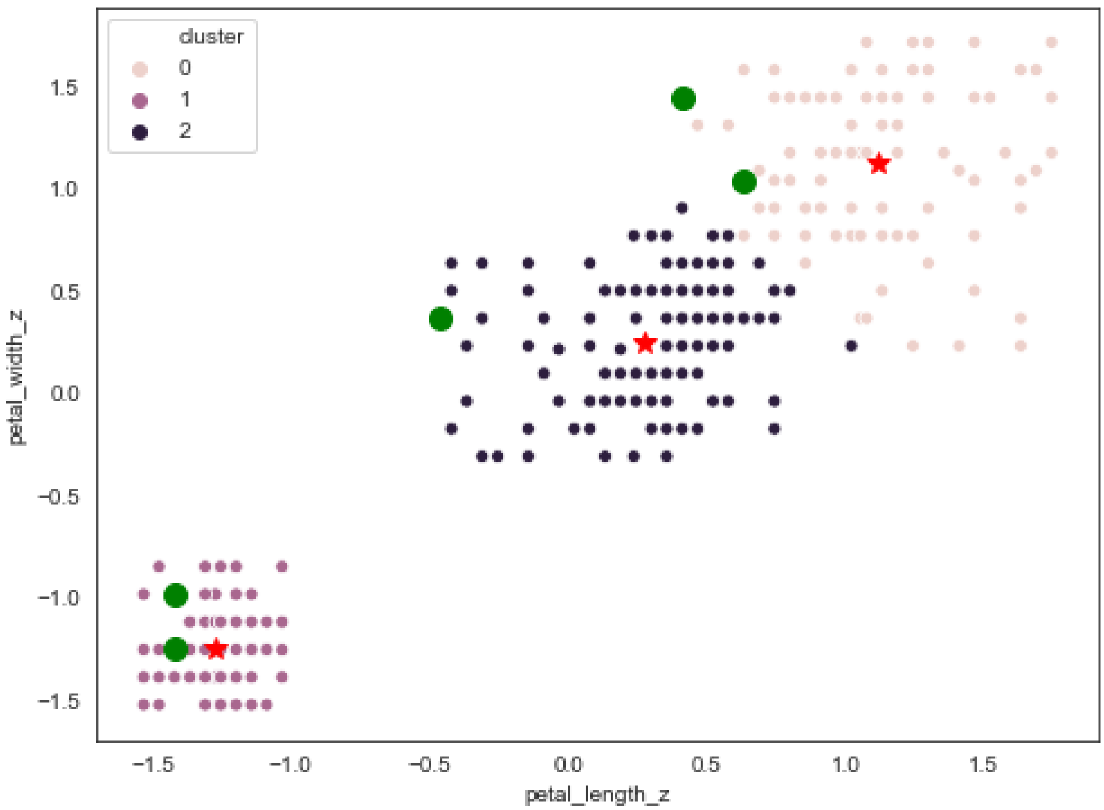
[107]:

	petal_length	petal_width	petal_length_z	petal_width_z	cluster
0	4.50	2.3	0.409627	1.439765	0
1	2.92	1.5	-0.465948	0.362765	2
2	1.20	0.3	-1.419106	-1.252735	1
3	1.20	0.5	-1.419106	-0.983485	1
4	4.90	2.0	0.631291	1.035890	0

[108]:
```
#Plot clusters
plt.figure(figsize=(8,6))
sns.scatterplot(plants_cluster['petal_length_z'],
                plants_cluster['petal_width_z'],
                hue=plants_cluster['cluster'])

#Plot centroids of the clusters
plt.plot(cluster_center[:,0],
         cluster_center[:,1],
         'r*',
         markersize=10)

#Plot predictions
plt.plot(newplant_z.iloc[:,0],
```

```
        newplant_z.iloc[:,1],
        'go',
        markersize=10)

# Graph shows where predicted flowers should lie with green dots
```

[108]: [<matplotlib.lines.Line2D at 0x12b4e27b8>]



1.4 Classification

[109]:
```
#--Preview Data and drop non-predictors
plants.
 ↪drop(['ID','sepal_length_z','sepal_width_z','petal_length_z','petal_width_z','SpeciesName']
 ↪axis = 1, inplace = True)
plants.head()
```

[109]:

	sepal_length	sepal_width	petal_length	petal_width	species
0	4.3	2.8	1.9	0.299057	0
1	4.8	3.4	1.6	0.200000	0
2	5.0	3.0	1.8	0.400000	0
3	4.8	3.0	1.4	0.300000	0
4	5.1	3.8	1.6	0.200000	0

[110]:
```
# establish predictors
outcome = 'species'
predictors = [c for c in plants.columns if c != outcome]
predictors
```

[110]:
```
['sepal_length', 'sepal_width', 'petal_length', 'petal_width']
```

[111]:
```
# --Split training and testing
# Test size of 30% used which is around the industry standard
X = plants.drop('species',axis=1) # -- features --
y = plants['species']             # -- target --

x_train, x_test, y_train, y_test = train_test_split(X,y,
                                                    test_size = 0.3,
                                                    random_state=1)
```

[112]:
```
# -- train neural nets and fit model--
# Solver type is lbfgs
# Hidden layer sizes is 3
ann_clf = MLPClassifier(hidden_layer_sizes = (3),
                        activation = 'logistic',
                        solver = 'lbfgs', random_state = 1)

ann_clf.fit(x_train,y_train)
```

[112]:
```
MLPClassifier(activation='logistic', alpha=0.0001, batch_size='auto',
              beta_1=0.9, beta_2=0.999, early_stopping=False, epsilon=1e-08,
              hidden_layer_sizes=3, learning_rate='constant',
              learning_rate_init=0.001, max_iter=200, momentum=0.9,
              n_iter_no_change=10, nesterovs_momentum=True, power_t=0.5,
              random_state=1, shuffle=True, solver='lbfgs', tol=0.0001,
              validation_fraction=0.1, verbose=False, warm_start=False)
```

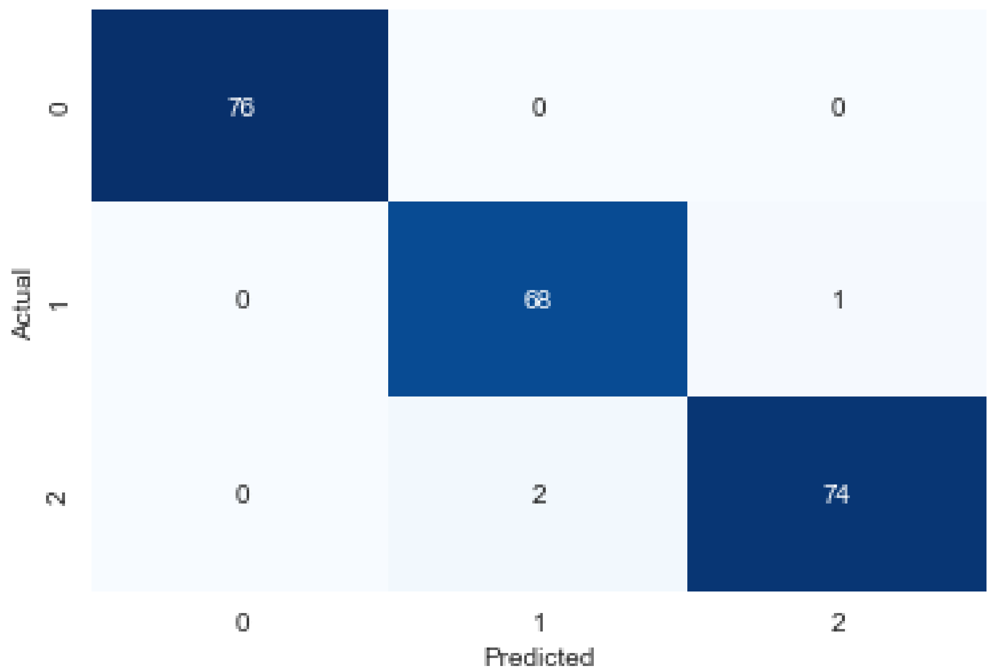
[113]:
```
# -- confusion matrix --

metrics.confusion_matrix(y_true = y_train,
                         y_pred = ann_clf.predict(x_train))
```

[113]:
```
array([[76,  0,  0],
       [ 0, 68,  1],
       [ 0,  2, 74]])
```

[114]:
```
# -- Use sklearn.metrics to present confustion_matrix --

# -- use seaborn heatmapt to present the confusion matrix --
# -- This is based on TRAINING DATA --
%matplotlib inline

sns.heatmap(metrics.confusion_matrix(y_true = y_train,
                                     y_pred = ann_clf.predict(x_train)),
```

```
                                                annot=True,
                                                cbar=False,
                                                fmt='g',
                                                cmap = plt.cm.get_cmap('Blues'))
plt.ylabel('Actual')
plt.xlabel('Predicted')
```

[114]: Text(0.5, 16.0, 'Predicted')



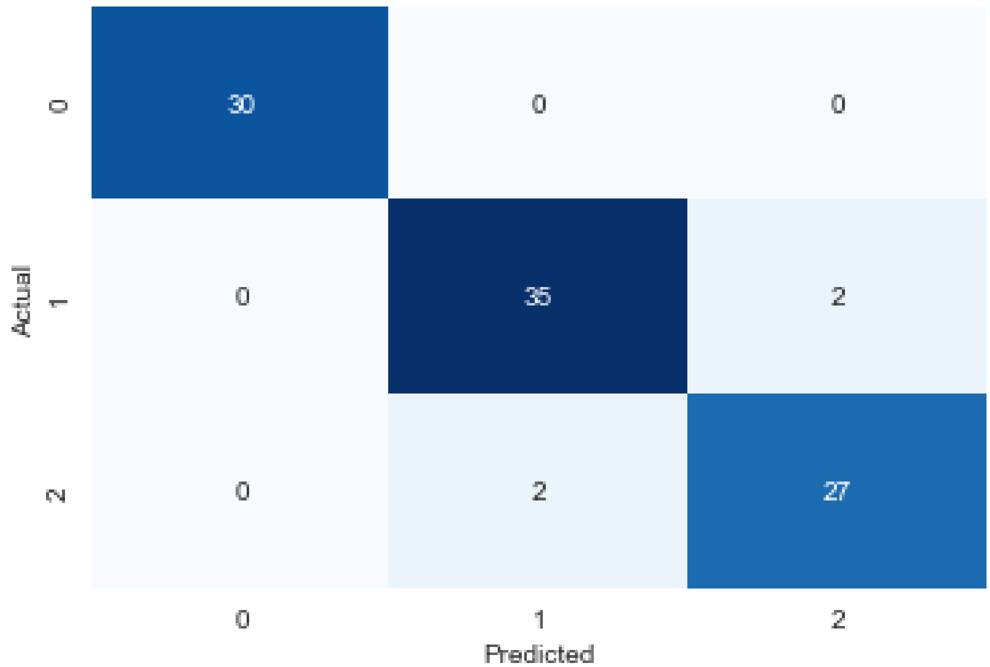
[115]:
```
# -- Validation performance --
# -- Use test data --
metrics.confusion_matrix(y_true = y_test,
                         y_pred=ann_clf.predict(x_test))
```

[115]:
```
array([[30,  0,  0],
       [ 0, 35,  2],
       [ 0,  2, 27]])
```

[116]:
```
# --- Print Confusion Matrix Using Panda's crosstab function ---
sns.set_style('white')
print('--- Confusion Matrix (predict on rows, actual on columns ---')
cmtab = metrics.confusion_matrix(y_test,ann_clf.predict(x_test))

# confusion_matrix = pd.crosstab(preds, y_test,rownames=['Predicted'],␣
 ↪colnames=['Actual'])
ax = sns.heatmap(cmtab, annot=True,fmt='g',cbar=False,cmap='Blues')
ax.set(xlabel="Predicted",ylabel="Actual");
```

```
# The confusion matrix shows that nearly all of the predicted values were␣
↪correctly identified. There were 2 flowers
# in classes 1 and 2 were misidentified. This is very minimal in the grand␣
↪scheme of the dataset
```

```
--- Confusion Matrix (predict on rows, actual on columns ---
```



[117]:

```python
# show metrics
print(metrics.classification_report(y_true = y_test,
                                     y_pred = ann_clf.predict(x_test)))

# The model has high performance in all areas. Especially the accuracy,␣
↪precision, and F1 score which are
# good metrics for this model because our biggest concern is classifying␣
↪flowers correctly and avoiding false positives
```

```
              precision    recall  f1-score   support

           0       1.00      1.00      1.00        30
           1       0.95      0.95      0.95        37
           2       0.93      0.93      0.93        29

    accuracy                           0.96        96
   macro avg       0.96      0.96      0.96        96
```

```
weighted avg       0.96      0.96      0.96        96
```