DS201 Exam 2, part 2

The exam is due **Nov 13 at midnight**. Submit `DS201_Exam2_LastFirst.ipynb` file on canvas.

Dataset: `BreastCancer_data.csv` (on Canvas under the Exam#2 module or loaded in this file)

About this Dataset: Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image.

Attribute Information:

1) ID number

2) Diagnosis (M = malignant, B = benign)

3-32) Ten real-valued features are computed for each cell nucleus: All feature values are recoded with four significant digits.

Missing attribute values: none

Class distribution: 357 benign, 212 malignant

```
import pandas as pd
df = pd.read_csv('http://lidicky.name/DS201/BreastCancer_data.csv')
df.head()
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	smoo
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	

5 rows × 33 columns

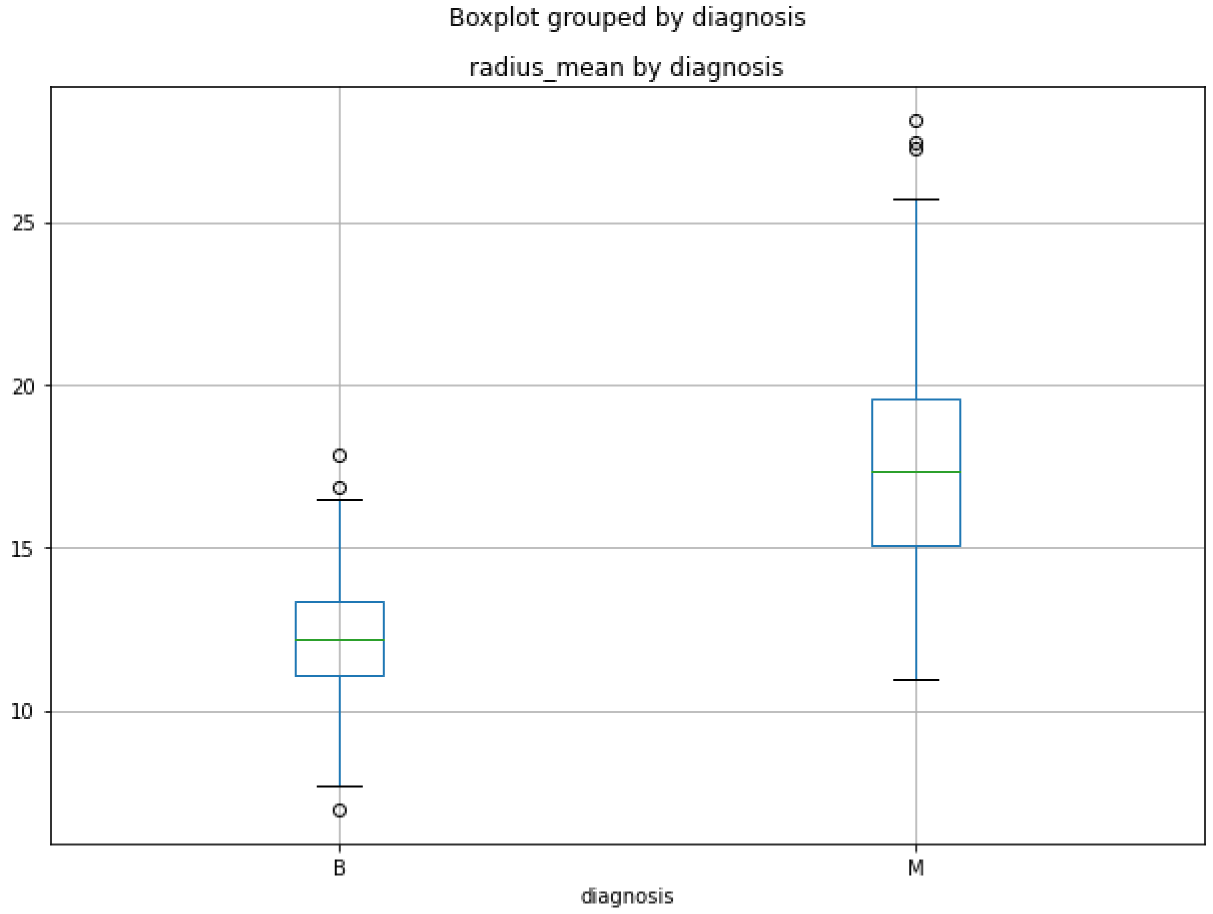
(10 points) Create a simple box plot of `radius_mean` by `diagnosis`. Your X axis need to be `diagnosis`.

What can you tell from the graph?

The radius mean by diagnosis for benign has a median of 12 and the minimum radius_mean being 4 and a maximum being 17. The radius_mean by diagnosis for malignant has a median of approximately 17.5 and the minimum radius_mean being 11 and maximum being 29. This means the size of the benign cell is smaller than that of malignant cell.

```
import pandas as pd
import matplotlib.pyplot as plt
df = df.drop_duplicates()
df = df.reset_index(drop = True)
df.boxplot(column = 'radius_mean', by = 'diagnosis', figsize = (10, 7))
plt.title('radius_mean by diagnosis')
plt.show()
```

```
    /usr/local/lib/python3.7/dist-packages/matplotlib/cbook/__init__.py:1376: Visibl
      X = np.atleast_1d(X.T if isinstance(X, np.ndarray) else np.asarray(X))
```



(10 points) Create a pairplot by following columns:

`"radius_mean","texture_mean", "perimeter_mean", "area_mean" , "smoothness_mean", "compactness_mean"`. Separate colors by `'diagnosis'`.

Which pairs seems to corellated and why? CORRELATED PAIRS:

RADIUS MEAN & PERIMETER MEAN

RADIUS MEAN & AREA MEAN

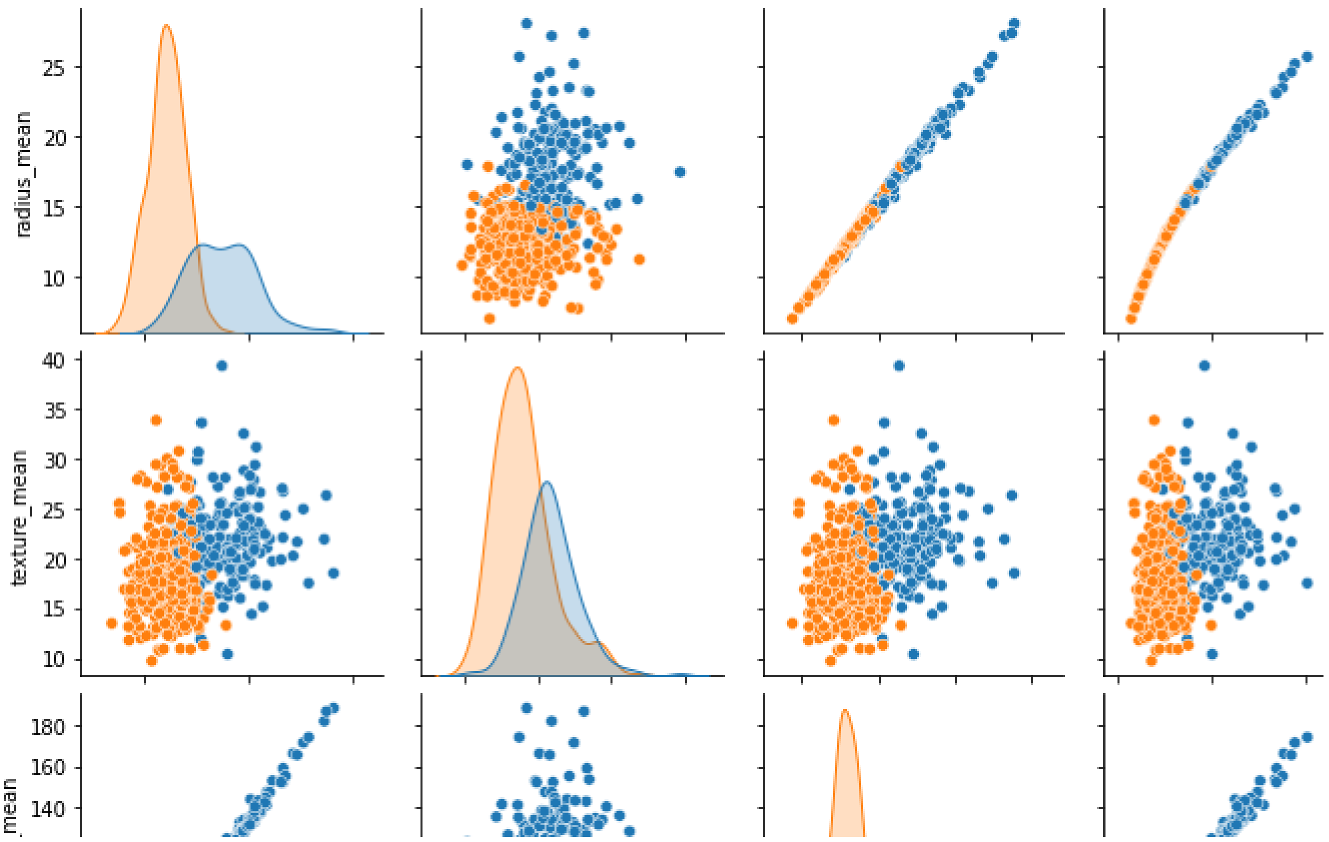
PERIMETER MEAN & AREA MEAN

SINCE THESE PAIRS SHOW LINEAR REGRESSION, THEY ARE CORRELATED

Which pair would you use for logostic regression to predict `'diagnosis'` and why?

PERIMETER MEAN AND AREA MEAN

```
import seaborn as sns
import numpy as np
df1 = df[['diagnosis', 'radius_mean','texture_mean','perimeter_mean','area_mean','smoc
sns.pairplot(df1, hue = 'diagnosis')
plt.show()
```



(20 points) Create a bokeh Scatter plot as following:

- Saperate Benign and Malignant data
- x axis: `area_mean`
- y axis: `texture_mean`
- the size of datapoints: `radius_mean`
- Benign datapoints: green circle
- Malignant datapoints: red triangle
- title: Benign and Malignant texture_mean(Y) by area_mean(X) with size by Radius
- use the lower alpha value (transparency) for Benign to allow Malignant data to be cleary visible
- legend location: top_left

Make output of bokeh included in the notebook.

Based on the plot, which classifier would you use to get a `'diagnosis'` and why? I WOULD USE MALIGNANT TO GET DIAGNOSIS SINCE IT IS SPREAD MORE UNIFORMLY AND THROUGHOUT THE PLOT THAN BENIGN.

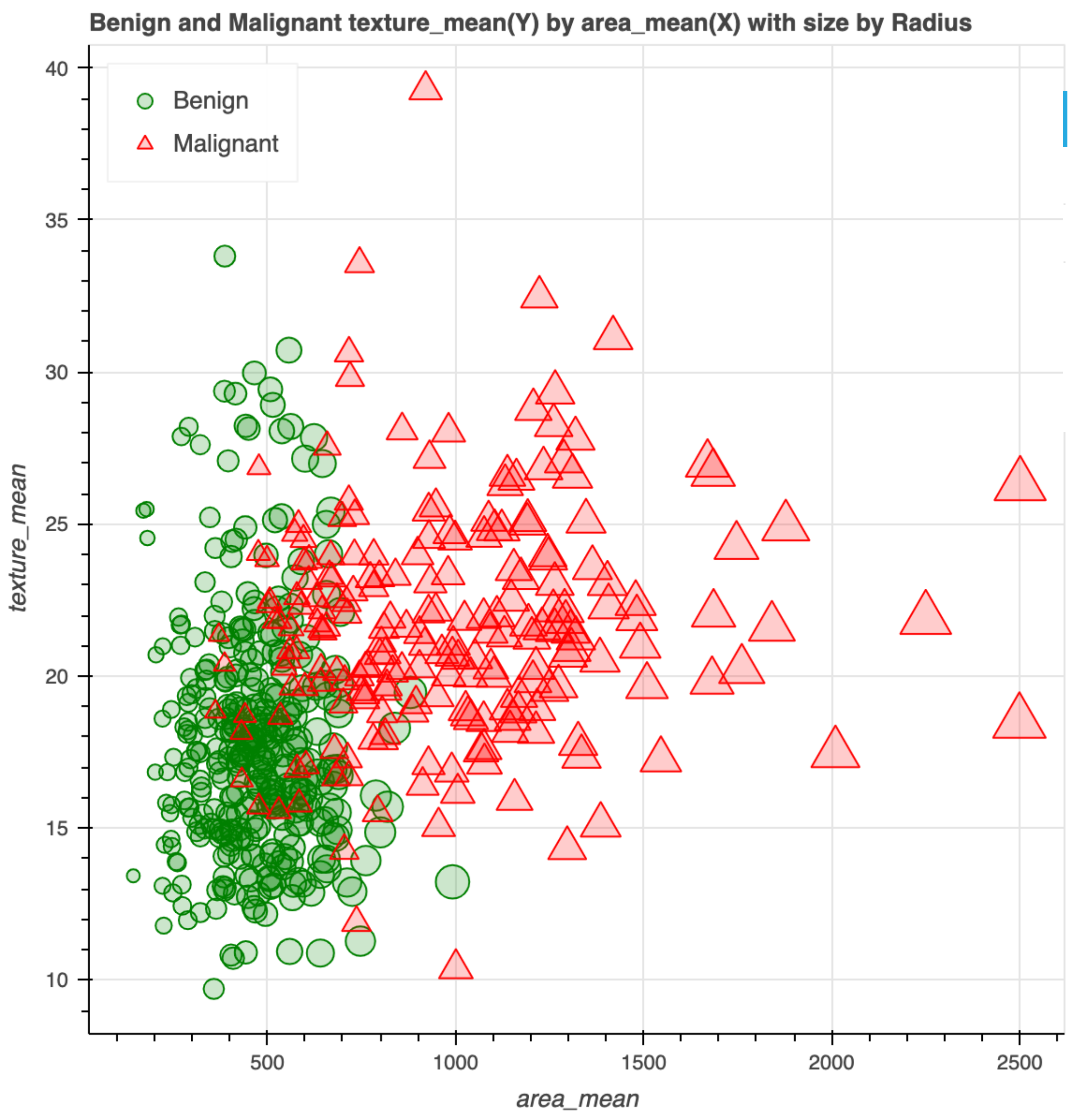
```
from bokeh.models import ColumnDataSource
from bokeh.io import output_notebook, show
from bokeh.plotting import figure

# separate benign and malignant
```

```
benign = df[df['diagnosis'] == 'B']
malignant = df[df['diagnosis'] == 'M']
p = figure(title = "Benign and Malignant texture_mean(Y) by area_mean(X) with size by
p.circle('area_mean', 'texture_mean', source = benign, color = 'green', size = 'radius
p.triangle('area_mean', 'texture_mean', source = malignant, color = 'red', size = 'rad
p.legend.location = "top_left"
p.xaxis.axis_label = 'area_mean'
p.yaxis.axis_label = 'texture_mean'
```

```
    BokehDeprecationWarning: 'legend' keyword is deprecated, use explicit 'legend_lal
    BokehDeprecationWarning: 'legend' keyword is deprecated, use explicit 'legend_lal
```

```
show(p)
```



(30 points) create a classifier to classify each observation to two class, Benign and Malignant:

- Label: Benign or Malignant
- train/test size: 80:20
- random_state=1
- features columns X : "radius_mean","texture_mean","perimeter_mean","area_mean","smoothness_mean","compactness_mean"
- report Logistic Regression accuracy of X,Y using `accuracy_score`
- report KNN accuracy of X,Y when k=5 using `accuracy_score`
- loop k=1 to k=25 and plot KNN accuracy of X,Y

Based on the last plot, what value of k in kNN would you use and why? I WOULD USE VALUE OF K AS 10 BECAUSE THAT WILL BE EQUIDISTANT TO ALL THE POINTS. SINCE OUR task is to calculate the distance and identify which categories are closest to our unknown entity, K=10 IS THE BEST POSSIBLE SOLUTION.

```
from sklearn.model_selection import train_test_split
from sklearn.metrics import accuracy_score
from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
import matplotlib.pyplot as plt
X = df[['radius_mean','texture_mean','perimeter_mean','area_mean','smoothness_mean','c
Y = df[['diagnosis']]
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size = 0.2, random_stat

# print out the shape of X,y,X_train, X_test, Y_train,Y_test
print(X.shape, Y.shape, X_train.shape, X_test.shape, Y_train.shape, Y_test.shape)

# report Logistic Regression accuracy of X,Y
log_reg_1 = LogisticRegression()
log_reg_1.fit(X, Y)
log_accuracy = log_reg_1.score(X_test, Y_test)
print(log_accuracy)

# report KNN accuracy of X,Y when k=5
knn = KNeighborsClassifier(n_neighbors = 5)
knn.fit(X, Y)
preds = knn.predict(X_test)
knn_accuracy = accuracy_score(y_true = Y_test, y_pred = preds)
print(knn_accuracy)

# loop k1-k25 and plot KNN accuracy of X,Y
neighbours = list(range(1, 25))
score = []
for i in neighbours:
    clf = KNeighborsClassifier(n_neighbors = i)
    clf.fit(X_train, Y_train)
    preds_neighbors = clf.predict(X_test)
    score.append(accuracy_score(y_true = Y_test, y_pred = preds_neighbors))
```

```
plt.plot(neighbours, score)
plt.xlabel('Value of K for KNN of X')
plt.ylabel('Testing Accuracy')
plt.show()
```

```
(569, 6) (569, 1) (455, 6) (114, 6) (455, 1) (114, 1)
0.8771929824561403
0.9035087719298246
/usr/local/lib/python3.7/dist-packages/sklearn/utils/validation.py:993: DataConv
  y = column_or_1d(y, warn=True)
/usr/local/lib/python3.7/dist-packages/sklearn/linear_model/_logistic.py:818: Co
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regressio
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG,
/usr/local/lib/python3.7/dist-packages/sklearn/neighbors/_classification.py:198:
  return self._fit(X, y)
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  return self._fit(X, y)
/usr/local/lib/python3.7/dist-packages/sklearn/neighbors/_classification.py:198:
  return self._fit(X, y)
```
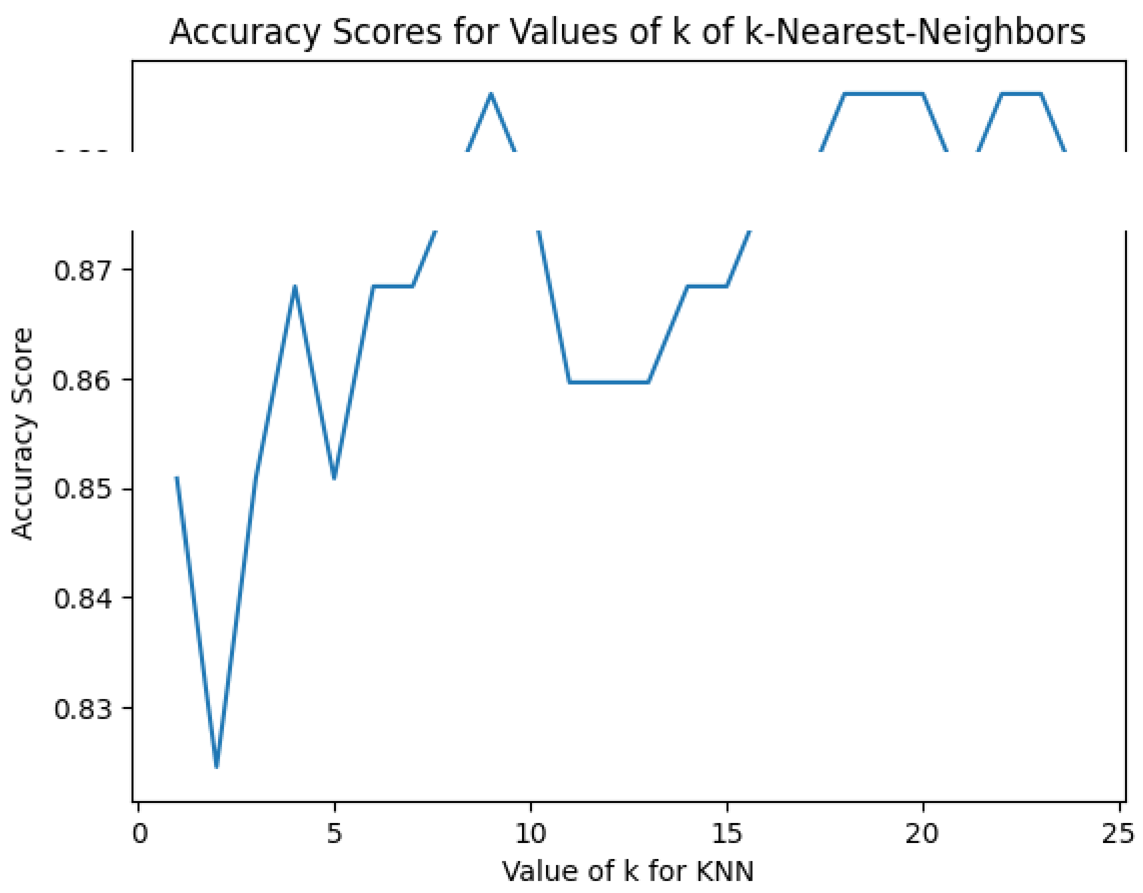

```
# Here below is an example of a plot we are looking for in the previous question
```



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