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Homework 1

CSCE 421 500

September 15, 2022

Question 1: Predicting patient post-surgery survival:

(a.i) Using the training data, compute the number of samples belonging to each class. Are the classes equally distributed?

Code

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

(a.i) Using the training data, compute the number of samples belonging to each class. Are the classes equally distributed?

```
#Constants
class1 = 1
class2 = 2

#Read the data from 'data_train.csv'
df_train= pd.read_csv('data_train.csv', header=None)
data_train = df_train.to_numpy()
print(df_train)

#Collect counts of the classes
inClass1 = 0;
inClass2 = 0;

for row in data_train:
    if row[3] == class1:
        inClass1 += 1
    else:
        inClass2 += 1

print("Sample in class 1 is " + str(inClass1))
print("Sample in class 2 is " + str(inClass2))
```

Output

```
      0   1   2  3
0    38  66   0  1
1    38  66  11  1
2    38  60   1  1
3    38  67   5  1
4    39  66   0  2
..   ..  ..  .. ..
240  75  62   1  1
241  76  67   0  1
242  77  65   3  1
243  78  65   1  2
244  83  58   2  2

[245 rows x 4 columns]
Sample in class 1 is 173
Sample in class 2 is 72
```

Reflections

The two classes are not equally distributed since the sample of class 1 is 173 and the sample of class 2 is 72.

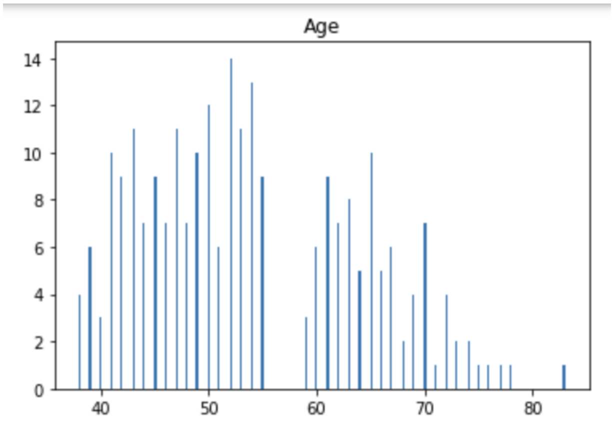
(a.ii) Using the training data, plot the histogram of each feature (i.e., 3 total histograms). How are the features distributed (e.g., unimodal, bimodal, uniform distributions)?

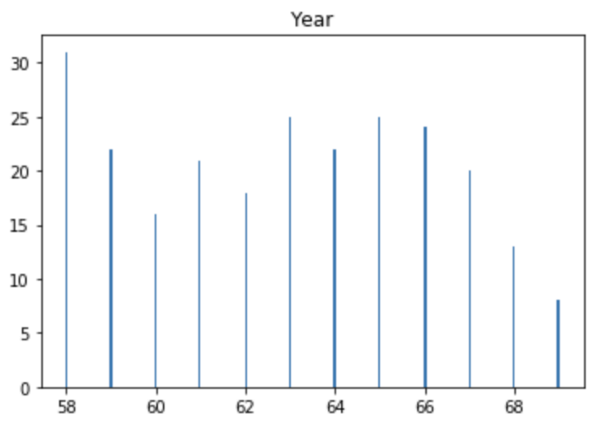
Code

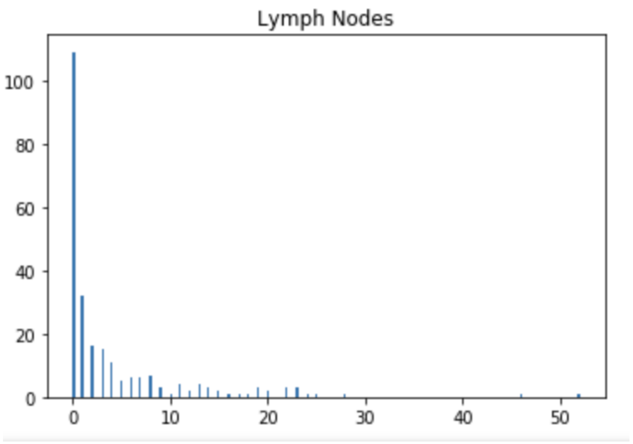
(a.ii) Using the training data, plot the histogram of each feature (i.e., 3 total histograms). How are the features distributed (e.g., unimodal, bimodal, uniform distributions)?

```
age = df_train[0].to_numpy()
year = df_train[1].to_numpy()
posLymphNodes = df_train[2].to_numpy()

plt.hist(age, bins=len(age))
plt.title('Age')
plt.show()

plt.hist(year, bins=len(year))
plt.title('Year')
plt.show()

plt.hist(posLymphNodes, bins=len(posLymphNodes))
plt.title('Lymph Nodes')
plt.show()
```

Output







Reflections

The histogram for Age is bimodal. The histogram for Year is somewhat uniformly distributed. The histogram for Lymph Nodes is skewed to the right.

(a.iii) Using the training data, plot scatter plots of all pairs of features (i.e., 3 total scatter plots). Use a color-coding to indicate the class in which the samples belong (e.g., blue circle for class 1, green star for class 2). What do you observe? How separable do the classes look? Are there feature combinations for which the two classes are more separable?

Code

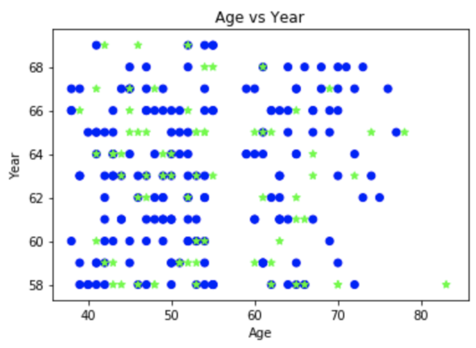
(a.iii) Using the training data, plot scatter plots of all pairs of features (i.e., 3 total scatter plots). Use a color-coding to indicate the class in which the samples belong to (e.g., blue circle for class 1, green star for class 2). What do you observe? How separable do the classes look? Are there feature combinations for which the two classes are more separable?

```
# Create two tuples for the colors of each class
one = (0, 0, 1)
two = (0, 1, 0)

#Separate each feature into respective classes
age_one = []
age_two = []

year_one = []
year_two = []

posLymphNodes_one = []
posLymphNodes_two = []

class_one = []
class_two = []

#Load each feature based on the class
for row in data_train:
    if row[3] == class1:
        age_one.append(row[0])
        year_one.append(row[1])
        posLymphNodes_one.append(row[2])
        class_one.append(one)
    else:
        age_two.append(row[0])
        year_two.append(row[1])
        posLymphNodes_two.append(row[2])
        class_two.append(two)
```

Output

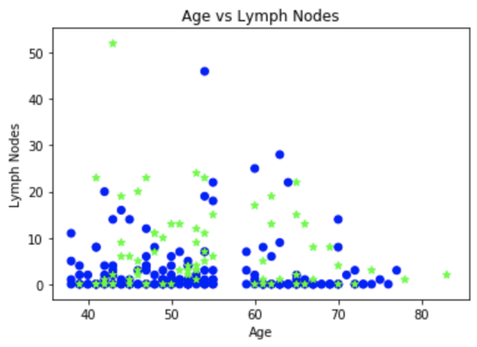
```
plt.scatter(
    x=age_one,
    y=year_one,
    c=class_one,
)
plt.scatter(
    x=age_two,
    y=year_two,
    c=class_two,
    marker='*'
)
plt.xlabel("Age")
plt.ylabel("Year")
plt.title("Age vs Year")
```

```
Text(0.5, 1.0, 'Age vs Year')
```



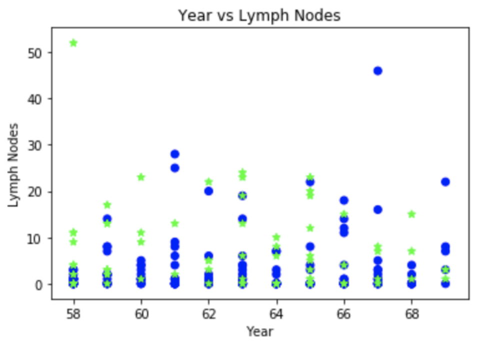
```
plt.scatter(
    x=age_one,
    y=posLymphNodes_one,
    c=class_one,
)
plt.scatter(
    x=age_two,
    y=posLymphNodes_two,
    c=class_two,
    marker='*'
)
plt.xlabel("Age")
plt.ylabel("Lymph Nodes")
plt.title("Age vs Lymph Nodes")
```

```
Text(0.5, 1.0, 'Age vs Lymph Nodes')
```



```
plt.scatter(
    x=year_one,
    y=posLymphNodes_one,
    c=class_one,
)
plt.scatter(
    x=year_two,
    y=posLymphNodes_two,
    c=class_two,
    marker='*'
)
plt.xlabel("Year")
plt.ylabel("Lymph Nodes")
plt.title("Year vs Lymph Nodes")
```

```
Text(0.5, 1.0, 'Year vs Lymph Nodes')
```

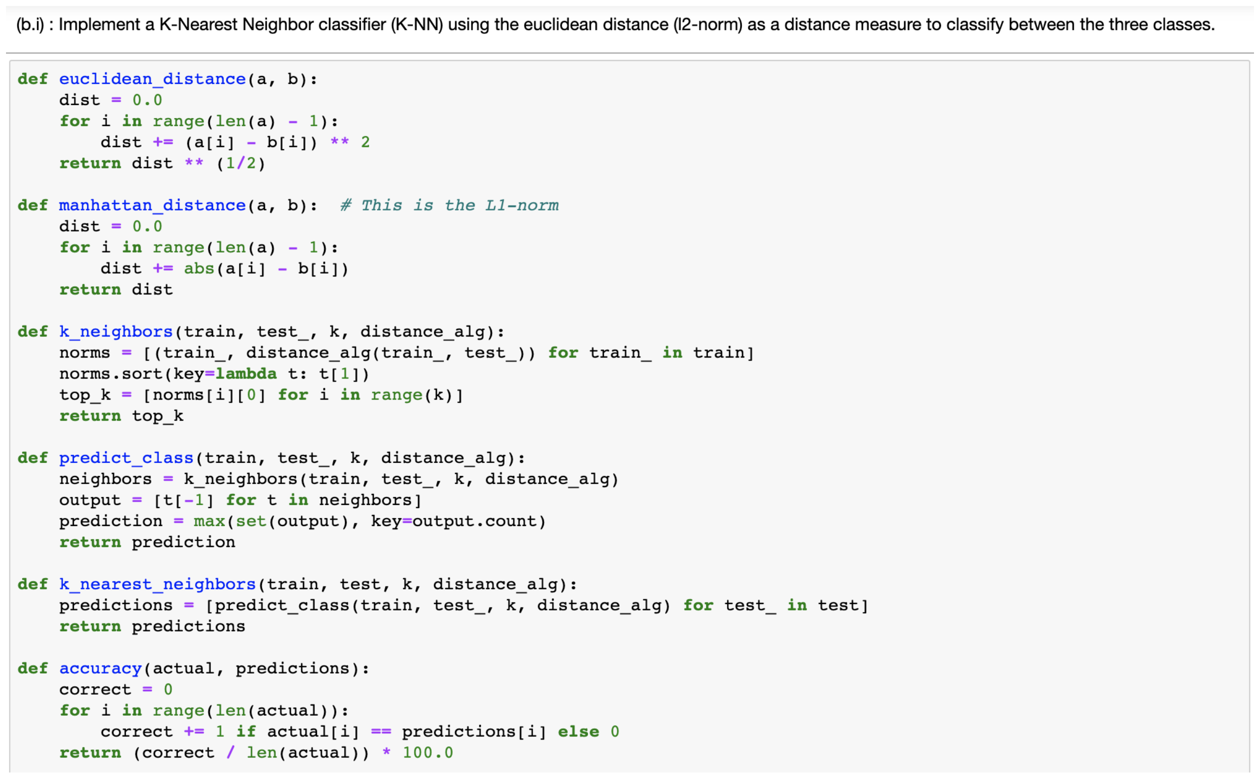


Reflections

From the graphs above, we can see that none of the classes are easily separable. However, the feature combination, Age vs. Lymph Nodes, seems more separable in comparison to the other feature combinations.

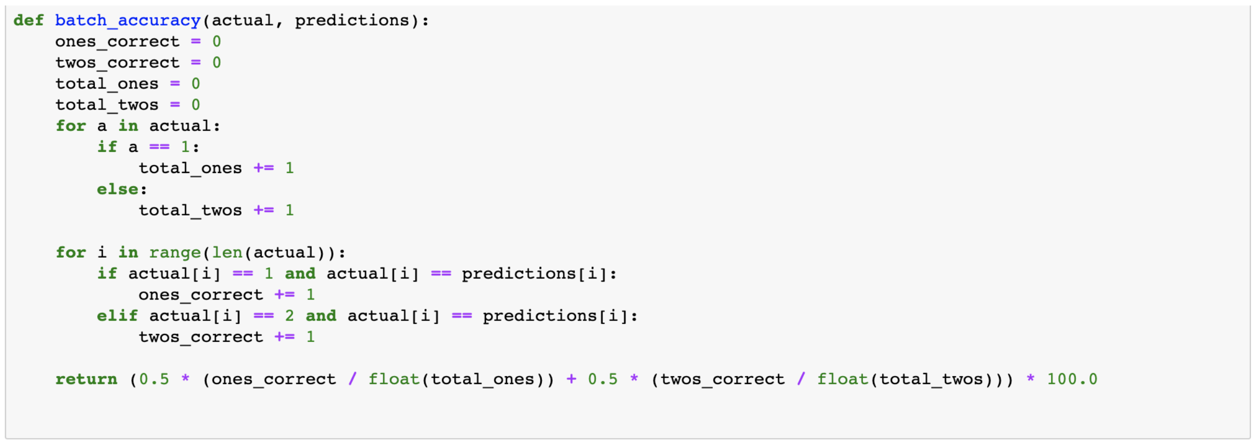
(b.i) Implement a K-Nearest Neighbor classifier (K-NN) using the euclidean distance (l2-norm) as a distance measure to classify between the three classes.

Code



(b.i) : Implement a K-Nearest Neighbor classifier (K-NN) using the euclidean distance (l2-norm) as a distance measure to classify between the three classes.

```python
def euclidean_distance(a, b):
    dist = 0.0
    for i in range(len(a) - 1):
        dist += (a[i] - b[i]) ** 2
    return dist ** (1/2)

def manhattan_distance(a, b):  # This is the L1-norm
    dist = 0.0
    for i in range(len(a) - 1):
        dist += abs(a[i] - b[i])
    return dist

def k_neighbors(train, test_, k, distance_alg):
    norms = [(train_, distance_alg(train_, test_)) for train_ in train]
    norms.sort(key=lambda t: t[1])
    top_k = [norms[i][0] for i in range(k)]
    return top_k

def predict_class(train, test_, k, distance_alg):
    neighbors = k_neighbors(train, test_, k, distance_alg)
    output = [t[-1] for t in neighbors]
    prediction = max(set(output), key=output.count)
    return prediction

def k_nearest_neighbors(train, test, k, distance_alg):
    predictions = [predict_class(train, test_, k, distance_alg) for test_ in test]
    return predictions

def accuracy(actual, predictions):
    correct = 0
    for i in range(len(actual)):
        correct += 1 if actual[i] == predictions[i] else 0
    return (correct / len(actual)) * 100.0
```



```python
def batch_accuracy(actual, predictions):
    ones_correct = 0
    twos_correct = 0
    total_ones = 0
    total_twos = 0
    for a in actual:
        if a == 1:
            total_ones += 1
        else:
            total_twos += 1

    for i in range(len(actual)):
        if actual[i] == 1 and actual[i] == predictions[i]:
            ones_correct += 1
        elif actual[i] == 2 and actual[i] == predictions[i]:
            twos_correct += 1

    return (0.5 * (ones_correct / float(total_ones)) + 0.5 * (twos_correct / float(total_twos))) * 100.0
```

Output

There is no output; this question was just to write out the algorithm for KNN.

(b.ii) Explore different values of K = 1, 3, 5, 7, 9, 11. You will train one model for each of the six values of K using the train data and compute the classification accuracy (ACC) and balanced classification accuracy (BAcc) of the model on the development set. Plot the Acc and BAcc metrics on the dev set against the different values of K. Please report the best hyper-parameter K*based on the ACC metric and the best hyper-parameter Kbased on the BAcc metric. Please implement this procedure, including computing the accuracy metrics, from scratch and do not use available libraries. Hint: Acc = # correctly classified samples / # samples BAcc = 0.5 ·# correctly classified samples from class 1 / # samples from class 1 + 0.5 ·# correctly classified samples from class 2 / # samples from class 2**

Code

(b.ii) Explore different values of K = 1, 3, 5, 7, 9, 11. You will train one model for each of the six values of K using the train data and compute the classification accuracy (Acc) and balanced classification accuract (BAcc) of the model on the development set. Plot the Acc and BAcc metrics on the dev set against the different values of K. Please report the best hyper-parameter K∗based on the Acc metric and the best hyper-parameter K∗∗based on the BAcc metric. Please implement this procedure, including computing the accuracy metrics, from scratch and do not use available libraries. Hint: Acc = # correctly classified samples / # samples BAcc = 0.5 ·# correctly classified samples from class 1 / # samples from class 1 + 0.5 ·# correctly classified samples from class 2 / # samples from class 2

```python
df_dev = pd.read_csv('data_dev.csv')
data_dev = df_dev.to_numpy()

train = data_train
test = data_dev

K = [1, 3, 5, 7, 9, 11]
# k=5 is the best hyper-parameter
for k in K:
    predictions = k_nearest_neighbors(train, test, k, euclidean_distance)
    actual = [row[-1] for row in test]
    print(predictions)
    print(actual)

    acc = accuracy(actual, predictions)
    bacc = batch_accuracy(actual, predictions)
    print('Acc: ' + str(acc) + '%')
    print('B-Acc: ' + str(bacc) + '%')
    print('\n\n')
```

Output

```
[1, 1, 1, 1, 1, 1, 1, 1, 2, 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, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 86.20689655172413%
B-Acc: 48.07692307692308%



[1, 1, 1, 1, 1, 1, 1, 1, 2, 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, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 86.20689655172413%
B-Acc: 48.07692307692308%



[1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
[1, 1, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 89.65517241379311%
B-Acc: 64.74358974358975%



[1, 1, 1, 1, 1, 1, 1, 1, 2, 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, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 86.20689655172413%
B-Acc: 48.07692307692308%



[1, 1, 1, 1, 1, 1, 1, 1, 2, 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, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 86.20689655172413%
B-Acc: 48.07692307692308%



[1, 1, 1, 1, 1, 1, 1, 1, 2, 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, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 86.20689655172413%
B-Acc: 48.07692307692308%
```

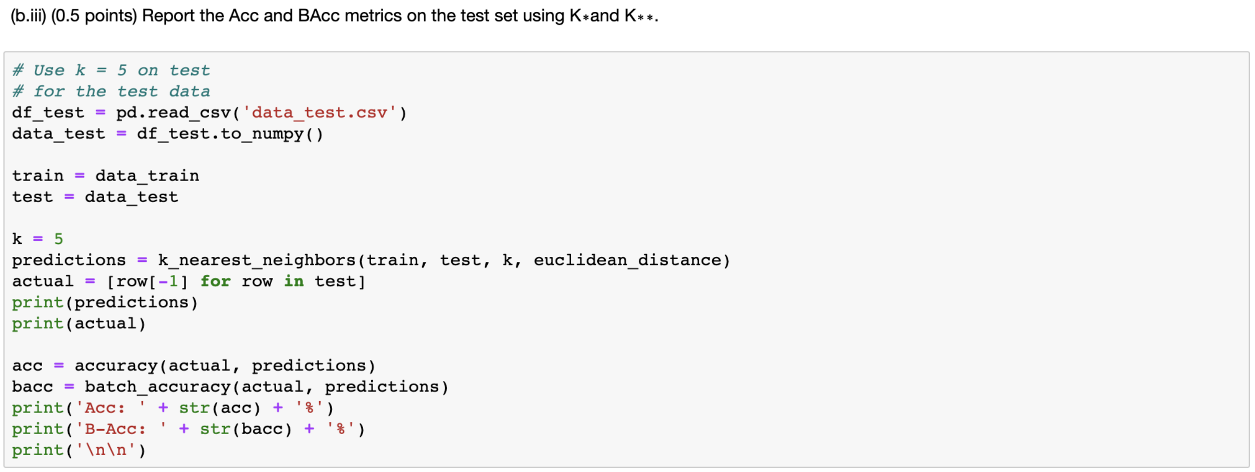
Reflections

From the output above, we can see that the best K was 5, with the ACC of 89.65517 and B-Acc of 64.7535897. The code below utilizes K at 5 to perform on the test data.

(b.iii) (0.5 points) Report the Acc and BAcc metrics on the test set using K*and K**.

Code

K at 5 was performed on the test data.



(b.iii) (0.5 points) Report the Acc and BAcc metrics on the test set using K∗and K∗∗.

```
# Use k = 5 on test
# for the test data
df_test = pd.read_csv('data_test.csv')
data_test = df_test.to_numpy()

train = data_train
test = data_test

k = 5
predictions = k_nearest_neighbors(train, test, k, euclidean_distance)
actual = [row[-1] for row in test]
print(predictions)
print(actual)

acc = accuracy(actual, predictions)
bacc = batch_accuracy(actual, predictions)
print('Acc: ' + str(acc) + '%')
print('B-Acc: ' + str(bacc) + '%')
print('\n\n')
```

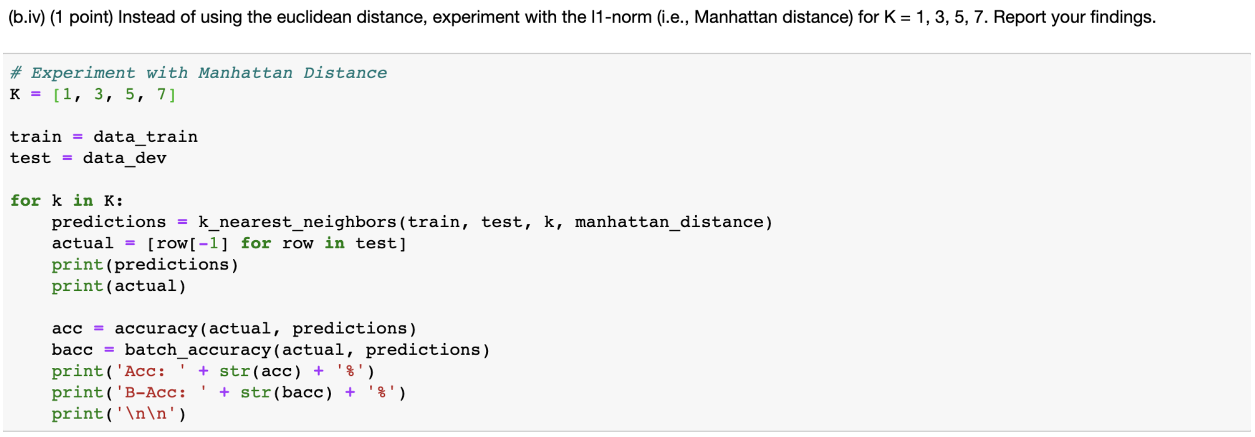
Output

```
[2, 1, 1, 1, 1, 1, 1, 1, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1]
[2, 2, 1, 1, 1, 1, 1, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1]
Acc: 83.33333333333334%
B-Acc: 64.58333333333334%
```

(b.iv) (1 point) Instead of using the euclidean distance, experiment with the l1-norm (i.e., Manhattan distance) for K = 1, 3, 5, 7. Report your findings.

Code

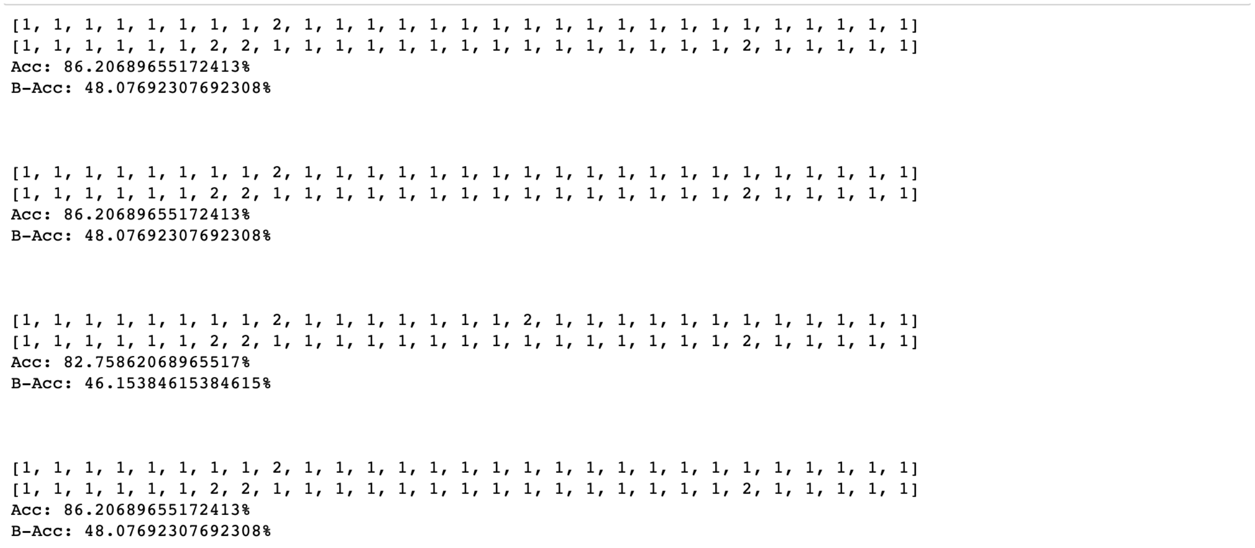
The algorithm for manhattan distance is in the image in part b.i



(b.iv) (1 point) Instead of using the euclidean distance, experiment with the l1-norm (i.e., Manhattan distance) for K = 1, 3, 5, 7. Report your findings.

```python
# Experiment with Manhattan Distance
K = [1, 3, 5, 7]

train = data_train
test = data_dev

for k in K:
    predictions = k_nearest_neighbors(train, test, k, manhattan_distance)
    actual = [row[-1] for row in test]
    print(predictions)
    print(actual)

    acc = accuracy(actual, predictions)
    bacc = batch_accuracy(actual, predictions)
    print('Acc: ' + str(acc) + '%')
    print('B-Acc: ' + str(bacc) + '%')
    print('\n\n')
```

Output



```
[1, 1, 1, 1, 1, 1, 1, 1, 2, 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, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 86.20689655172413%
B-Acc: 48.07692307692308%



[1, 1, 1, 1, 1, 1, 1, 1, 2, 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, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 86.20689655172413%
B-Acc: 48.07692307692308%



[1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1]
[1, 1, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 82.75862068965517%
B-Acc: 46.15384615384615%



[1, 1, 1, 1, 1, 1, 1, 1, 2, 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, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1]
Acc: 86.20689655172413%
B-Acc: 48.07692307692308%
```

Reflections

From the output above, we can see that K at 1, 3, and 7 are all tied. So the code below, I chose K at 1 to perform on the test data.

```python
# k = 1, 5, 7 performed the same
# for the test data
K = [1]

train = data_train
test = data_test

for k in K:
    predictions = k_nearest_neighbors(train, test, k, manhattan_distance)
    actual = [row[-1] for row in test]
    print(predictions)
    print(actual)

    acc = accuracy(actual, predictions)
    bacc = batch_accuracy(actual, predictions)
    print('Acc: ' + str(acc) + '%')
    print('B-Acc: ' + str(bacc) + '%')
    print('\n\n')
```

```
[2, 1, 1, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1]
[2, 2, 1, 1, 1, 1, 1, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1]
Acc: 90.0%
B-Acc: 75.0%
```

(c) ML deployment: Assume that the Memorial Herman Hospital in Houston, TX, is planning to deploy this system over the next months in order to predict patient post-surgery mortality rate. What would be your thoughts/questions/concerns regarding this?
Some questions or concerns regarding the deployment of this system are to consider if the data given is sufficient enough to predict patient post-surgery mortality rate accurately. We also need to consider if the feature provided in the system is enough or if there are more factors that play a role in determining the mortality rate after surgery. There also needs to be more testing done with the system, along with determining its scalability for it to be fully implemented for Memorial Herman.

Question 2: Bonus Survey
Completed