CSC 587 HW 4

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Homework 4

1. Given a data tuple having the values ”systems”, ”26_30”, and ”46K_50K” for the attributes department, age, and salary, respectively, what would a naive Bayesian classification of the status according to the data above? Notice that Count column is NOT an attribute. It just tells how many times a row occurs in our database and status is our target variable.

```
# create a data frame
data = {'department': ['sales', 'sales', 'sales', 'systems', 'systems', 'systems', 'systems', 'marketing

df = pd.DataFrame(data)

# df.head()
print (df)
```

department age salary status count 0 sales 31_35 46K_50K senior 30 1 sales 26_30 26K_30K junior 40 2 sales 31_35 31K_35K junior 40 3 systems 21_25 46K_50K junior 20 4 systems 31_35 66K_70K senior 5 5 systems 26_30 46K_50K junior 3 6 systems 41_45 66K_70K senior 3 7 marketing 36_40 46K_50K senior 10 8 marketing 31_35 41K_45K junior 4 9 secretary 46_50 36K_40K senior 4 10 secretary 26_30 26K_30K junior 6

```
# calculate the probability of each status
sum_total = sum(df['count'])
print("Total:",sum_total)
```

Total: 165

```
senior_total = sum(df['count'][df['status'] == 'senior'])
print("Senior Total:",senior_total)
```

Senior Total: 52

```
junior_total = sum(df['count'][df['status'] == 'junior'])
print("Junior Total:",junior_total)
```

Junior Total: 113

```
PStaus_Senior = (senior_total / sum_total)

print("P(Staus = Senior)",round(PStaus_Senior,2))
```

P(Staus = Senior) 0.32

```
PStaus_Junior = (junior_total / sum_total)

print("P(Staus = Junior)",round(PStaus_Junior,2))
```

P(Staus = Junior) 0.68

```
# calculate the probability of systems department
systems_total = sum(df['count'][df['department'] == 'systems'])
print("Department Total:",systems_total)
```

Department Total: 31

```
PDept_Systems = (systems_total / sum_total)
print("P(Department = Systems)",round(PDept_Systems,2))
```

P(Department = Systems) 0.19

```
# calculate the probability of age 26_30
age_total = sum(df['count'][df['age'] == '26_30'])
print("Age Total:",age_total)
```

Age Total: 49

```
PAge_26_30 = (age_total / sum_total)
print("P(Age = 26_30)",round(PAge_26_30,2))
```

P(Age = 26_30) 0.3

```
# calculate the probability of salary 46K_50K
salary_total = sum(df['count'][df['salary'] == '46K_50K'])
print("Salary Total:",salary_total)
```

Salary Total: 63

```
PSalary_46K_50K = (salary_total / sum_total)
print("P(Salary = 46K_50K)",round(PSalary_46K_50K,2))
```

P(Salary = 46K_50K) 0.38

```
# calculate the probability of status senior given department systems, age 26_30, and salary 46K_50K
PStatus_Senior_x = (PDept_Systems * PAge_26_30 * PSalary_46K_50K * PStaus_Senior)
print("P(Status = Senior | Department = Systems, Age = 26_30, Salary = 46K_50K)",round(PStatus_Senior_x
```

P(Status = Senior | Department = Systems, Age = 26_30, Salary = 46K_50K) 0.01

```
# calculate the probability of status junior given department systems, age 26_30, and salary 46K_50K
PStatus_Junior_x = (PDept_Systems * PAge_26_30 * PSalary_46K_50K * PStaus_Junior)
print("P(Status = Junior | Department = Systems, Age = 26_30, Salary = 46K_50K)",round(PStatus_Junior_x
```

P(Status = Junior | Department = Systems, Age = 26_30, Salary = 46K_50K) 0.01

2. split your diabetes data into two parts for training and testing purposes. Namely, reserve last 10 rows of the diabetes_train.csv for the test set. Then fit a SVM classifier on the bigger portion of this data and test it on these 10 rows you had reserved. Please feel free to modify existing codes. Notice that you're not going to read diabetes_test.csv anymore since you're going to split the bigger data. Please submit your Python code and your prediction results

```
# read the diabetes data
diabetes = pd.read_csv('diabetes_train.csv')

# split the data into training and testing reserves last 10 rows for testing
test = diabetes.iloc[-10:]
train = diabetes.iloc[:-10]

print(test)
```

preg plas pres skin insu mass pedi age class

748 3 187 70 22 200 36.4 0.408 36 tested_positive 749 6 162 62 0 0 24.3 0.178 50 tested_positive 750 4 136 70 0 0 31.2 1.182 22 tested_positive 751 1 121 78 39 74 39.0 0.261 28 tested_negative 752 3 108 62 24 0 26.0 0.223 25 tested_negative 753 0 181 88 44 510 43.3 0.222 26 tested_positive 754 8 154 78 32 0 32.4 0.443 45 tested_positive 755 1 128 88 39 110 36.5 1.057 37 tested_positive 756 7 137 90 41 0 32.0 0.391 39 tested_negative 757 0 123 72 0 0 36.3 0.258 52 tested_positive

```
print(train)
```

preg plas pres skin insu mass pedi age class

0 6 148 72 35 0 33.6 0.627 50 tested_positive 1 1 85 66 29 0 26.6 0.351 31 tested_negative 2 8 183 64 0 0 23.3 0.672 32 tested_positive 3 1 89 66 23 94 28.1 0.167 21 tested_negative 4 0 137 40 35 168 43.1 2.288 33 tested_positive .. .. 743 9 140 94 0 0 32.7 0.734 45 tested_positive 744 13 153 88 37 140 40.6 1.174 39 tested_negative 745 12 100 84 33 105 30.0 0.488 46 tested_negative 746 1 147 94 41 0 49.3 0.358 27 tested_positive 747 1 81 74 41 57 46.3 1.096 32 tested_negative

[748 rows x 9 columns]

```
# fit a SVM classifier
from sklearn import svm
clf = svm.SVC()
clf.fit(train.iloc[:,:-1], train.iloc[:,-1])
```

SVC()

```
# test the classifier
prediction = clf.predict(test.iloc[:,:-1])

# print the prediction results
print("Predicted Results =",prediction)
```

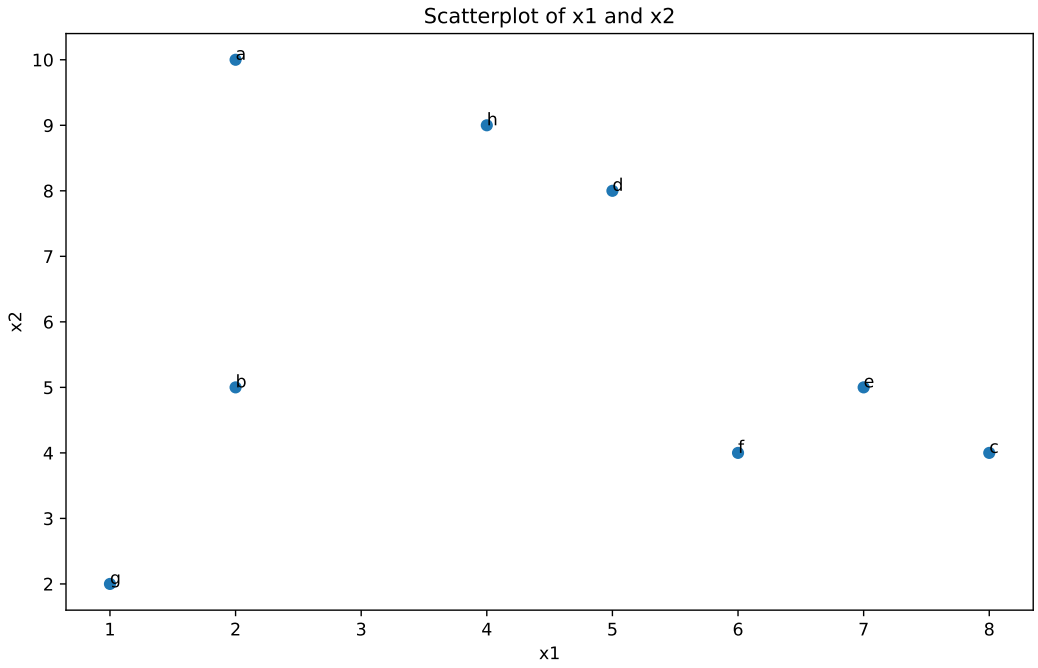
Predicted Results = ['tested_positive' 'tested_positive' 'tested_negative' 'tested_negative' 'tested_negative' 'tested_positive' 'tested_positive' 'tested_negative' 'tested_negative' 'tested_negative']

3.

```
# create a data frame
classes = ['a','b','c','d','e','f','g','h']
data = {'x1': [2, 2, 8, 5, 7, 6, 1, 4],'x2': [10, 5, 4, 8, 5, 4, 2, 9]}
P3_df = pd.DataFrame(data, index=classes)
print(P3_df)
```

x1 x2 a 2 10 b 2 5 c 8 4 d 5 8 e 7 5 f 6 4 g 1 2 h 4 9

```
# build a scatterplot of the df
plt.figure(figsize=(10, 6))
plt.scatter(P3_df['x1'], P3_df['x2'])
plt.xlabel('x1')
plt.ylabel('x2')
plt.title('Scatterplot of x1 and x2')
for i, txt in enumerate(classes):
    plt.annotate(txt, (P3_df['x1'][i], P3_df['x2'][i]))

plt.show()
```



(a) If h and c are selected as the initial centers for your k-means clustering, assign memberships for other points, and compute the means (centroids) of your initial clusters. You can use Manhattan distance.

```
# initial centers
c1 = P3_df.loc['h']
c2 = P3_df.loc['c']
print(c1)
```

x1 4 x2 9 Name: h, dtype: int64

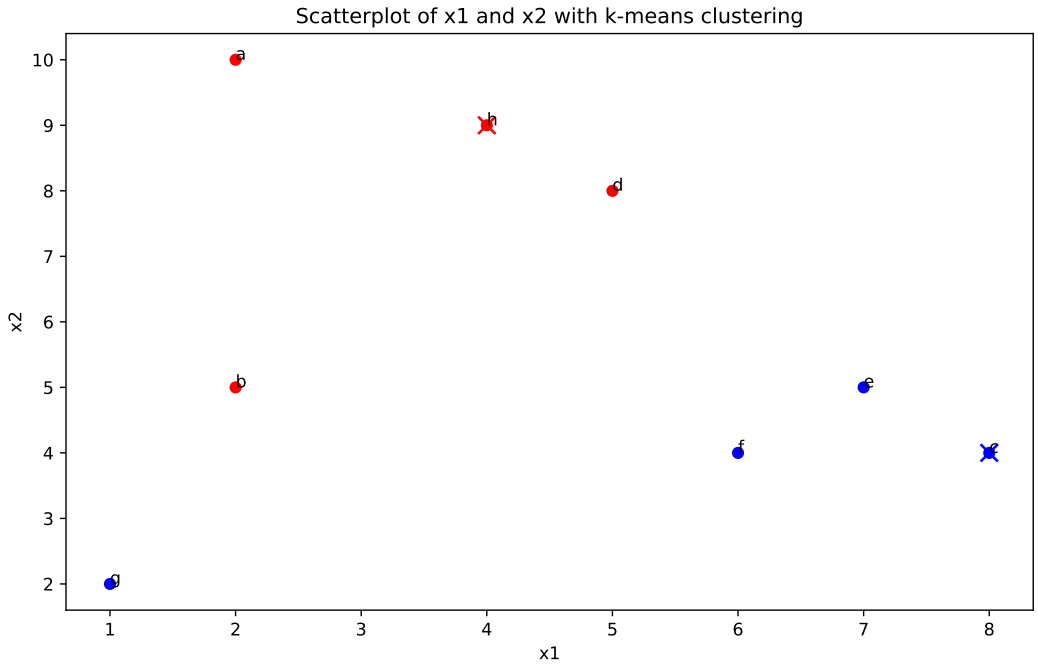
```
print(c2)
```

x1 8 x2 4 Name: c, dtype: int64

```
# assign memberships
P3_df['d_c1'] = np.sqrt((P3_df['x1'] - c1['x1'])**2 + (P3_df['x2'] - c1['x2'])**2)
P3_df['d_c2'] = np.sqrt((P3_df['x1'] - c2['x1'])**2 + (P3_df['x2'] - c2['x2'])**2)
P3_df['mem'] = np.where(P3_df['d_c1'] < P3_df['d_c2'], 'c1', 'c2')

print(P3_df)
```

x1 x2 d_c1 d_c2 mem a 2 10 2.236068 8.485281 c1 b 2 5 4.472136 6.082763 c1 c 8 4 6.403124 0.000000 c2 d 5 8 1.414214 5.000000 c1 e 7 5 5.000000 1.414214 c2 f 6 4 5.385165 2.000000 c2 g 1 2 7.615773 7.280110 c2 h 4 9 0.000000 6.403124 c1

```
# build a visualization of the k-means clustering
plt.figure(figsize=(10, 6))
plt.scatter(P3_df['x1'], P3_df['x2'], c=P3_df['mem'].map({'c1': 'red', 'c2': 'blue'}))
plt.scatter(c1['x1'], c1['x2'], color='red', marker='x', s=100)
plt.scatter(c2['x1'], c2['x2'], color='blue', marker='x', s=100)
plt.xlabel('x1')
plt.ylabel('x2')
plt.title('Scatterplot of x1 and x2 with k-means clustering')
for i, txt in enumerate(classes):
    plt.annotate(txt, (P3_df['x1'][i], P3_df['x2'][i]))

plt.show()
```

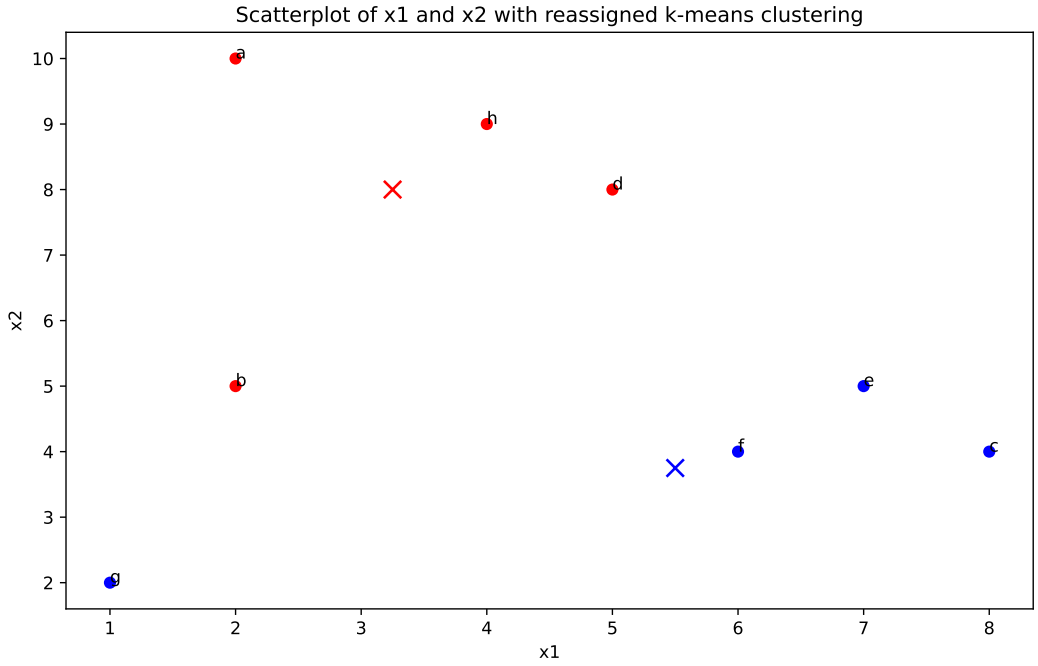


(b) Based on the centroids you found above reassign the memberships by using Manhattan distance

```
# reassign memberships
c1 = P3_df[P3_df['mem'] == 'c1'][['x1', 'x2']].mean()
c2 = P3_df[P3_df['mem'] == 'c2'][['x1', 'x2']].mean()


P3_df['d_c1'] = np.sqrt((P3_df['x1'] - c1['x1'])**2 + (P3_df['x2'] - c1['x2'])**2)
P3_df['d_c2'] = np.sqrt((P3_df['x1'] - c2['x1'])**2 + (P3_df['x2'] - c2['x2'])**2)
P3_df['mem'] = np.where(P3_df['d_c1'] < P3_df['d_c2'], 'c1', 'c2')

print(P3_df)
```

x1 x2 d_c1 d_c2 mem a 2 10 2.358495 7.163274 c1 b 2 5 3.250000 3.716517 c1 c 8 4 6.209871 2.512469 c2 d 5 8 1.750000 4.279311 c1 e 7 5 4.802343 1.952562 c2 f 6 4 4.854122 0.559017 c2 g 1 2 6.408003 4.828302 c2 h 4 9 1.250000 5.460082 c1

```
# build a visualization of the reassigned k-means clustering
plt.figure(figsize=(10, 6))
plt.scatter(P3_df['x1'], P3_df['x2'], c=P3_df['mem'].map({'c1': 'red', 'c2': 'blue'}))
plt.scatter(c1['x1'], c1['x2'], color='red', marker='x', s=100)
plt.scatter(c2['x1'], c2['x2'], color='blue', marker='x', s=100)
plt.xlabel('x1')
plt.ylabel('x2')
plt.title('Scatterplot of x1 and x2 with reassigned k-means clustering')
for i, txt in enumerate(classes):
    plt.annotate(txt, (P3_df['x1'][i], P3_df['x2'][i]))

plt.show()
```



4. Given the distance matrix below answer the following questions. Notice that this is a distance matrix,

meaning the distance between any pair of points can be found by checking the corresponding cell.

```
# create a data frame
classes = ['b','c','d','e','f','g','h']
data = {'a': [5, 8, 4, 7, 7, 8, 2],'b': [0, 6, 4, 5, 4, 3, 4],'c': [0, 0, 5, 1, 2, 7, 6],'d': [0, 0, 0,
P4_df = pd.DataFrame(data, index=classes)
print(P4_df)
```

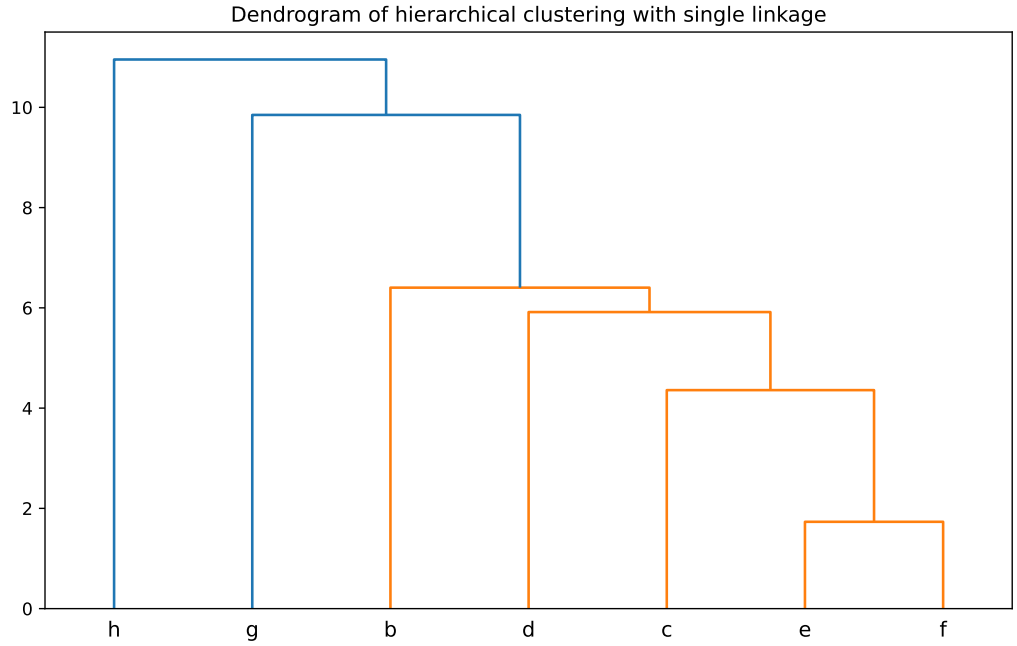
a b c d e f g b 5 0 0 0 0 0 0 c 8 6 0 0 0 0 0 d 4 4 5 0 0 0 0 e 7 5 1 4 0 0 0 f 7 4 2 4 1 0 0 g 8 3 7 7 7 5 0 h 2 4 6 1 5 5 8

(a) Apply the hierarchical clustering algorithm with single linkage to the data above. Draw the final dendrogram.

```
# apply hierarchical clustering with single linkage
from scipy.cluster.hierarchy import linkage, dendrogram
Z = linkage(P4_df, 'single')
plt.figure(figsize=(10, 6))
dendrogram(Z, labels=classes)
```

{'icoord': [[55.0, 55.0, 65.0, 65.0], [45.0, 45.0, 60.0, 60.0], [35.0, 35.0, 52.5, 52.5], [25.0, 25.0, 43.75, 43.75], [15.0, 15.0, 34.375, 34.375], [5.0, 5.0, 24.6875, 24.6875]], 'dcoord': [[0.0, 1.7320508075688772, 1.7320508075688772, 0.0], [0.0, 4.358898943540674, 4.358898943540674, 1.7320508075688772], [0.0, 5.916079783099616, 5.916079783099616, 4.358898943540674], [0.0, 6.4031242374328485, 6.4031242374328485, 5.916079783099616], [0.0, 9.848857801796104, 9.848857801796104, 6.4031242374328485], [0.0, 10.954451150103322, 10.954451150103322, 9.848857801796104]], 'ivl': ['h', 'g', 'b', 'd', 'c', 'e', 'f'], 'leaves': [6, 5, 0, 2, 1, 3, 4], 'color_list': ['C1', 'C1', 'C1', 'C1', 'C0', 'C0'], 'leaves_color_list': ['C0', 'C0', 'C1', 'C1', 'C1', 'C1', 'C1']}

```
plt.title('Dendrogram of hierarchical clustering with single linkage')
plt.show()
```



(b) Determine whether a point is core based on eps = 6 and 'minPts' = 2. (Recall that a point p is a core point if at least 'minPts' points are within distance eps of it (including p).

```
# determine core points
eps = 6
minPts = 2
core_points = []
for i in range(len(P4_df)):
    if sum(P4_df.iloc[i] <= eps) >= minPts:
        core_points.append(classes[i])

print("Core Points:",core_points)
```

Core Points: ['b', 'c', 'd', 'e', 'f', 'g', 'h']