Machine Learning Laboratory

November 2, 2019

1 Find S

Implement and demonstrate the FIND-S algorithm for finding the most specific hypothesis based on a given set of training data samples. Read the training data from a .CSV file.

[1]:
```
import pandas as pd  # Pandas must be installed.Pandas used for reading data␣
 ↪from .csv file.

df = pd.read_csv('Datasets/EnjoySport.csv')
df = df.drop(['slno'], axis=1)
#ensure csv file exists in the same folder as the python code.
column_length = df.shape[1]  #obtain number of columns
df.head()
```

[1]:
```
     sky airTemp humidity    wind water forecast enjoySport
0  sunny    warm   normal  strong  warm     same        yes
1  sunny    warm     high  strong  warm     same        yes
2  rainy    cold     high  strong  warm   change         no
3  sunny    warm     high  strong  cool   change        yes
```

[2]:
```
h = ['0'] * (column_length - 1)
#initialize list hp i.e list of hypotheses for positive training examples
hp = []
hn = []
```

[3]:
```
#this loop is used to build the hypothesis list for every row.
for training_example in df.values:
    #if the trainingExample is positive, then it is appended to hp else to hn
    if training_example[-1] != 'no':
        hp.append(list(training_example))
    else:
        hn.append(list(training_example))
```

[4]:
```
#update the hypothesis h from most specific to maximally specific
for i in range(len(hp)):
    #if the hypothesis attribute value is 0, it is updated to the attributes in␣
 ↪the first hypothesis
    for j in range(column_length - 1):
        if (h[j] == '0'):
```

```
            h[j] = hp[i][j]
        #if the attribute value in the hypothesis is not same as the attribute␣
↪value in the successive hypotheses
        if (h[j] != hp[i][j]):
            #then it is updated to '?' indicating that any value is acceptable.
            h[j] = '?'
        #if the attribute in the hypothesis is the same as the attribute value␣
↪in the successive hypotheses
        else:
            #then the same attribute value is retained
            h[j] = hp[i][j]
```

[5]:
```
print(f'Positive Hypotheses:\n{hp}')
print(f'Negative Hypotheses:\n{hn}')
print(f'Maximally Specific Hypothesis:\n{h}')
```

```
Positive Hypotheses:
[['sunny', 'warm', 'normal', 'strong', 'warm', 'same', 'yes'], ['sunny', 'warm',
'high', 'strong', 'warm', 'same', 'yes'], ['sunny', 'warm', 'high', 'strong',
'cool', 'change', 'yes']]
Negative Hypotheses:
[['rainy', 'cold', 'high', 'strong', 'warm', 'change', 'no']]
Maximally Specific Hypothesis:
['sunny', 'warm', '?', 'strong', '?', '?']
```

2 Candidate Elimination

For a given set of training data examples stored in a .CSV file, implement and demonstrate the Candidate-Elimination algorithm to output a description of the set of all hypotheses consistent with the training examples.

[6]:
```
import pandas as pd

df = pd.read_csv('Datasets/EnjoySport.csv')
df = df.drop(['slno'], axis=1)
concepts = df.values[:, :-1]
target = df.values[:, -1]
df.head()
```

[6]:

	sky	airTemp	humidity	wind	water	forecast	enjoySport
0	sunny	warm	normal	strong	warm	same	yes
1	sunny	warm	high	strong	warm	same	yes
2	rainy	cold	high	strong	warm	change	no
3	sunny	warm	high	strong	cool	change	yes

[7]:
```
def learn(concepts, target):
    specific_h = concepts[0].copy()
    general_h = [["?" for i in range(len(specific_h))]
                 for i in range(len(specific_h))]
```

```
    for i, h in enumerate(concepts):
        if target[i] == "yes":
            for x in range(len(specific_h)):
                if h[x] != specific_h[x]:
                    specific_h[x] = '?'
                    general_h[x][x] = '?'
        if target[i] == "no":
            for x in range(len(specific_h)):
                if h[x] != specific_h[x]:
                    general_h[x][x] = specific_h[x]
                else:
                    general_h[x][x] = '?'
    indices = [
        i for i, val in enumerate(general_h)
        if val == ['?', '?', '?', '?', '?', '?']
    ]
    for i in indices:
        general_h.remove(['?', '?', '?', '?', '?', '?'])
    return specific_h, general_h
```

[8]:
```
s_final, g_final = learn(concepts, target)
print(f"Final S: {s_final}")
print(f"Final G: {g_final}")
```

```
Final S: ['sunny' 'warm' '?' 'strong' '?' '?']
Final G: [['sunny', '?', '?', '?', '?', '?'], ['?', 'warm', '?', '?', '?', '?']]
```

3 Decision Tree based on ID3

Write a program to demonstrate the working of the decision tree based ID3 algorithm. Use an appropriate data set for building the decision tree and apply this knowledge to classify a new sample.

[9]:
```
def infoGain(P, N):  #Claculate Information gain or Class entropy
    import math
    return -P / (P + N) * math.log2(P / (P + N)) - N / (P + N) * math.log2(N /␣
 ↪(P + N))
```

[10]:
```
def insertNode(tree, addTo, Node):
    for k, v in tree.items():  #Traversal of tree
        if isinstance(v, dict):
            tree[k] = insertNode(v, addTo, Node)
    if addTo in tree:  #If d is found then add Node
        if isinstance(tree[addTo], dict):
            tree[addTo][Node] = 'None'
        else:
            tree[addTo] = {Node: 'None'}
    return tree
```

[11]:
```
def insertConcept(tree, addTo, Node):
    for k, v in tree.items():  #Traversal of tree
        if isinstance(v, dict):
            tree[k] = insertConcept(v, addTo, Node)
    if addTo in tree:  #If d is found then add Node
        tree[addTo] = Node
    return tree
```

[12]:
```
def getNextNode(data, AttributeList, concept, conceptVals, tree, addTo):
    Total = data.shape[0]
    if Total == 0:  #If Attibutes are empty, then return current value of tree
        return tree

    countC = {}
    #If Example is positive then return positive and If negative then return␣
↪negative
    for cVal in conceptVals:
        #Get data for specific concept
        dataCC = data[data[concept] == cVal]

        #Get the count of data for specific concept
        countC[cVal] = dataCC.shape[0]

    #If all examples are Positive(Not Negative), return single node Positive
    if countC[conceptVals[0]] == 0:
        tree = insertConcept(tree, addTo, conceptVals[1])
        return tree
    #If all examples are Negative (Not Positive), return single node Negative
    if countC[conceptVals[1]] == 0:
        tree = insertConcept(tree, addTo, conceptVals[0])
        return tree

    #Calculate Class Entropy for data
    ClassEntropy = infoGain(countC[conceptVals[0]], countC[conceptVals[1]])

    #Attribute dict holding list of possible values
    Attr = {}
    for a in AttributeList:
        Attr[a] = list(set(data[a]))

    AttrCount = {}  #Get the attribute values being positive and negative
    EntropyAttr = {}  #Attribute Entropy
    for att in Attr:
        for vals in Attr[att]:
            for c in conceptVals:
                #Get data for specific attribute
                iData = data[data[att] == vals]
```

```
                #Get data for specific attribute and concept
                dataAtt = iData[iData[concept] == c]

                #Get the count of data for specific attribute and concept
                AttrCount[c] = dataAtt.shape[0]

            #Total Attribute
            TotalInfo = AttrCount[conceptVals[0]] + AttrCount[conceptVals[1]]

            if AttrCount[conceptVals[0]] == 0 or AttrCount[conceptVals[1]] == 0:
                InfoGain = 0
            else:
                #Calculate InfoGain for each  attr
                InfoGain = infoGain(AttrCount[conceptVals[0]],␣
↪AttrCount[conceptVals[1]])

            #Calculate Entropy for each attr
            if att not in EntropyAttr:
                EntropyAttr[att] = (TotalInfo / Total) * InfoGain
            else:
                EntropyAttr[att] = EntropyAttr[att] + (TotalInfo / Total) *␣
↪InfoGain

    Gain = {}
    for g in EntropyAttr:
        #Calculate gain
        Gain[g] = ClassEntropy - EntropyAttr[g]

    #Get root node
    Node = max(Gain, key=Gain.get)

    #Add Node to tree
    tree = insertNode(tree, addTo, Node)
    for nD in Attr[Node]:
        #Insert Attribute value to tree
        tree = insertNode(tree, Node, nD)

        #Get new data with Attribute value nD and removing rows with column␣
↪value Node
        newData = data[data[Node] == nD].drop(Node, axis=1)

        #New Attribute List
        AttributeList = list(newData)[:-1]

        #Call the function recursively
```

```
        tree = getNextNode(newData, AttributeList, concept, conceptVals, tree,␣
↪nD)
    return tree
```

[13]:
```
import pandas as pd


def main():
    data = pd.read_csv('Datasets/PlayTennis.csv')  #Read CSV
    if 'Unnamed: 0' in data.columns:
        data = data.drop('Unnamed: 0', axis=1)


#     data = data.drop('slno', axis=1)
    AttributeList = list(data)[:-1]  #Get Attribute List
    concept = str(list(data)[-1])  #Get concept list
    conceptVals = list(set(data[concept]))  #Get Concept values
    tree = getNextNode(data, AttributeList, concept, conceptVals,
                       {'root': 'None'}, 'root')
    return tree  #Call recursive function with initial value of tree and Node␣
↪as root
```

[14]:
```
tree = main()['root']
```

[15]:
```
df = pd.read_csv('Datasets/PlayTennis.csv')


def test(tree, d):
    for k in tree:
        for v in tree[k]:
            if (d[k] == v and isinstance(tree[k][v], dict)):
                test(tree[k][v], d)
            elif (d[k] == v):
                print("Classification: " + tree[k][v])
```

[16]:
```
if 'Unnamed: 0' in df.columns:
    df = df.drop('Unnamed: 0', axis=1)
df.head()
```

[16]:

	Outlook	Temperature	Humidity	Wind	PlayTennis
0	Sunny	Hot	High	Weak	No
1	Sunny	Hot	High	Strong	No
2	Overcast	Hot	High	Weak	Yes
3	Rain	Mild	High	Weak	Yes
4	Rain	Cool	Normal	Weak	Yes

[17]:
```
print(tree)
```

```
{'Outlook': {'Sunny': {'Humidity': {'Normal': 'Yes', 'High': 'No'}}, 'Rain':
{'Wind': {'Strong': 'No', 'Weak': 'Yes'}}, 'Overcast': 'Yes'}}
```

[18]:
```
test(tree, df.loc[0, :])
```

```
Classification: No
```

4 Neural Network with Backpropogation Algorithm

Build an Artificial Neural Network by implementing the Backpropagation algorithm and test the same using appropriate data sets.

[19]:
```
import numpy as np

X = np.array(([2, 9], [1, 5], [3, 6]), dtype=float)
y = np.array(([92], [86], [89]), dtype=float)
X = X / np.amax(X, axis=0)
y = y / 100
```

[20]:
```
def sigmoid(x):
    return 1 / (1 + np.exp(-x))



def derivatives_sigmoid(x):
    return x * (1 - x)
```

[21]:
```
epoch = 1000  #number of iterations
learning_rate = 0.6  #learning rate eta
inputlayer_neurons = 2  #number of neurons in input layer
hiddenlayer_neurons = 3  #number of neurons in hidden layer
output_neurons = 1  #number of neurons in output layer
```

[22]:
```
wh = np.random.uniform(size=(inputlayer_neurons, hiddenlayer_neurons)) ␣
 ↪#wh=hidden layer weights
bh = np.random.uniform(size=(1, hiddenlayer_neurons))  #bh=hidden layer bias
wo = np.random.uniform(size=(hiddenlayer_neurons, output_neurons))  #wo=output␣
 ↪layer weights
bo = np.random.uniform(size=(1, output_neurons))  #bo=output layer bias
```

[23]:
```
for i in range(epoch):
    #Forward Propogation
    net_h = np.dot(X, wh) + bh  #net_h=net input for hidden layer
    sigma_h = sigmoid(net_h)  #sigma_h=output of sigmoid function of hidden␣
 ↪layer
    net_o = np.dot(sigma_h, wo) + bo  #net_o=net input for output layer
    output = sigmoid(net_o)  #output= is the output of output layer i.e sigmoid␣
 ↪of net_o

    #Backpropagation
    deltaK = (y - output) * derivatives_sigmoid(output)  ##calculate deltak
    deltaH = deltaK.dot(wo.T) * derivatives_sigmoid(sigma_h)  #deltaH
```

```
    wo = wo + sigma_h.T.dot(deltaK) * learning_rate  #Update output layer␣
↪weights
    wh = wh + X.T.dot(deltaH) * learning_rate  #Update hidden layer weights
```

[24]:
```
print("Input: \n" + str(X))
print("Actual Output: \n" + str(y))
print("Predicted Output: \n", output)
```

```
Input:
[[0.66666667 1.        ]
 [0.33333333 0.55555556]
 [1.         0.66666667]]
Actual Output:
[[0.92]
 [0.86]
 [0.89]]
Predicted Output:
 [[0.89475654]
 [0.88220315]
 [0.89303989]]
```

5 Naive Bayes Classifier from Scratch

Write a program to implement the naïve Bayesian classifier for a sample training data set stored as a .CSV file. Compute the accuracy of the classifier, considering few test data sets.

[25]:
```
def probAttr(data, attr, val):
    Total = data.shape[0]  #Get column length
    cnt = len(data[data[attr] == val])  #Count of Attribute [attr] equal to val
    return cnt, cnt / Total
```

[26]:
```
def train(data, Attr, conceptVals, concept):
    conceptProbs = {}  #P(A)
    countConcept = {}

    #Get probablity and count of Yes and No
    for cVal in conceptVals:
        countConcept[cVal], conceptProbs[cVal] = probAttr(data, concept, cVal)

    #P(X/A)
    AttrConcept = {}

    #P(X)
    probability_list = {}

    #Create a tree for attribute
    for att in Attr:
        probability_list[att] = {}
```

```
        AttrConcept[att] = {}

        #Create Tree for Attribute value
        for val in Attr[att]:
            AttrConcept[att][val] = {}

            #Get Probablity for att equal to val
            a, probability_list[att][val] = probAttr(data, att, val)

            #Create Tree to hold yes and no values
            for cVal in conceptVals:

                #Calculate att equal to val and concept equal to cVal
                dataTemp = data[data[att] == val]

                AttrConcept[att][val][cVal] = len(dataTemp[dataTemp[concept] ==␣
↪cVal])/countConcept[cVal]

    print("P(A) : ", conceptProbs, "\n")
    print("P(X/A) : ", AttrConcept, "\n")
    print("P(X) : ", probability_list, "\n")
    return conceptProbs, AttrConcept, probability_list
```

[27]:
```
def test(examples, Attr, concept_list, conceptProbs, AttrConcept,
         probability_list):
    misclassification_count = 0

    #Get Number of testing set
    Total = len(examples)
    for ex in examples:

        #Dict to hold final value
        px = {}

        #Iterrate thorugh the Tree with Attributes (Refer problem to find the␣
↪tree)
        for a in Attr:

            #Iterrate thorugh the Tree for given example
            for x in ex:

                #Iterrate thorugh the Tree using concepts
                for c in concept_list:

                    #Check if the value of x refering in same sub-tree of P(X/
↪A)
                    if x in AttrConcept[a]:
```

```
                        #If c not in px multiply P(A) with 1st Itteration (for␣
↪1st value of x)
                        if c not in px:
                            px[c] = conceptProbs[c] * AttrConcept[a][x][c] /␣
↪probability_list[a][x]

                        #multiply px in next Itterations (for next values of x)
                        else:
                            px[c] = px[c] * AttrConcept[a][x][c] /␣
↪probability_list[a][x]
        print(px)

        #Key of Maximum of px is required Classification
        classification = max(px, key=px.get)
        print("Classification :", classification, "Expected :", ex[-1])
        if (classification != ex[-1]):
            misclassification_count += 1
    misclassification_rate = misclassification_count * 100 / Total
    accuracy = 100 - misclassification_rate
    print("Misclassification Count={}".format(misclassification_count))
    print("Misclassification Rate={}%".format(misclassification_rate))
    print("Accuracy={}%".format(accuracy))
```

[28]:
```
def main():
    import pandas as pd
    data = pd.read_csv('Datasets/PlayTennis.csv')
    data.drop(['Unnamed: 0'], axis=1, inplace=True)
    print(data)
    concept = str(list(data)[-1])
    print(concept)
    concept_list = set(data[concept])
    print(concept_list)
    Attr = {}
    for a in list(data)[:-1]:  #Get attribute values
        Attr[a] = set(data[a])
        print(Attr[a])
    conceptProbs, AttrConcept, probability_list = train(
        data, Attr, concept_list, concept)

    examples = pd.read_csv('Datasets/PlayTennis.csv')
    #print(examples)
    test(examples.values, Attr, concept_list, conceptProbs, AttrConcept,
         probability_list)
```

[29]:
```
main()
```

```
     Outlook Temperature Humidity    Wind PlayTennis
0      Sunny         Hot     High    Weak         No
1      Sunny         Hot     High  Strong         No
2   Overcast         Hot     High    Weak        Yes
3       Rain        Mild     High    Weak        Yes
4       Rain        Cool   Normal    Weak        Yes
5       Rain        Cool   Normal  Strong         No
6   Overcast        Cool   Normal  Strong        Yes
7      Sunny        Mild     High    Weak         No
8      Sunny        Cool   Normal    Weak        Yes
9       Rain        Mild   Normal    Weak        Yes
10     Sunny        Mild   Normal  Strong        Yes
11  Overcast        Mild     High  Strong        Yes
12  Overcast         Hot   Normal    Weak        Yes
13      Rain        Mild     High  Strong         No
PlayTennis
{'Yes', 'No'}
{'Sunny', 'Rain', 'Overcast'}
{'Hot', 'Cool', 'Mild'}
{'Normal', 'High'}
{'Strong', 'Weak'}
P(A) :  {'Yes': 0.6428571428571429, 'No': 0.35714285714285715}

P(X/A) :  {'Outlook': {'Sunny': {'Yes': 0.2222222222222222, 'No': 0.6}, 'Rain':
{'Yes': 0.3333333333333333, 'No': 0.4}, 'Overcast': {'Yes': 0.4444444444444444,
'No': 0.0}}, 'Temperature': {'Hot': {'Yes': 0.2222222222222222, 'No': 0.4},
'Cool': {'Yes': 0.3333333333333333, 'No': 0.2}, 'Mild': {'Yes':
0.4444444444444444, 'No': 0.4}}, 'Humidity': {'Normal': {'Yes':
0.6666666666666666, 'No': 0.2}, 'High': {'Yes': 0.3333333333333333, 'No': 0.8}},
'Wind': {'Strong': {'Yes': 0.3333333333333333, 'No': 0.6}, 'Weak': {'Yes':
0.6666666666666666, 'No': 0.4}}}

P(X) :  {'Outlook': {'Sunny': 0.35714285714285715, 'Rain': 0.35714285714285715,
'Overcast': 0.2857142857142857}, 'Temperature': {'Hot': 0.2857142857142857,
'Cool': 0.2857142857142857, 'Mild': 0.42857142857142855}, 'Humidity': {'Normal':
0.5, 'High': 0.5}, 'Wind': {'Strong': 0.42857142857142855, 'Weak':
0.5714285714285714}}

{'Yes': 0.2419753086419753, 'No': 0.9408000000000002}
Classification : No Expected : No
{'Yes': 0.16131687242798354, 'No': 1.8816000000000002}
Classification : No Expected : No
{'Yes': 0.6049382716049383, 'No': 0.0}
Classification : Yes Expected : Yes
{'Yes': 0.4839506172839506, 'No': 0.41813333333333335}
Classification : Yes Expected : Yes
{'Yes': 1.0888888888888888, 'No': 0.07840000000000004}
Classification : Yes Expected : Yes
```

```
{'Yes': 0.7259259259259259, 'No': 0.15680000000000005}
Classification : Yes Expected : No
{'Yes': 1.2098765432098766, 'No': 0.0}
Classification : Yes Expected : Yes
{'Yes': 0.3226337448559671, 'No': 0.6272000000000001}
Classification : No Expected : No
{'Yes': 0.7259259259259256, 'No': 0.11760000000000002}
Classification : Yes Expected : Yes
{'Yes': 0.9679012345679012, 'No': 0.10453333333333338}
Classification : Yes Expected : Yes
{'Yes': 0.43017832647462273, 'No': 0.31360000000000005}
Classification : Yes Expected : Yes
{'Yes': 0.5377229080932785, 'No': 0.0}
Classification : Yes Expected : Yes
{'Yes': 1.2098765432098766, 'No': 0.0}
Classification : Yes Expected : Yes
{'Yes': 0.3226337448559671, 'No': 0.8362666666666669}
Classification : No Expected : No
Misclassification Count=1
Misclassification Rate=7.142857142857143%
Accuracy=92.85714285714286%
```

6 Naive Bayes Classifer using an API

Assuming a set of documents that need to be classified, use the naïve Bayesian Classifier model to perform this task. Built-in Java classes/API can be used to write the program. Calculate the accuracy, precision, and recall for your data set.

[30]:
```python
import pandas as pd

msg = pd.read_csv('Datasets/document.csv', names=['message', 'label'])
print("Total Instances of Dataset: ", msg.shape[0])
msg['labelnum'] = msg.label.map({'pos': 1, 'neg': 0})
```

```
Total Instances of Dataset:  18
```

[31]:
```python
X = msg.message
y = msg.labelnum
from sklearn.feature_extraction.text import CountVectorizer
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y)
count_v = CountVectorizer()
X_train_dm = count_v.fit_transform(X_train)
X_test_dm = count_v.transform(X_test)
```

[32]:
```python
df = pd.DataFrame(X_train_dm.toarray(), columns=count_v.get_feature_names())
# df[0:5]
```

[33]:
```
from sklearn.naive_bayes import MultinomialNB

clf = MultinomialNB()
clf.fit(X_train_dm, y_train)
pred = clf.predict(X_test_dm)
for doc, p in zip(X_train, pred):
    p = 'pos' if p == 1 else 'neg'
    print(f"{doc} -> {p}")
```

```
He is my sworn enemy -> pos
We will have good fun tomorrow -> pos
My boss is horrible -> neg
I feel very good about these beers -> pos
What a great holiday -> neg
```

[34]:
```
from sklearn.metrics import (accuracy_score, confusion_matrix, precision_score,
                             recall_score)

print('Accuracy Metrics: \n')
print('Accuracy: ', accuracy_score(y_test, pred))
print('Recall: ', recall_score(y_test, pred))
print('Precision: ', precision_score(y_test, pred))
print('Confusion Matrix: \n', confusion_matrix(y_test, pred))
```

```
Accuracy Metrics:

Accuracy:  0.8
Recall:  1.0
Precision:  0.6666666666666666
Confusion Matrix:
 [[2 1]
 [0 2]]
```

7 Bayesian Network using an API

Write a program to construct a Bayesian network considering medical data. Use this model to demonstrate the diagnosis of heart patients using standard Heart Disease Data Set. You can use Java/Python ML library classes/API.

[35]:
```
from pgmpy.models import BayesianModel

cancer_model = BayesianModel([('Pollution', 'Cancer'), ('Smoker', 'Cancer'),
                              ('Cancer', 'Xray'), ('Cancer', 'Dyspnoea')])
```

[36]:
```
print(cancer_model)
```

[37]:
```
cancer_model.nodes()
```

[37]:
```
NodeView(('Pollution', 'Cancer', 'Smoker', 'Xray', 'Dyspnoea'))
```

[38]:
```
cancer_model.edges()
```

[38]:
```
OutEdgeView([('Pollution', 'Cancer'), ('Cancer', 'Xray'), ('Cancer',
'Dyspnoea'), ('Smoker', 'Cancer')])
```

[39]:
```
cancer_model.get_cpds()
```

[39]:
```
[]
```

[40]:
```
from pgmpy.factors.discrete import TabularCPD

cpd_poll = TabularCPD(variable='Pollution',
                      variable_card=2,
                      values=[[0.9], [0.1]])
cpd_smoke = TabularCPD(variable='Smoker',
                       variable_card=2,
                       values=[[0.3], [0.7]])
cpd_cancer = TabularCPD(variable='Cancer',
                        variable_card=2,
                        values=[[0.03, 0.05, 0.001, 0.02],
                                [0.97, 0.95, 0.999, 0.98]],
                        evidence=['Smoker', 'Pollution'],
                        evidence_card=[2, 2])
cpd_xray = TabularCPD(variable='Xray',
                      variable_card=2,
                      values=[[0.9, 0.2], [0.1, 0.8]],
                      evidence=['Cancer'],
                      evidence_card=[2])
cpd_dysp = TabularCPD(variable='Dyspnoea',
                      variable_card=2,
                      values=[[0.65, 0.3], [0.35, 0.7]],
                      evidence=['Cancer'],
                      evidence_card=[2])
```

[41]:
```
# Associating the parameters with the model structure.
cancer_model.add_cpds(cpd_poll, cpd_smoke, cpd_cancer, cpd_xray, cpd_dysp)
# Checking if the cpds are valid for the model.
cancer_model.check_model()
```

[41]:
```
True
```

[42]:
```
cancer_model.get_cpds()
```

[42]:
```
[<TabularCPD representing P(Pollution:2) at 0x7ff9d085fa10>,
 <TabularCPD representing P(Smoker:2) at 0x7ff9d085fa50>,
 <TabularCPD representing P(Cancer:2 | Smoker:2, Pollution:2) at
0x7ff9d085fa90>,
 <TabularCPD representing P(Xray:2 | Cancer:2) at 0x7ff9d085f9d0>,
```

```
<TabularCPD representing P(Dyspnoea:2 | Cancer:2) at 0x7ff9d085f990>]
```

[43]:
```python
print(cancer_model.get_cpds('Pollution'))
print(cancer_model.get_cpds('Smoker'))
print(cancer_model.get_cpds('Xray'))
print(cancer_model.get_cpds('Dyspnoea'))
print(cancer_model.get_cpds('Cancer'))
```

```
+-------------+-----+
| Pollution_0 | 0.9 |
+-------------+-----+
| Pollution_1 | 0.1 |
+-------------+-----+
+----------+-----+
| Smoker_0 | 0.3 |
+----------+-----+
| Smoker_1 | 0.7 |
+----------+-----+
+--------+----------+----------+
| Cancer | Cancer_0 | Cancer_1 |
+--------+----------+----------+
| Xray_0 | 0.9      | 0.2      |
+--------+----------+----------+
| Xray_1 | 0.1      | 0.8      |
+--------+----------+----------+
+------------+----------+----------+
| Cancer     | Cancer_0 | Cancer_1 |
+------------+----------+----------+
| Dyspnoea_0 | 0.65     | 0.3      |
+------------+----------+----------+
| Dyspnoea_1 | 0.35     | 0.7      |
+------------+----------+----------+
+-----------+-------------+-------------+-------------+-------------+
| Smoker    | Smoker_0    | Smoker_0    | Smoker_1    | Smoker_1    |
+-----------+-------------+-------------+-------------+-------------+
| Pollution | Pollution_0 | Pollution_1 | Pollution_0 | Pollution_1 |
+-----------+-------------+-------------+-------------+-------------+
| Cancer_0  | 0.03        | 0.05        | 0.001       | 0.02        |
+-----------+-------------+-------------+-------------+-------------+
| Cancer_1  | 0.97        | 0.95        | 0.999       | 0.98        |
+-----------+-------------+-------------+-------------+-------------+
```

[44]:
```python
cancer_model.local_independencies('Xray')
cancer_model.local_independencies('Pollution')
cancer_model.local_independencies('Smoker')
cancer_model.local_independencies('Dyspnoea')
cancer_model.local_independencies('Cancer')
```

[44]: (Cancer _|_ Dyspnoea, Xray | Smoker, Pollution)

[45]:
```
cancer_model.get_independencies()
```

[45]:
```
(Pollution _|_ Smoker)
(Pollution _|_ Dyspnoea, Xray | Cancer)
(Pollution _|_ Xray | Dyspnoea, Cancer)
(Pollution _|_ Dyspnoea, Xray | Cancer, Smoker)
(Pollution _|_ Dyspnoea | Cancer, Xray)
(Pollution _|_ Xray | Dyspnoea, Cancer, Smoker)
(Pollution _|_ Dyspnoea | Cancer, Xray, Smoker)
(Smoker _|_ Pollution)
(Smoker _|_ Dyspnoea, Xray | Cancer)
(Smoker _|_ Xray | Dyspnoea, Cancer)
(Smoker _|_ Dyspnoea | Cancer, Xray)
(Smoker _|_ Dyspnoea, Xray | Cancer, Pollution)
(Smoker _|_ Xray | Dyspnoea, Cancer, Pollution)
(Smoker _|_ Dyspnoea | Cancer, Xray, Pollution)
(Xray _|_ Dyspnoea, Smoker, Pollution | Cancer)
(Xray _|_ Smoker, Pollution | Dyspnoea, Cancer)
(Xray _|_ Dyspnoea, Pollution | Cancer, Smoker)
(Xray _|_ Dyspnoea, Smoker | Cancer, Pollution)
(Xray _|_ Pollution | Dyspnoea, Cancer, Smoker)
(Xray _|_ Smoker | Dyspnoea, Cancer, Pollution)
(Xray _|_ Dyspnoea | Cancer, Pollution, Smoker)
(Dyspnoea _|_ Smoker, Xray, Pollution | Cancer)
(Dyspnoea _|_ Xray, Pollution | Cancer, Smoker)
(Dyspnoea _|_ Smoker, Pollution | Cancer, Xray)
(Dyspnoea _|_ Smoker, Xray | Cancer, Pollution)
(Dyspnoea _|_ Pollution | Cancer, Xray, Smoker)
(Dyspnoea _|_ Xray | Cancer, Pollution, Smoker)
(Dyspnoea _|_ Smoker | Cancer, Xray, Pollution)
```

[46]:
```python
# Doing exact inference using Variable Elimination
from pgmpy.inference import VariableElimination

cancer_infer = VariableElimination(cancer_model)
```

[71]:
```python
# Computing the probability of bronc given smoke.
q = cancer_infer.query(variables=['Cancer'], evidence={'Smoker': 1})
print(q['Cancer'])
```

```
+----------+---------------+
| Cancer   |   phi(Cancer) |
+==========+===============+
| Cancer_0 |        0.0029 |
+----------+---------------+
| Cancer_1 |        0.9971 |
+----------+---------------+
```

[48]:
```
# Computing the probability of bronc given smoke.
q = cancer_infer.query(variables=['Cancer'],
                       evidence={
                           'Smoker': 1,
                           'Pollution': 1
                       })
print(q['Cancer'])
```

```
+----------+---------------+
| Cancer   |   phi(Cancer) |
+==========+===============+
| Cancer_0 |        0.0200 |
+----------+---------------+
| Cancer_1 |        0.9800 |
+----------+---------------+
```

[49]:
```
import sys
import urllib
from urllib.request import urlopen

import matplotlib.pyplot as plt  # Visuals
import numpy as np
import pandas as pd
import seaborn as sns
import sklearn as skl
```

[50]:
```
Cleveland_data_URL = 'http://archive.ics.uci.edu/ml/machine-learning-databases/
 ↪heart-disease/processed.hungarian.data'
np.set_printoptions(threshold=sys.maxsize) #see a whole array when we output it
names = ['age', 'sex', 'cp', 'trestbps', 'chol', 'fbs', 'restecg', 'thalach',␣
 ↪'exang', 'oldpeak', 'slope', 'ca', 'thal', 'heartdisease']
heartDisease = pd.read_csv(urlopen(Cleveland_data_URL), names = names) #gets␣
 ↪Cleveland data
```

[51]:
```
del heartDisease['ca']
del heartDisease['slope']
del heartDisease['thal']
del heartDisease['oldpeak']

heartDisease = heartDisease.replace('?', np.nan)
```

[73]:
```
from pgmpy.estimators import BayesianEstimator, MaximumLikelihoodEstimator
from pgmpy.models import BayesianModel

model = BayesianModel([('age', 'trestbps'), ('age', 'fbs'),
                       ('sex', 'trestbps'), ('sex', 'trestbps'),
                       ('exang', 'trestbps'), ('trestbps', 'heartdisease'),
                       ('fbs', 'heartdisease'), ('heartdisease', 'restecg'),
```

```
                        ('heartdisease', 'thalach'), ('heartdisease', 'chol')])

# Learing CPDs using Maximum Likelihood Estimators
model.fit(heartDisease, estimator=MaximumLikelihoodEstimator)
#for cpd in model.get_cpds():
#    print("CPD of {variable}:".format(variable=cpd.variable))
#   print(cpd)
```

[53]:
```
print(model.get_cpds('age'))
print(model.get_cpds('chol'))
print(model.get_cpds('sex'))
```

```
+---------+------------+
| age(28) | 0.00383142 |
+---------+------------+
| age(29) | 0.00383142 |
+---------+------------+
| age(30) | 0.00383142 |
+---------+------------+
| age(31) | 0.00766284 |
+---------+------------+
| age(32) | 0.0153257  |
+---------+------------+
| age(33) | 0.00766284 |
+---------+------------+
| age(34) | 0.0153257  |
+---------+------------+
| age(35) | 0.0191571  |
+---------+------------+
| age(36) | 0.0191571  |
+---------+------------+
| age(37) | 0.0306513  |
+---------+------------+
| age(38) | 0.0191571  |
+---------+------------+
| age(39) | 0.0344828  |
+---------+------------+
| age(40) | 0.0191571  |
+---------+------------+
| age(41) | 0.0383142  |
+---------+------------+
| age(42) | 0.0268199  |
+---------+------------+
| age(43) | 0.0421456  |
+---------+------------+
| age(44) | 0.0268199  |
+---------+------------+
| age(45) | 0.0229885  |
```

age(46)	0.045977
age(47)	0.0344828
age(48)	0.0613027
age(49)	0.0421456
age(50)	0.045977
age(51)	0.0344828
age(52)	0.0574713
age(53)	0.0383142
age(54)	0.0842912
age(55)	0.0536398
age(56)	0.0306513
age(57)	0.0191571
age(58)	0.0344828
age(59)	0.0229885
age(60)	0.00766284
age(61)	0.00766284
age(62)	0.00766284
age(63)	0.00383142
age(65)	0.0114943
age(66)	0

heartdisease	heartdisease(0)	heartdisease(1)
chol(100)	0.006134969325153374	0.0
chol(117)	0.0	0.01020408163265306

chol(129)	0.006134969325153374	0.0
chol(132)	0.006134969325153374	0.0
chol(147)	0.012269938650306749	0.0
chol(156)	0.0	0.01020408163265306
chol(160)	0.012269938650306749	0.01020408163265306
chol(161)	0.006134969325153374	0.0
chol(163)	0.006134969325153374	0.0
chol(164)	0.0	0.01020408163265306
chol(166)	0.006134969325153374	0.0
chol(167)	0.006134969325153374	0.0
chol(168)	0.006134969325153374	0.0
chol(171)	0.006134969325153374	0.0
chol(172)	0.0	0.01020408163265306
chol(173)	0.006134969325153374	0.0
chol(175)	0.0	0.01020408163265306
chol(179)	0.012269938650306749	0.0
chol(180)	0.006134969325153374	0.01020408163265306
chol(182)	0.012269938650306749	0.01020408163265306
chol(184)	0.018404907975460124	0.0
chol(186)	0.006134969325153374	0.01020408163265306
chol(187)	0.006134969325153374	0.0
chol(188)	0.012269938650306749	0.0
chol(190)	0.006134969325153374	0.0
chol(193)	0.006134969325153374	0.02040816326530612

chol(194)	0.012269938650306749	0.0
chol(195)	0.018404907975460124	0.0
chol(196)	0.018404907975460124	0.01020408163265306
chol(198)	0.012269938650306749	0.01020408163265306
chol(200)	0.012269938650306749	0.0
chol(201)	0.012269938650306749	0.01020408163265306
chol(202)	0.006134969325153374	0.01020408163265306
chol(204)	0.006134969325153374	0.0
chol(205)	0.0	0.01020408163265306
chol(206)	0.0	0.01020408163265306
chol(207)	0.012269938650306749	0.01020408163265306
chol(208)	0.006134969325153374	0.0
chol(209)	0.012269938650306749	0.0
chol(210)	0.006134969325153374	0.0
chol(211)	0.018404907975460124	0.01020408163265306
chol(212)	0.0	0.01020408163265306
chol(213)	0.006134969325153374	0.02040816326530612
chol(214)	0.006134969325153374	0.01020408163265306
chol(215)	0.024539877300613498	0.0
chol(216)	0.012269938650306749	0.02040816326530612
chol(217)	0.006134969325153374	0.0
chol(218)	0.006134969325153374	0.0
chol(219)	0.006134969325153374	0.01020408163265306
chol(220)	0.018404907975460124	0.0

chol(221)	0.006134969325153374	0.0
chol(222)	0.006134969325153374	0.02040816326530612
chol(223)	0.012269938650306749	0.01020408163265306
chol(224)	0.018404907975460124	0.01020408163265306
chol(225)	0.012269938650306749	0.01020408163265306
chol(226)	0.0	0.01020408163265306
chol(227)	0.006134969325153374	0.0
chol(228)	0.006134969325153374	0.0
chol(229)	0.006134969325153374	0.0
chol(230)	0.024539877300613498	0.01020408163265306
chol(231)	0.0	0.02040816326530612
chol(233)	0.0	0.01020408163265306
chol(234)	0.0	0.01020408163265306
chol(237)	0.012269938650306749	0.01020408163265306
chol(238)	0.024539877300613498	0.0
chol(240)	0.006134969325153374	0.0
chol(241)	0.006134969325153374	0.0
chol(242)	0.0	0.01020408163265306
chol(243)	0.012269938650306749	0.0
chol(245)	0.012269938650306749	0.0
chol(246)	0.012269938650306749	0.030612244897959183
chol(247)	0.0	0.01020408163265306
chol(248)	0.0	0.030612244897959183
chol(249)	0.012269938650306749	0.0

chol(250)	0.012269938650306749	0.0
chol(251)	0.006134969325153374	0.0
chol(253)	0.012269938650306749	0.0
chol(254)	0.012269938650306749	0.0
chol(255)	0.0	0.01020408163265306
chol(256)	0.006134969325153374	0.0
chol(257)	0.006134969325153374	0.01020408163265306
chol(259)	0.006134969325153374	0.0
chol(260)	0.018404907975460124	0.01020408163265306
chol(263)	0.006134969325153374	0.030612244897959183
chol(264)	0.006134969325153374	0.02040816326530612
chol(265)	0.0	0.02040816326530612
chol(266)	0.006134969325153374	0.01020408163265306
chol(267)	0.0	0.01020408163265306
chol(268)	0.006134969325153374	0.02040816326530612
chol(269)	0.006134969325153374	0.0
chol(270)	0.006134969325153374	0.01020408163265306
chol(271)	0.006134969325153374	0.0
chol(272)	0.006134969325153374	0.01020408163265306
chol(273)	0.012269938650306749	0.0
chol(274)	0.006134969325153374	0.0
chol(275)	0.012269938650306749	0.02040816326530612
chol(276)	0.012269938650306749	0.0
chol(277)	0.006134969325153374	0.01020408163265306

chol(279)	0.0	0.01020408163265306
chol(280)	0.006134969325153374	0.01020408163265306
chol(281)	0.006134969325153374	0.0
chol(282)	0.0	0.01020408163265306
chol(283)	0.006134969325153374	0.0
chol(284)	0.012269938650306749	0.0
chol(285)	0.0	0.01020408163265306
chol(287)	0.006134969325153374	0.0
chol(288)	0.0	0.030612244897959183
chol(289)	0.006134969325153374	0.01020408163265306
chol(290)	0.0	0.01020408163265306
chol(291)	0.006134969325153374	0.02040816326530612
chol(292)	0.012269938650306749	0.01020408163265306
chol(294)	0.006134969325153374	0.01020408163265306
chol(295)	0.006134969325153374	0.0
chol(297)	0.012269938650306749	0.0
chol(298)	0.006134969325153374	0.01020408163265306
chol(303)	0.0	0.01020408163265306
chol(305)	0.006134969325153374	0.0
chol(306)	0.0	0.01020408163265306
chol(307)	0.006134969325153374	0.0
chol(308)	0.012269938650306749	0.0
chol(309)	0.0	0.0
chol(312)	0.006134969325153374	0.0

chol(315)	0.006134969325153374	0.0
chol(318)	0.006134969325153374	0.0
chol(320)	0.012269938650306749	0.0
chol(326)	0.006134969325153374	0.0
chol(328)	0.006134969325153374	0.0
chol(329)	0.0	0.01020408163265306
chol(331)	0.0	0.01020408163265306
chol(336)	0.0	0.01020408163265306
chol(338)	0.0	0.01020408163265306
chol(339)	0.006134969325153374	0.0
chol(340)	0.006134969325153374	0.0
chol(341)	0.0	0.02040816326530612
chol(342)	0.0	0.02040816326530612
chol(344)	0.006134969325153374	0.0
chol(347)	0.006134969325153374	0.0
chol(355)	0.0	0.01020408163265306
chol(358)	0.006134969325153374	0.0
chol(365)	0.006134969325153374	0.0
chol(388)	0.0	0.01020408163265306
chol(392)	0.0	0.01020408163265306
chol(393)	0.0	0.01020408163265306
chol(394)	0.006134969325153374	0.0
chol(404)	0.0	0.01020408163265306
chol(412)	0.006134969325153374	0.0

chol(466)	0.0	0.0
chol(468)	0.0	0.0
chol(491)	0.0	0.01020408163265306
chol(518)	0.0	0.01020408163265306
chol(529)	0.0	0.01020408163265306
chol(603)	0.0	0.01020408163265306
chol(85)	0.006134969325153374	0.0

sex(0)	0.264368
sex(1)	0.735632

[54]:
```
model.get_independencies()
```

[54]:
```
(age _|_ exang, sex)
(age _|_ exang | sex)
(age _|_ sex | exang)
(age _|_ thalach, restecg, chol | heartdisease)
(age _|_ exang, sex | fbs)
(age _|_ thalach, restecg, chol | heartdisease, sex)
(age _|_ exang | sex, fbs)
(age _|_ thalach, chol, restecg | exang, heartdisease)
(age _|_ sex | exang, fbs)
(age _|_ thalach, chol | heartdisease, restecg)
(age _|_ thalach, chol, restecg | heartdisease, fbs)
(age _|_ chol, restecg | heartdisease, thalach)
(age _|_ thalach, restecg | heartdisease, chol)
(age _|_ thalach, restecg, chol | trestbps, heartdisease)
(age _|_ thalach, restecg, heartdisease, chol | trestbps, fbs)
(age _|_ thalach, restecg, chol | exang, sex, heartdisease)
(age _|_ thalach, chol | heartdisease, sex, restecg)
(age _|_ thalach, restecg, chol | heartdisease, sex, fbs)
(age _|_ restecg, chol | heartdisease, sex, thalach)
(age _|_ thalach, restecg | heartdisease, sex, chol)
(age _|_ thalach, restecg, chol | trestbps, heartdisease, sex)
(age _|_ thalach, restecg, heartdisease, chol | trestbps, sex, fbs)
(age _|_ thalach, chol | exang, restecg, heartdisease)
(age _|_ thalach, chol, restecg | exang, fbs, heartdisease)
(age _|_ chol, restecg | exang, thalach, heartdisease)
(age _|_ thalach, restecg | exang, chol, heartdisease)
```

```
(age _|_ thalach, chol, restecg | trestbps, exang, heartdisease)
(age _|_ heartdisease, chol, thalach, restecg | trestbps, exang, fbs)
(age _|_ thalach, chol | heartdisease, restecg, fbs)
(age _|_ chol | heartdisease, restecg, thalach)
(age _|_ thalach | heartdisease, restecg, chol)
(age _|_ thalach, chol | trestbps, heartdisease, restecg)
(age _|_ chol, restecg | heartdisease, fbs, thalach)
(age _|_ thalach, restecg | heartdisease, chol, fbs)
(age _|_ thalach, chol, restecg | trestbps, heartdisease, fbs)
(age _|_ restecg | heartdisease, chol, thalach)
(age _|_ chol, restecg | trestbps, heartdisease, thalach)
(age _|_ thalach, restecg | trestbps, heartdisease, chol)
(age _|_ thalach, chol, heartdisease | trestbps, restecg, fbs)
(age _|_ heartdisease, chol, restecg | trestbps, thalach, fbs)
(age _|_ thalach, restecg, heartdisease | trestbps, chol, fbs)
(age _|_ thalach, chol | exang, sex, heartdisease, restecg)
(age _|_ thalach, restecg, chol | exang, sex, fbs, heartdisease)
(age _|_ restecg, chol | exang, sex, thalach, heartdisease)
(age _|_ thalach, restecg | exang, sex, heartdisease, chol)
(age _|_ thalach, restecg, chol | trestbps, exang, sex, heartdisease)
(age _|_ heartdisease, restecg, thalach, chol | trestbps, exang, sex, fbs)
(age _|_ thalach, chol | heartdisease, sex, fbs, restecg)
(age _|_ chol | heartdisease, sex, thalach, restecg)
(age _|_ thalach | heartdisease, chol, sex, restecg)
(age _|_ thalach, chol | trestbps, heartdisease, sex, restecg)
(age _|_ restecg, chol | heartdisease, sex, fbs, thalach)
(age _|_ thalach, restecg | heartdisease, sex, fbs, chol)
(age _|_ thalach, restecg, chol | trestbps, heartdisease, sex, fbs)
(age _|_ restecg | heartdisease, sex, thalach, chol)
(age _|_ restecg, chol | trestbps, heartdisease, sex, thalach)
(age _|_ thalach, restecg | trestbps, heartdisease, sex, chol)
(age _|_ thalach, chol, heartdisease | trestbps, sex, fbs, restecg)
(age _|_ heartdisease, restecg, chol | trestbps, thalach, sex, fbs)
(age _|_ thalach, restecg, heartdisease | trestbps, sex, fbs, chol)
(age _|_ thalach, chol | exang, restecg, fbs, heartdisease)
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(chol _|_ thalach, restecg, fbs | sex, age, exang, heartdisease, trestbps)
(chol _|_ trestbps, exang, thalach | sex, age, heartdisease, restecg, fbs)
(chol _|_ trestbps, exang, fbs | sex, age, heartdisease, thalach, restecg)
(chol _|_ exang, fbs, thalach | sex, age, heartdisease, restecg, trestbps)
(chol _|_ trestbps, exang, restecg | sex, age, heartdisease, thalach, fbs)
(chol _|_ exang, restecg, thalach | sex, age, heartdisease, fbs, trestbps)
(chol _|_ exang, restecg, fbs | sex, age, heartdisease, thalach, trestbps)
(chol _|_ exang | sex, age, restecg, fbs, trestbps)
(chol _|_ exang | sex, age, thalach, restecg, trestbps)
(chol _|_ exang | sex, age, thalach, fbs, trestbps)
(chol _|_ age, thalach, trestbps | sex, exang, heartdisease, restecg, fbs)
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(chol _|_ age | sex, exang, thalach, fbs, trestbps)
(chol _|_ age, exang, trestbps | sex, heartdisease, thalach, restecg, fbs)
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(chol _|_ age, exang, fbs | sex, heartdisease, thalach, restecg, trestbps)
(chol _|_ age, exang, restecg | sex, heartdisease, thalach, fbs, trestbps)
(chol _|_ age, exang | sex, thalach, restecg, fbs, trestbps)
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(chol _|_ exang, sex | age, thalach, restecg, fbs, trestbps)
(chol _|_ age, sex, trestbps | thalach, exang, restecg, fbs, heartdisease)
```

```
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(chol _|_ exang | sex, age, thalach, restecg, fbs, trestbps)
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(chol _|_ sex | age, exang, thalach, restecg, fbs, trestbps)
(chol _|_ exang, sex | age, heartdisease, thalach, restecg, fbs, trestbps)
(chol _|_ age, sex | thalach, exang, restecg, fbs, heartdisease, trestbps)
(chol _|_ trestbps | sex, age, exang, heartdisease, restecg, fbs, thalach)
(chol _|_ thalach | sex, age, exang, heartdisease, restecg, fbs, trestbps)
(chol _|_ fbs | sex, age, exang, heartdisease, restecg, thalach, trestbps)
(chol _|_ restecg | sex, age, exang, heartdisease, thalach, fbs, trestbps)
(chol _|_ exang | sex, age, heartdisease, thalach, restecg, fbs, trestbps)
(chol _|_ age | sex, exang, heartdisease, restecg, fbs, thalach, trestbps)
(chol _|_ sex | age, exang, heartdisease, restecg, fbs, thalach, trestbps)
```

[55]:
```python
from pgmpy.inference import VariableElimination

HeartDisease_infer = VariableElimination(model)
```

[75]:
```python
q = HeartDisease_infer.query(variables=['heartdisease'], evidence={'age': 28})
print(q['heartdisease'])
```

```
+----------------+---------------------+
| heartdisease   |   phi(heartdisease) |
+================+=====================+
| heartdisease_0 |              0.6333 |
```

```
+----------------+---------------------+
| heartdisease_1 |              0.3667 |
+----------------+---------------------+
```

[57]:
```
q = HeartDisease_infer.query(variables=['heartdisease'], evidence={'chol': 100})
print(q['heartdisease'])
```

```
+----------------+---------------------+
| heartdisease   |   phi(heartdisease) |
+================+=====================+
| heartdisease_0 |              1.0000 |
+----------------+---------------------+
| heartdisease_1 |              0.0000 |
+----------------+---------------------+
```

8 K-Means and E-M Algorithm

Apply EM algorithm to cluster a set of data stored in a .CSV file. Use the same dataset for clustering using k-Means algorithm. Compare the results of these two algorithms and comment on the quality of clustering. You can add Java/Python ML library classes/API in the program.

[58]:
```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import sklearn.metrics as sm
from sklearn import preprocessing
from sklearn.cluster import KMeans
from sklearn.datasets import load_iris
from sklearn.mixture import GaussianMixture
```

[59]:
```
dataset = load_iris()
dataset
```

[59]:
```
{'data': array([[5.1, 3.5, 1.4, 0.2],
        [4.9, 3. , 1.4, 0.2],
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        [5. , 3.6, 1.4, 0.2],
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        [4.6, 3.4, 1.4, 0.3],
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```

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```

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```

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```

```
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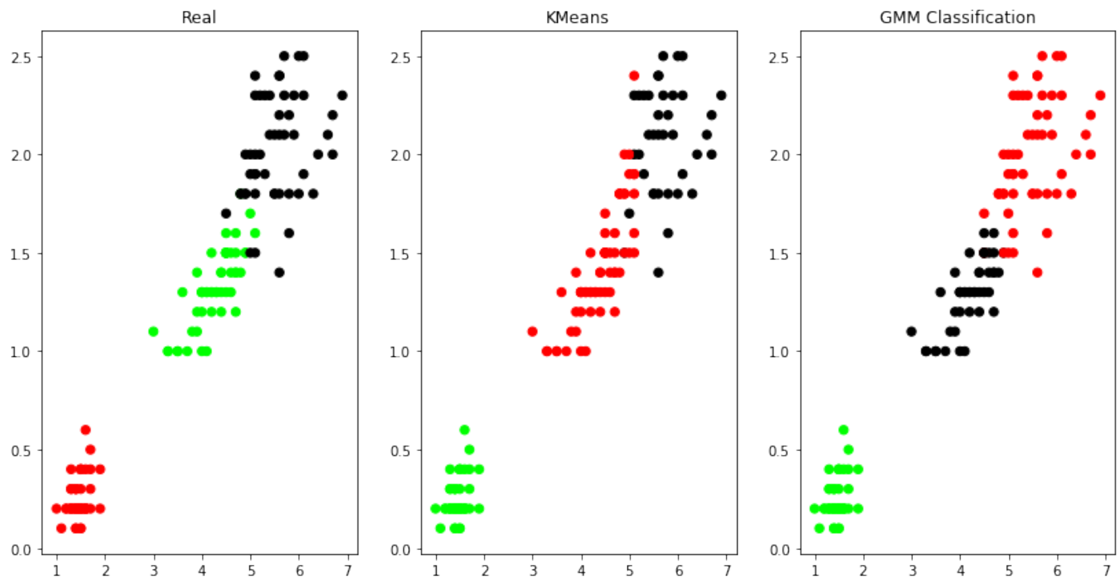
 'target_names': array(['setosa', 'versicolor', 'virginica'], dtype='<U10'),
 'DESCR': '.. _iris_dataset:\n\nIris plants
dataset\n--------------------\n\n**Data Set Characteristics:**\n\n    :Number of
Instances: 150 (50 in each of three classes)\n    :Number of Attributes: 4
numeric, predictive attributes and the class\n    :Attribute Information:\n
- sepal length in cm\n        - sepal width in cm\n        - petal length in
cm\n        - petal width in cm\n        - class:\n                - Iris-
Setosa\n                - Iris-Versicolour\n                - Iris-Virginica\n
\n    :Summary Statistics:\n\n    ============== ==== ==== ======= =====
====================\n                    Min  Max   Mean    SD   Class
Correlation\n    ============== ==== ==== ======= ===== ====================\n
sepal length:   4.3  7.9   5.84   0.83    0.7826\n    sepal width:    2.0  4.4
3.05   0.43   -0.4194\n    petal length:   1.0  6.9   3.76   1.76    0.9490
(high!)\n    petal width:    0.1  2.5   1.20   0.76    0.9565  (high!)\n
============== ==== ==== ======= ===== ====================\n\n    :Missing
Attribute Values: None\n    :Class Distribution: 33.3% for each of 3 classes.\n
:Creator: R.A. Fisher\n    :Donor: Michael Marshall
(MARSHALL%PLU@io.arc.nasa.gov)\n    :Date: July, 1988\n\nThe famous Iris
database, first used by Sir R.A. Fisher. The dataset is taken\nfrom Fisher\'s
paper. Note that it\'s the same as in R, but not as in the UCI\nMachine Learning
Repository, which has two wrong data points.\n\nThis is perhaps the best known
database to be found in the\npattern recognition literature.  Fisher\'s paper is
a classic in the field and\nis referenced frequently to this day.  (See Duda &
Hart, for example.)  The\ndata set contains 3 classes of 50 instances each,
where each class refers to a\ntype of iris plant.  One class is linearly
separable from the other 2; the\nlatter are NOT linearly separable from each
other.\n\n.. topic:: References\n\n   - Fisher, R.A. "The use of multiple
measurements in taxonomic problems"\n     Annual Eugenics, 7, Part II, 179-188
(1936); also in "Contributions to\n     Mathematical Statistics" (John Wiley,
NY, 1950).\n   - Duda, R.O., & Hart, P.E. (1973) Pattern Classification and
Scene Analysis.\n     (Q327.D83) John Wiley & Sons.  ISBN 0-471-22361-1.  See
page 218.\n   - Dasarathy, B.V. (1980) "Nosing Around the Neighborhood: A New
System\n     Structure and Classification Rule for Recognition in Partially
Exposed\n     Environments".  IEEE Transactions on Pattern Analysis and
Machine\n     Intelligence, Vol. PAMI-2, No. 1, 67-71.\n   - Gates, G.W. (1972)
"The Reduced Nearest Neighbor Rule".  IEEE Transactions\n     on Information
Theory, May 1972, 431-433.\n   - See also: 1988 MLC Proceedings, 54-64.
Cheeseman et al"s AUTOCLASS II\n     conceptual clustering system finds 3
classes in the data.\n   - Many, many more ...',
 'feature_names': ['sepal length (cm)',
  'sepal width (cm)',
  'petal length (cm)',
  'petal width (cm)'],
 'filename': '/home/akshayrb22/.local/lib/python3.7/site-
packages/sklearn/datasets/data/iris.csv'}
```

[60]:
```python
X = pd.DataFrame(dataset.data)
X.columns = ['Sepal_Length', 'Sepal_Width', 'Petal_Length', 'Petal_Width']
y = pd.DataFrame(dataset.target)
y.columns = ['Targets']
#print(X)
```

[61]:
```python
plt.figure(figsize=(14, 7))
colormap = np.array(['red', 'lime', 'black'])
#REAL PLOT
plt.subplot(1, 3, 1)
plt.scatter(X.Petal_Length, X.Petal_Width, c=colormap[y.Targets], s=40)
plt.title('Real')
#K-PLOT
plt.subplot(1, 3, 2)
model = KMeans(n_clusters=3)
model.fit(X)
predY = np.choose(model.labels_, [0, 1, 2]).astype(np.int64)
plt.scatter(X.Petal_Length, X.Petal_Width, c=colormap[predY], s=40)
plt.title('KMeans')
#GMM PLOT
scaler = preprocessing.StandardScaler()
scaler.fit(X)
xsa = scaler.transform(X)
xs = pd.DataFrame(xsa, columns=X.columns)
gmm = GaussianMixture(n_components=3)
gmm.fit(xs)
y_cluster_gmm = gmm.predict(xs)
plt.subplot(1, 3, 3)
plt.scatter(X.Petal_Length, X.Petal_Width, c=colormap[y_cluster_gmm], s=40)
plt.title('GMM Classification')
```

[61]:
```
Text(0.5, 1.0, 'GMM Classification')
```



9 KNN Algorithm

Write a program to implement k-Nearest Neighbour algorithm to classify the iris data set. Print both correct and wrong predictions. Java/Python ML library classes can be used for this problem.

[62]:
```
import numpy as np
from sklearn.datasets import load_iris
from sklearn.model_selection import train_test_split
from sklearn.neighbors import KNeighborsClassifier
```

[63]:
```
dataset = load_iris()
#print(dataset)
X_train, X_test, y_train, y_test = train_test_split(dataset["data"],␣
↪dataset["target"], random_state=0)
```

[64]:
```
kn = KNeighborsClassifier(n_neighbors=1)
kn.fit(X_train, y_train)
```

[64]:
```
KNeighborsClassifier(algorithm='auto', leaf_size=30, metric='minkowski',
                     metric_params=None, n_jobs=None, n_neighbors=1, p=2,
                     weights='uniform')
```

[65]:
```
prediction = kn.predict(X_test)
confusion_matrix(y_test, prediction)
```

[65]:
```
array([[13,  0,  0],
       [ 0, 15,  1],
       [ 0,  0,  9]])
```

10 Locally weighted regression

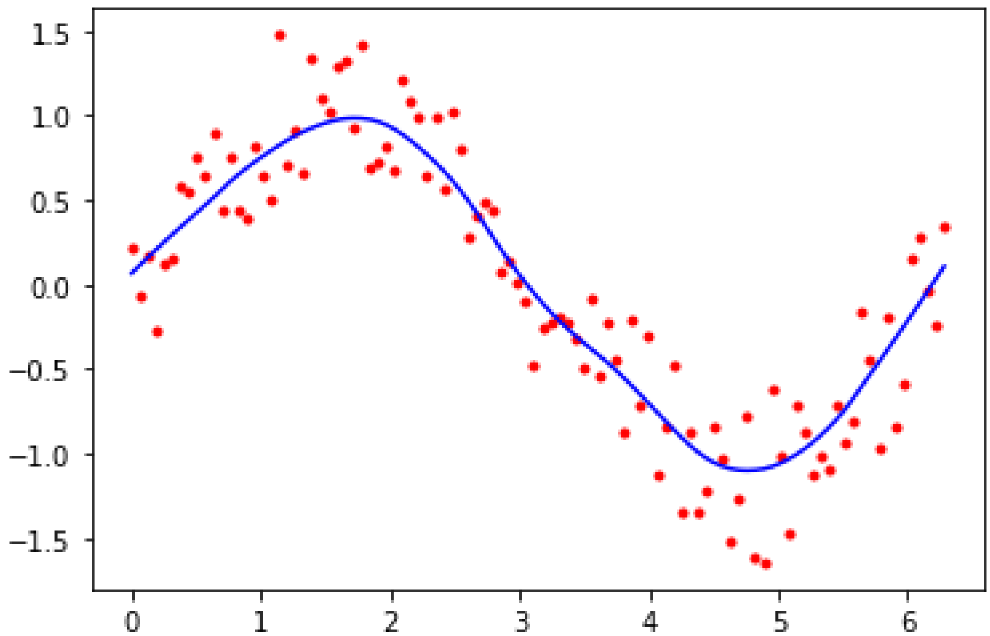
Implement the non-parametric Locally Weighted Regression algorithm in order to fit data points. Select appropriate data set for your experiment and draw graphs.

[66]:
```
from math import ceil

import numpy as np
from scipy import linalg
```

[67]:
```
def lowess(x, y, f, iterations):
    n = len(x)
    r = int(ceil(f * n))
    h = [np.sort(np.abs(x - x[i]))[r] for i in range(n)]
    w = np.clip(np.abs((x[:, None] - x[None, :]) / h), 0.0, 1.0)
    w = (1 - w**3)**3
    yest = np.zeros(n)
    delta = np.ones(n)
    for iteration in range(iterations):
        for i in range(n):
            weights = delta * w[:, i]
            b = np.array([np.sum(weights * y), np.sum(weights * y * x)])
            A = np.array([[np.sum(weights),
                           np.sum(weights * x)],
                          [np.sum(weights * x),
                           np.sum(weights * x * x)]])
            beta = linalg.solve(A, b)
            yest[i] = beta[0] + beta[1] * x[i]

        residuals = y - yest
        s = np.median(np.abs(residuals))
        delta = np.clip(residuals / (6.0 * s), -1, 1)
        delta = (1 - delta**2)**2

    return yest
```

[68]:
```
def main():
    import math
    n = 100
    x = np.linspace(0, 2 * math.pi, n)
    y = np.sin(x) + 0.3 * np.random.randn(n)
    f = 0.25
    iterations = 3
    yest = lowess(x, y, f, iterations)

    import matplotlib.pyplot as plt
    plt.plot(x, y, "r.")
    plt.plot(x, yest, "b-")
```

[69]:
```
main()
```



[ ]:
```
```