COMP3308 Assignment 2 Bayesian Networks

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1 Aim

The aim of this assignment is to build Bayesian networks for diagnostic problems and verify the independence statements by using existing tools such as JavaBayes and implementing an inference algorithm to compute posterior probabilities.

2 Methods

2.1 Bayesian Networks

Bayesian networks are simple, probabilistic graphical models that represent sets of random variables and their conditional dependencies. In general, they are acylic directed graphs, which are used to set up a scenario and calculate probabilities of events based on evidence and dependecies.

2.2 Variable Elimination

Variable elimination is an exact inference method which eliminates/marginalises the non-evidence non-query variables individually by distributing the sum over the product (i.e. summation for discrete variables and integration for continuous variables). This method allows us to avoid duplicate (possibly expensive) computations and also to simplify large queries to a normalised message which can be calculated and passed along more easily.

2.3 Likelihood Weighting

Likelihood weighting is used to avoid the potentially large amount of samples that rejection sampling rejects. It runs similarly to rejection sampling. However, when an observed node is reached, instead of rejecting it if it does not match the evidence, the probability of the observed node given the evidence is calculated. The product of all these probabilities is then the weight for the sample over the entire network.

3 Results and Discussion

3.1 Question 1

Metastatic cancer is a possible cause of a brain tumour and is also an explanation for increased total serum calcium. In turn, either of these could explain a patient falling into a coma. Severe headache is also possibly associated with a brain tumour.

- The prior probability of metastatic cancer P(m) is 0.2.
- The conditional probability of increased total serum calcium P(I|M) is: P(i|m) = 0.8 and $P(i|\neg m) = 0.2$
- The conditional probability of brain tumor P(B|M) is: P(b|m) = 0.2 and $P(b|\neg m) = 0.05$
- The conditional probability of coma P(C|I,B) is: P(c|i,b) = 0.8, $P(c|\neg i,b) = 0.8$, $P(c|i,\neg b) = 0.8$ and $P(c|\neg i,\neg b) = 0.05$.
- The conditional probability of severe headache P(S|B) is P(s|b) = 0.8 and P(s|b) = 0.6.
- a) Construct and show the equivalent graphical model.

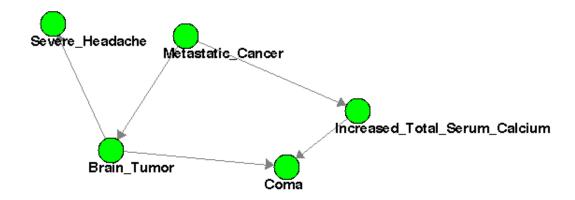


Figure 1: Equivalent graphical model created using JavaBayes

b) What is the prior probability of coma P(C)?

Figure 2: Probability of coma query output using JavaBayes

Using the Query function in JavaBayes, P(C) = 0.32.

c) What is the probability of metastatic cancer given the patient has severe headaches and has not fallen into coma?

Figure 3: $P(M|S, \neg C)$ query output using JavaBayes

Using the Observe and Query functions in JavaBayes, $P(M|S, \neg C) = 0.12087912087912088$.

d) What is the Markov blanket of coma?

In a Bayesian network, the Markov blanket of node A includes its parents, children and the other parents of all of its children.

Therefore the Markov blanket of coma are brain tumor and increased total serum calcium.

e) Are increased total serum calcium and brain tumor independent given coma? Explain.

No, because of explaining away otherwise known as Berkson's Paradox.

Normally, total serum calcium and brain tumor are independent, but if we are given coma they become dependent since they share the same child.

f) What is the probability of fallen into coma given the patient has metastatic cancer?

Figure 4: P(C|M) query output using JavaBayes

Using the Observe and Query functions in JavaBayes, P(C|M) = 0.68.

3.2 Question 2

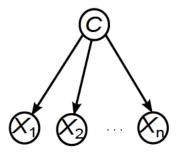


Figure 5: Naive Bayes Classifer

a)

$$P(C|X_1,\ldots,X_n) = \frac{P(C)P(X_1,\ldots,X_n|C)}{P(X_1,\ldots,X_n)}$$
 Bayes' Theorem
$$P(C|X_1,\ldots,X_n) = \frac{P(C,X_1,\ldots,X_n)}{P(X_1,\ldots,X_n)}$$
 conditional probability
$$P(C|X_1,\ldots,X_n)P(X_1,\ldots,X_n) = P(C,X_1,\ldots,X_n)$$

$$P(C,X_1,\ldots,X_n) = P(X_1,\ldots,X_n)\frac{P(C)P(X_1,\ldots,X_n|C)}{P(X_1,\ldots,X_n)}$$

$$P(C,X_1,\ldots,X_n) = P(C)P(X_1,\ldots,X_n|C)$$

$$P(X_1,\ldots,X_n|C) = \prod_{i=1}^n P(X_i|C)$$

which is the distribution for X_1, \ldots, X_n which can be given by the product of each node's probability given its parent which is C. Therefore, $P(C, x_1, \ldots, x_n) = P(C) \prod_{i=1}^n P(x_i|C)$

b)

$$\log\left(\frac{P(C=c|X_1,\ldots,X_n)}{P(C=\neg c|X_1,\ldots,X_n)}\right) = \log\left(\frac{P(C=c)}{P(C=\neg c)}\prod_{i=1}^n\frac{P(x_i|C=c)}{P(x_i|C=\neg c)}\right) \qquad \text{from part a})$$

$$= \log\left(\frac{P(C=c)}{P(C=\neg c)}\right) + \log\left(\prod_{i=1}^n\frac{P(x_i|C=c)}{P(x_i|C=\neg c)}\right)$$

$$= \alpha_0 + \log\left(\prod_{i=1}^n\frac{P(x_i|C=c)}{P(x_i|C=\neg c)}\right) \qquad \text{where } \alpha_0 = \log\left(\frac{P(C=c)}{P(C=\neg c)}\right)$$

$$= \alpha_0 + \sum_{i=1}^n\log\left(\frac{P(x_i|C=c)}{P(x_i|C=\neg c)}\right)$$

$$= \alpha_0 + \sum_{i=1}^n\alpha_iX_i \qquad \text{where } \alpha_i = \log\left(\frac{P(x_i|C=c)}{P(x_i|C=\neg c)}\right)$$

3.3 Question 3

Based on some of the common causes of coronary heart disease, we wanted to build a Bayesian network that would help us detect if a patient has heart disease.

3.3.1 Random Variables

- Age (A): Age of the patient. We will divide this up into four ranges. Under 19, 20-30, 31-50, above 50.
- Gender (G): Male or female.
- Physically active (PA): If the patient is physically active. True or False.
- Smokes (S): If the patient smokes. True or False.
- Overweight (O): If the patient is currently overweight. True or False.
- High cholesterol (HC): If the patient has high cholesterol. True of False.
- High blood pressure (HBP): If the patient has high blood pressure. True or False.
- Diabetes (DI): If the patient has diabetes. Type1, Type2 or None.
- Heart disease (HD): If the patient has heart disease. True or False.

3.3.2 Probability Distributions

$$\begin{split} P(A <= 19) &= 0.16, \, P(19 < A <= 30) = 0.21, \, P(30 < A <= 50) = 0.24, \, P(A > 50) = 0.39 \\ P(G = male) &= 0.62, P(G = female) = 0.38 \\ P(PA) &= 0.54 \\ P(S) &= 0.367 \\ P(O|PA) &= 0.66 \\ P(O|\neg PA) &= 0.01 \\ P(HC|O) &= 0.374 \\ P(HC|\neg O) &= 0.15 \end{split}$$

```
P(HBP|S, O) = 0.215
   P(HBP|S, \neg O) = 0.11
   P(HBP|\neg S, O) = 0.08
   P(HBP|\neg S, \neg O) = 0.05
   P(D = type1|O) =, P(D = type1|\neg O) =
P(D = type2|O) =, P(D = type2|\neg O) =
P(D = none|O) =, P(D = none|\neg O) =
   P(HD|A \le 19, G = male, D = type1, HBP, HC) = 0.3
P(HD|A \le 19, G = male, D = type1, HBP, \neg HC) = 0.2
P(HD|A \le 19, G = male, D = type1, \neg HBP, HC) = 0.2
P(HD|A \le 19, G = male, D = type1, \neg HBP, \neg HC) = 0.1
P(HD|A \le 19, G = male, D = type2, HBP, HC) = 0.3
P(HD|A \le 19, G = male, D = type2, HBP, \neg HC) = 0.2
P(HD|A \le 19, G = male, D = type2, \neg HBP, HC) = 0.2
P(HD|A \le 19, G = male, D = type2, \neg HBP, \neg HC) = 0.1
P(HD|A \le 19, G = male, D = none, HBP, HC) = 0.2
P(HD|A \le 19, G = male, D = none, HBP, \neg HC) = 0.1
P(HD|A \le 19, G = male, D = none, \neg HBP, HC) = 0.1
P(HD|A \le 19, G = male, D = none, \neg HBP, \neg HC) = 0.05
P(HD|A \le 19, G = female, D = type1, HBP, HC) = 0.2
P(HD|A \le 19, G = female, D = type1, HBP, \neg HC) = 0.15
P(HD|A \le 19, G = female, D = type1, \neg HBP, HC) = 0.1
P(HD|A \leq 19, G = female, D = type1, \neg HBP, \neg HC) = 0.05
P(HD|A \le 19, G = female, D = type2, HBP, HC) = 0.2
P(HD|A \le 19, G = female, D = type2, HBP, \neg HC) = 0.15
P(HD|A \leq 19, G = female, D = type2, \neg HBP, HC) = 0.1
P(HD|A \le 19, G = female, D = type2, \neg HBP, \neg HC) = 0.05
P(HD|A \le 19, G = female, D = none, HBP, HC) = 0.1
P(HD|A \le 19, G = female, D = none, HBP, \neg HC) = 0.05
P(HD|A \le 19, G = female, D = none, \neg HBP, HC) = 0.1
P(HD|A \le 19, G = female, D = none, \neg HBP, \neg HC) = 0.05
P(HD|19 < A \le 30, G = male, D = type1, HBP, HC) = 0.4
P(HD|19 < A \le 30, G = male, D = type1, HBP, \neg HC) = 0.3
P(HD|19 < A \le 30, G = male, D = type1, \neg HBP, HC) = 0.3
P(HD|19 < A \le 30, G = male, D = type1, \neg HBP, \neg HC) = 0.2
P(HD|19 < A \le 30, G = male, D = type2, HBP, HC) = 0.4
P(HD|19 < A < 30, G = male, D = type2, HBP, \neg HC) = 0.3
P(HD|19 < A \le 30, G = male, D = type2, \neg HBP, HC) = 0.3
P(HD|19 < A < 30, G = male, D = type2, \neg HBP, \neg HC) = 0.2
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P(HD|19 < A < 30, G = male, D = none, HBP, HC) = 0.3
P(HD|19 < A < 30, G = male, D = none, HBP, \neg HC) = 0.2
P(HD|19 < A < 30, G = male, D = none, \neg HBP, HC) = 0.2
P(HD|19 < A \le 30, G = male, D = none, \neg HBP, \neg HC) = 0.1
P(HD|19 < A \le 30, G = female, D = type1, HBP, HC) = 0.3
P(HD|19 < A < 30, G = female, D = type1, HBP, \neg HC) = 0.2
P(HD|19 < A < 30, G = female, D = type1, \neg HBP, HC) = 0.2
P(HD|19 < A \le 30, G = female, D = type1, \neg HBP, \neg HC) = 0.1
P(HD|19 < A \le 30, G = female, D = type2, HBP, HC) = 0.3
P(HD|19 < A < 30, G = female, D = type2, HBP, \neg HC) = 0.2
P(HD|19 < A \le 30, G = female, D = type2, \neg HBP, HC) = 0.2
P(HD|19 < A \le 30, G = female, D = type2, \neg HBP, \neg HC) = 0.1
P(HD|19 < A < 30, G = female, D = none, HBP, HC) = 0.2
P(HD|19 < A \le 30, G = female, D = none, HBP, \neg HC) = 0.1
P(HD|19 < A < 30, G = female, D = none, \neg HBP, HC) = 0.1
P(HD|19 < A \leq 30, G = female, D = none, \neg HBP, \neg HC) = 0.05
P(HD|30 < A \le 50, G = male, D = type1, HBP, HC) = 0.6
P(HD|30 < A \le 50, G = male, D = type1, HBP, \neg HC) = 0.4
P(HD|30 < A \le 50, G = male, D = type1, \neg HBP, HC) = 0.5
P(HD|30 < A \le 50, G = male, D = type1, \neg HBP, \neg HC) = 0.3
P(HD|30 < A \le 50, G = male, D = type2, HBP, HC) = 0.6
P(HD|30 < A \le 50, G = male, D = type2, HBP, \neg HC) = 0.4
P(HD|30 < A \le 50, G = male, D = type2, \neg HBP, HC) = 0.5
P(HD|30 < A \le 50, G = male, D = type2, \neg HBP, \neg HC) = 0.3
P(HD|30 < A \le 50, G = male, D = none, HBP, HC) = 0.5
P(HD|30 < A \le 50, G = male, D = none, HBP, \neg HC) = 0.3
P(HD|30 < A \le 50, G = male, D = none, \neg HBP, HC) = 0.4
P(HD|30 < A \le 50, G = male, D = none, \neg HBP, \neg HC) = 0.2
P(HD|30 < A \le 50, G = female, D = type1, HBP, HC) = 0.4
P(HD|30 < A \le 50, G = female, D = type1, HBP, \neg HC) = 0.3
P(HD|30 < A \le 50, G = female, D = type1, \neg HBP, HC) = 0.3
P(HD|30 < A \le 50, G = female, D = type1, \neg HBP, \neg HC) = 0.2
P(HD|30 < A \le 50, G = female, D = type2, HBP, HC) = 0.4
P(HD|30 < A \le 50, G = female, D = type2, HBP, \neg HC) = 0.3
P(HD|30 < A \le 50, G = female, D = type2, \neg HBP, HC) = 0.3
P(HD|30 < A \le 50, G = female, D = type2, \neg HBP, \neg HC) = 0.2
P(HD|30 < A < 50, G = female, D = none, HBP, HC) = 0.3
P(HD|30 < A \le 50, G = female, D = none, HBP, \neg HC) = 0.2
P(HD|30 < A < 50, G = female, D = none, \neg HBP, HC) = 0.2
P(HD|30 < A \leq 50, G = female, D = none, \neg HBP, \neg HC) = 0.1
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P(HD|A > 50, G = male, D = type1, HBP, HC) = 0.7
P(HD|A > 50, G = male, D = type1, HBP, \neg HC) = 0.5
P(HD|A > 50, G = male, D = type1, \neg HBP, HC) = 0.6
P(HD|A > 50, G = male, D = type1, \neg HBP, \neg HC) = 0.4
P(HD|A > 50, G = male, D = type2, HBP, HC) = 0.7
P(HD|A > 50, G = male, D = type2, HBP, \neg HC) = 0.5
P(HD|A > 50, G = male, D = type2, \neg HBP, HC) = 0.6
P(HD|A > 50, G = male, D = type2, \neg HBP, \neg HC) = 0.4
P(HD|A > 50, G = male, D = none, HBP, HC) = 0.6
P(HD|A > 50, G = male, D = none, HBP, \neg HC) = 0.4
P(HD|A > 50, G = male, D = none, \neg HBP, HC) = 0.5
P(HD|A > 50, G = male, D = none, \neg HBP, \neg HC) = 0.3
P(HD|A > 50, G = female, D = type1, HBP, HC) = 0.5
P(HD|A > 50, G = female, D = type1, HBP, \neg HC) = 0.4
P(HD|A > 50, G = female, D = type1, \neg HBP, HC) = 0.4
P(HD|A > 50, G = female, D = type1, \neg HBP, \neg HC) = 0.3
P(HD|A > 50, G = female, D = type2, HBP, HC) = 0.5
P(HD|A > 50, G = female, D = type2, HBP, \neg HC) = 0.4
P(HD|A > 50, G = female, D = type2, \neg HBP, HC) = 0.4
P(HD|A > 50, G = female, D = type2, \neg HBP, \neg HC) = 0.3
P(HD|A > 50, G = female, D = none, HBP, HC) = 0.4
P(HD|A > 50, G = female, D = none, HBP, \neg HC) = 0.3
P(HD|A > 50, G = female, D = none, \neg HBP, HC) = 0.3
P(HD|A > 50, G = female, D = none, \neg HBP, \neg HC) = 0.2
```

3.3.3 Method

Firstly, we did some research on the Internet, looking at the medical and health websites that were discussing heart disease in Australia and the common causes. Based on this list of common causes, we determined which one could be used as random variables in our Bayes net. Taking these variables, we researched further to find statistics to model our probability distribution.

We then tried to link these variables and found the following from research various sources on the Internet:

- Physical activity greatly affects if a person is overweight or not.
- Smoking and being overweight can cause a person to have a high blood pressure.
- Being overweight can cause a person to have high cholesterol.
- Being overweight can cause a person to have diabetes.
- Age, gender, high blood pressure, high cholesterol and diabetes are causes of heart disease.

From here we assigned the probabilities for the variables. Age and gender were based on Australian age and gender demographics. Physically active, overweight and smoking were also taken from Australian

statistics found on the Internet. From these defined probability we used the Bayes theorem and conditional joint probability to calculate the rest of the probabilities. Some of these probability however were estimated and weighted.

Finally we drew up the Bayes network based on our finds and calculations which can seen below in Figure 6.

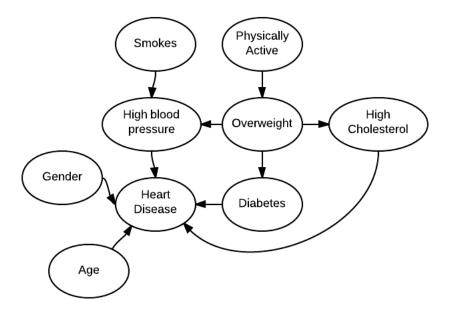


Figure 6: Heart disease diagnosis Bayes net

3.4 Question 4

3.4.1 Likelihood Weighting

We implemented the likelihood weighting in Python 2.7.5 to calculate the probability of P(cloudy | sprinkler, wetgrass).

Our program takes in the number of samples used to construct the estimate (N) as input and then runs M times which is set to 1000 by default. It then returns the mean, variance and standard deviation of the probability calculated using the likelihood weighting algorithm.

Below in Table 1, are the results for N=10, 100, 1000, 5000.

| N | Mean | Variance | Standard Deviation |
|------|-----------|-----------------|--------------------|
| 10 | 0.5069 | 0.02524239 | 0.158878538513 |
| 100 | 0.50004 | 0.0025593984 | 0.0505904971314 |
| 1000 | 0.499573 | 0.000222700671 | 0.0149231588814 |
| 5000 | 0.5001358 | 4.979223836e-05 | 0.00705636155253 |

Table 1: Accuracy results for likelihood weighting

3.4.2 Exact Inference using JavaBayes

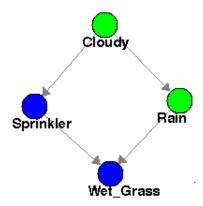


Figure 7: Equivalent graphical model created using JavaBayes. Sprinkler and Wet Grass set to true.

Figure 8: P(Cloudy|Sprinkler, WetGrass) query output using JavaBayes

4 Conclusions

As we input more samples to the program, the mean tends towards 0.5 and the variance and standard deviation also tend closer to 0. The low variance and standard deviation indicate that many of the values were closer to the mean, and as a result we can estimate the probability to be 0.5.

We noted also that as we increased the sample size, the program's runtime was increased, which was expected, as the algorithm must cover the entire network multiple times in order to create the distribution of interest.

JavaBayes uses exact inference, so we were able to obtain a much more concise result where the exact probability was calculated by doing the math. As seen above, we have a differing answer from our likelihood weighting output, which takes only random sampling and calculates a weight. Since the sampling is (psuedo) random, there are chances that we may get samples that are outliers and should be rejected, but are not, and thus contribute negatively to the outcome.

5 Reflection

Once again, the ability to work in a team proved beneficial to the completion of this task. It especially helped when we could compare results and confirm our findings, or discussing of various elements such as methods, calculations and interpretations of results.

Also, this assignment gave us further insight into the usage and understanding of probability graphical models, with challenging questions that required a lot of thought to deal with.

6 Code

Our implementation of Likelihood Weighting was written in Python 2.7.5.

This implementation was designed to work with any Bayesian network and not just the Cloudy-Rain-Sprinkler-WetGrass network.

6.1 XML Format

The program reads an XML file which has the structure of the network and probability values and makes the appropriate data structures.

The XML of the Cloudy-Rain-Sprinkler-WetGrass network can seen in the figure below.

```
<network>
        < node >
                <id>C</id>
                <name>Cloudy</name>
                cprobability>0.5</probability>
        </node>
        <node>
                <id>S</id>
                <name>Sprinkler</name>
                <parent>C</parent>
                <probability given="C">0.1</probability>
                <probability given="-C">0.5</probability>
        </node>
        < node >
                <id>R</id>
                <name>Rain</name>
                <parent>C</parent>
                <probability given="C">0.8</probability>
                <probability given="-C">0.2</probability>
        </node>
        <node>
                <id>W</id>
                <name>Wet Grass</name>
                <parent>S</parent>
                <parent>R</parent>
                <probability given="S,R">0.99</probability>
                <probability given="S,-R">0.9</probability>
                <probability given="-S,R">0.9</probability>
                <probability given="-S,-R">0.00</probability>
        </node>
</network>
```

Figure 9: Cloudy-Rain-Sprinkler-WetGrass-Network.xml

6.2 Instructions

To run our implementation, change directory to the where the code is. Make sure that Cloudy-Rain-Sprinkler-WetGrass-Network.xml file is present.

Then run:

```
{\rm python\ likelihood.py} < \! N \! \! >
```

where N is the number of samples used.

6.2.1 Example

N: 1000 M: 1000

Mean: 0.499573

Variance: 0.000222700671

Standard Deviation: 0.0149231588814