BNs for Genetic Inheritance PA Quiz

Quiz, 11 questions

11/11 points (100%)

Congratulations! You passed!

Next Item

1 / 1 point

1.

This quiz is a companion quiz to Programming Assignment: Bayes Nets for Genetic Inheritance. Please refer to the writeup for the programming assignment for instructions on how to complete this quiz.

James and Rene come to a genetic counselor because they are deciding whether to have another child or adopt. They want to know the probability that their un-born child will have cystic fibrosis.

Consider the Bayesian network for cystic fibrosis. We consider a person's phenotype variable to be "observed" if the person's phenotype is known. Order the probabilities of their un-born child having cystic fibrosis in the following situations from smallest to largest: (1) No phenotypes are observed (nothing clicked), (2) Jason has cystic fibrosis, (3) Sandra has cystic fibrosis.

- (1), (2), (3)
- (3), (2), (1)
- (1), (3), (2)

Correct

Since Benjamin's phenotype and genotype are not observed in all of these situations, the probability that he will have cystic fibrosis (CF) is equivalent to the probability that James and Rene's unborn child will have CF. Observing that Benjamin's cousin has CF makes Benjamin more likely to have CF because CF is a genetic disease. Observing that Benjamin's brother has CF makes Benjamin more likely to have CF than when observing that Benjamin's cousin has CF because Benjamin's brother is a more closely-related relative than his cousin is.

- (3), (1), (2)
- (2), (3), (1)

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1 / 1 point

2.

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James never knew his father Ira because Ira passed away in an accident when James was a few months old. Now James comes to the genetic counselor wanting to know if Ira had cystic fibrosis. The genetic counselor wants your help in determining the probability that Ira had cystic fibrosis. Consider the Bayesian network for cystic fibrosis. We consider a person's phenotype variable to be "observed" if the person's phenotype is known. Order the probabilities of Ira having had cystic fibrosis in the following situations from smallest to largest: (1) No phenotypes are observed (nothing clicked), (2) Benjamin has cystic fibrosis, (3) Benjamin and Robin have cystic fibrosis.

- (1), (3), (2)

Correct

Observing that Ira's grandson has cystic fibrosis (CF) makes Ira more likely to have CF because CF is a genetic disease. Observing that Ira's wife also has CF partially explains away why Ira has CF.

- (2), (3), (1)
- (1), (2), (3)
- (3), (1), (2)
- (3), (2), (1)

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1 / 1 point

3.

Recall that, for a trait with 2 alleles, the CPD for genotype given parents' genotypes has 27 entries, and 18 parameters were needed to specify the distribution. How many parameters would be needed if the trait had 3 alleles instead of 2?

180

Correct Response

There are 6 possible genotypes for each parent and for the child, so the size of the CPD is $6 \times 6 \times 6 = 216$. Since the probability of having a genotype is fully defined if the probabilities for having the other genotypes are known, there are $216 - (6 \times 6) = 180$ parameters.

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1 / 1 point

4.

You will now gain some intuition for why decoupling a Bayesian network can be worthwhile. Consider a **non-decoupled** Bayesian network for cystic fibrosis with **3 alleles** over the pedigree that was used in section 2.4 and 3.3. How many parameters are needed to specify all probability distributions across the entire network?

191

Correct Response

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There are 6 parameters for a phenotype given genotype factor, 5 parameters for a genotype given allele frequency factor, and 180 parameters for a child genotype given parents' genotypes factor. Since each type of factor has the same parameters, regardless of where it occurs in the network, the total number of parameters is $6 + 5 + 180 = 191$.

✔ 1 / 1 point

5.

Now consider the **decoupled** Bayesian network for cystic fibrosis with **3 alleles** over the pedigree that was used in section 2.4 and 3.3. How many parameters are needed to specify all of the probability distributions across the entire network?

Hint: A child cannot inherit an allele that is not present in either parent, so there aren't as many degrees of freedom here as there might be without that context-specific information.

20

Correct Response

There are 9 parameters for a phenotype given genotype factor, 2 parameters for a copy of gene given allele frequency factor, and 9 parameters for a child copy of gene given parent's copies of gene factor. Since each type of factor has the same parameters, regardless of where it occurs in the network, the total number of parameters is $9 + 2 + 9 = 20$.

✔ 1 / 1 point

6.

Consider the **decoupled** Bayesian network for cystic fibrosis with three alleles that you constructed in section 3.3. We consider a person's gene copy variable to be "observed" if the person's allele for that copy of the gene is known.

James and Rene are debating whether to have another child or adopt a child. They are concerned that, if they have a child, the child will have cystic fibrosis because both of them have one F allele observed (their other gene copy is not observed), even though neither of them have cystic fibrosis. You want to give them advice, but they refuse to tell you whether anyone else in their family has cystic fibrosis. What is the **probability** (NOT a percentage) that their unborn child will have cystic fibrosis?

0.4672

Correct Response

Knowing that James and Rene each have at least one F allele makes their child more likely to have cystic fibrosis, even though neither of them have CF.

✔ 1 / 1 point

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11/11 points (100%)

7.
Consider a Bayesian network for spinal muscular atrophy (SMA), in which there are multiple genes and 2 phenotypes.

Let n be the number of genes involved in SMA and m be the maximum number of alleles per gene. How many parameters are necessary if we use a table CPD for the probabilities for phenotype given copies of the genes from both parents?

- $O(4^n)$
- $O(m^{2n})$

Correct
There are two alleles per gene, so there are $O(m^2)$ allele combinations per gene. Therefore, there are $O(m^{2n})$ parameters for $n genes.

- $O(m+n)$
- $O(mn)$
- Depends on the phenotype
- $O(m^2)$
- $O(n)$
- $O(2^n)$

1 / 1 point

8.
Consider the Bayesian network for spinal muscular atrophy (SMA), in which there are multiple genes and two phenotypes.

Let n be the number of genes involved in SMA and m be the maximum number of alleles per gene. How many parameters are necessary if we use a sigmoid CPD for the probabilities for phenotype given copies of the genes from both parents?

- $O(mn)$

Correct
Each gene has up to m alleles, and there is an indicator for each allele for each copy of the gene. Therefore, if there were one gene, there would be $O(2m) = O(m)$ parameters. Since there are n genes, there are $O(mn)$ possible parameters.

- $O(m+n)$
- $O(m)$
- $O((mn)^2)$

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- $O(m^2n)$
- Depends on the phenotype
- $O(n)$
- $O(max(m,n))$

1 / 1 point

9.

Consider genes A and B that might be involved in spinal muscular atrophy. Assume that A has 2 alleles A_1 and A_2, and B has 2 alleles, B_1 and B_2. Which of the following relationships between A and B can a sigmoid CPD capture?

- [x] Allele A_1 makes a person more likely to have SMA, while allele B_1 independently makes a person less likely to have SMA.

Correct

A sigmoid CPD can capture this by making the weights for the inidicators for allele A_1 positive while making the weights for the indicators for allele B_1 negative.

- [x] Gene A contributes to SMA, but gene B does not contribute to SMA and thus does not affect the effects of gene A on SMA.

Correct

A sigmoid CPD can capture this by giving the alleles for copies of gene A positive weights and the alleles for copies of gene B zero weights.

- [ ] Allele A_1 and allele B_1 make a person more likely to be have SMA when both of these alleles are present, but neither affect SMA otherwise.

Un-selected is correct

- [ ] Allele A_1 and allele B_1 make a person equally more likely to have SMA, but when both are present the effect on SMA is the same as when only one is present.

Un-selected is correct

- [x] Neither gene A nor gene B contribute to SMA.

Correct

A sigmoid CPD can capture this by giving alleles for copies of gene A as well as alleles for copies of gene B weights with value zero.

- [ ] When the alleles are A_1 and B_2 or A_2 and B_1 the person has SMA; otherwise the person does not have SMA.

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Un-selected is correct

- [ ] Alleles A_1 and B_1 each independently make a person likely to have SMA.

Correct
Since their contributions are independent, a sigmoid CPD that weights the alleles for each gene based on the extent of their contribution would capture this perfectly.

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1 / 1 point

10.
Consider the Bayesian network for spinal muscular atrophy that we provided in spinalMuscularAtrophyBayesNet.net. We consider a person's gene copy variable to be "observed" if the person's allele for that copy of that gene is known.

Now say that Ira and Robin come to the genetic counselor because they are debating whether to have a biological child or adopt and are concerned that their child might have spinal muscular atrophy. They have some genetic information, but because sequencing is still far too expensive to be affordable for everyone, their information is limited to only a few genes and to only 1 chromosome in each pair of chromosomes.

Order the probabilities of their un-born child having spinal muscular atrophy in the following situations from smallest to largest: (1) No genetic information or phenotypes are observed (nothing clicked), (2) Ira and Robin each have at least 1 M allele, (3) Ira and Robin each have at least 1 B allele.

- (1), (3), (2)
- (3), (1), (2)
- (1), (2), (3)

Correct
Since James is unobserved, the probability that he will have spinal muscular atrophy (SMA) is equivalent to the probability that Ira and Robin's unborn child will have SMA. Observing that Ira and Robin each have an allele that is involved in causing SMA makes James more likely to have SMA than if no variables were observed. Observing that Ira and Robin each have alleles for 2 genes that are involved in causing SMA makes James even more likely to have SMA than if only 1 allele for 1 gene were observed.

- (2), (3), (1)
- (3), (2), (1)

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1 / 1 point

11.

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Consider the Bayesian network for spinal muscular atrophy that we provided in

No longer interested in finding out whether his father had cystic fibroisis, James comes to the genetic counselor with another question: Did his father have spinal muscular atrophy? The genetic counselor now wants your help in figuring this out. This time, however, James has other information for you: both he and Robin have spinal muscular atrophy.

What is the **probability** (NOT a percentage) that Ira had spinal muscular atrophy?

0.3541

Correct Response

Since Ira's wife has spinal muscular atrophy (SMA), this helps explain away why his child has SMA, so Ira is more likely to have SMA than he would be if no phenotypes were observed but is less likely to have SMA than he would be if only James were observed to have SMA.