A Primer on Bayesian Decision Analysis With an Application to a Kidney Transplant Decision

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Abstract: A clinical decision support system (CDSS) is a computer program, which is designed to assist health care professionals with decision making tasks. A well-developed CDSS weighs the benefits of therapy versus the cost in terms of loss of quality of life and financial loss and recommends the decision that can be expected to provide maximum overall benefit. This article provides an introduction to developing CDSSs using Bayesian networks; such CDSSs can help with the often complex decisions involving transplants. First, we review Bayes theorem in the context of medical decision making. Then, we introduce Bayesian networks, which can model probabilistic relationships among many related variables and are based on Bayes theorem. Next, we discuss influence diagrams, which are Bayesian networks augmented with decision and value nodes and which can be used to develop CDSSs that are able to recommend decisions that maximize the expected utility of the predicted outcomes to the patient. By way of comparison, we examine the benefit and challenges of using the Kidney Donor Risk Index as the sole decision tool. Finally, we develop a schema for an influence diagram that models generalized kidney transplant decisions and show how the influence diagram approach can provide the clinician and the potential transplant recipient with a valuable decision support tool.

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"Precision medicine is an emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle for each person."[1] To provide personalized medicine, we not only must take into account the patient's clinical and genomic profiles to determine the treatments most likely to be effective, but also consider the patient's trade-off between possible benefits of therapy versus loss of quality of life. There are numerous studies indicating that treatments can negatively affect quality of life, and so can outcomes, such as distant metastasis and locoregional occurrence.[2–4] For example, chemotherapy has a significant negative impact on immediate quality of life; however, a benefit is that it can decrease the chances of future metastasis. So, with no therapy, the patient would feel better now, but possibly be much worse off in the future. The utilities of these qualities of life to the patient and the chances of metastasis with and without chemotherapy are needed to determine the decision that maximizes expected utility. In general, even if we have all information available for a given patient, it is an arduous task to amass the information to reach a decision that maximizes the utility of the decision to the patient.

A clinical decision support system (CDSS) is a computer program, which is designed to assist health care professionals with decision making tasks, such as determining the diagnosis and treatment of a patient.[5] A CDSS provides the capability of integrating all patient information toward recommending a decision. There have been various hurdles to the development of CDSSs including lack of large-scale data.[6] However, we are now approaching the era of "big" data where abundant clinical and genomic data are becoming increasingly available. By using these data, we hold promise for developing CDSSs that can predict how treatment options and other decisions can affect outcomes, such as survival. Furthermore, our CDSSs should account for the extent to which these decisions can affect quality of life to recommend a decision. We provide an introduction to developing CDSSs using Bayesian networks and influence diagrams. Such CDSSs are able to recommend decisions that maximize the expected utility of the predicted outcomes to the patient.

This decision tool has particular applicability to transplant, where there are often complex decisions that require some estimate of the trade-off between potential benefit and potential harm. A recent decision support tool for the kidney transplant decision is the Kidney Donor Risk Index (KDRI).[7] As an example of current tools that assist us with complex transplant decisions, we briefly review the use of KDRI as a

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decision metric, and point out difficulties using the KDRI to make a decision that garners the greatest benefit to the patient. We then develop a schema for an influence diagram that models a particular kidney transplant decision and show how the influence diagram approach can resolve these difficulties and provide the potential transplant recipient with a true decision support tool.

Glossary

A glossary of terms used in this paper follows.

Bayesian network: A graphic model that succinctly represents a joint probability distribution. It consists of a directed acyclic graph (DAG) in which each node represents a random variable, and the conditional probability distribution of each node given its parents in the DAG.
Clinical decision support system (CDSS): A computer program, which is designed to assist healthcare professionals with decision making tasks, such as determining the diagnosis and treatment of a patient.
Decision analysis: The discipline that formally analyzes decision alternatives, and recommends the alternative that maximizes the expected utility of the outcome to the decision maker.
Decision tree: A tree-like graph that models decision alternatives, their possible outcomes, and the utilities of the outcomes. It is used to recommend the decision alternative that maximizes expected utility.
Directed acyclic graph (DAG): Pictorially, a node is a circle representing a variable or feature. A directed graph contains nodes and arrows (called edges) between the nodes. A DAG is a directed graph in which there is no sequence of edges leading from a node back to itself.
DSA: donor specific human leukocyte antigen.
Influence diagram: A Bayesian network augmented with decision nodes and value nodes. It models the same problems as a decision tree, and is used to recommend the decision alternative that maximizes expected utility.
Kidney Donor Risk Index (KDRI): A risk index for rate of graft failure relative to that of a healthy 40-year old donor.
Quality-adjusted life expectancy (QALE): Life expectancy computed using a time-trade-off quality of life adjustment.
Quality-adjusted life year (QALY): A measure of the utility of one year in a disease or treatment state that takes into account the quality of life in that state.

Bayesian Networks

A Bayesian network[8–11] is a graphical model for representing the probabilistic relationships among variables, which has been applied extensively to biomedical informatics.[12–15] Because Bayesian networks are an extension of Bayes theorem, we start by reviewing Bayes theorem.

Suppose Sam plans to marry, and to obtain a marriage license in the state in which he resides, one must take the blood test enzyme-linked immunosorbent assay (ELISA), which tests for the presence of human immunodeficiency virus (HIV). Sam takes the test and it comes back positive for HIV. How likely is it, that Sam is infected with HIV? Without knowing the accuracy of the test, Sam really has no way of knowing how probable it is that he is infected with HIV.

The data we ordinarily have on such tests are the true-positive rate (sensitivity) and the true-negative rate (specificity). The true-positive rate is the number of people who both have the infection and test positive divided by the total number of people who have the infection. For example, to obtain this number for ELISA, 10 000 people who were known to be infected with HIV were identified. This was done using the Western blot, which is the gold standard test for HIV. These people were then tested with ELISA, and 9990 tested positive. Therefore, the true-positive rate is 0.999. The true negative rate is the number of people who both do not have the infection and test negative divided by the total number of people who do not have the infection. To obtain this number for ELISA, 10 000 nuns who denied risk factors for HIV infection were tested. Of these, 9980 tested negative using the ELISA test. Furthermore, the 20 positive-testing nuns tested negative using the Western blot test. So, the true-negative rate is 0.998, which means that the false-positive rate (1-specificity) is 0.002. We therefore formulate the following random variables and subjective probabilities:

$$P(\text{ELISA} = \text{positive}|\text{HIV} = \text{present}) = 0.999 \qquad 1$$

$$P(\text{ELISA} = \text{positive}|\text{HIV} = \text{absent}) = 0.002.$$

The probabilities in Equation 1 are called conditional probabilities. They give the probability of the event to the left of the conditioning bar ("|") given the event to the right of the conditioning bar is known. The top probability states that if an individual has HIV, there is a 0.999 probability that the individual will test positive. The bottom probability states that if an individual does not have HIV, there is a 0.002 probability that the individual will test positive.

It might seem that Sam almost certainly is infected with HIV, because the test is so accurate. However, notice that neither of the above probabilities are the probability of Sam being infected with HIV. Because we know that Sam tested positive on ELISA, that probability is

$$P(\text{HIV} = \text{present}|\text{ELISA} = \text{positive}). \qquad 2$$

Equation 2 shows the probability of someone having HIV if that person has tested positive. We can compute that probability using Bayes Theorem if we know P (HIV = present), which is the prior probability of Sam having HIV before we found out that he tested positive. Recall that Sam took the blood test simply because the state required it. He did not take it because he thought for any reason he was infected with HIV. So, the only information we have about Sam before he took the test is that he is a man in the state in which

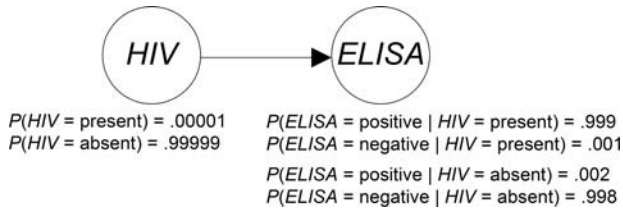


FIGURE 1. A 2-variable Bayesian network.

he resides. Therefore if 1 in 100 000 men in Sam's state is infected with HIV, we assign the following prior probability:

$$P(\text{HIV} = \text{present}) = 0.00001. \quad 3$$

We now use Bayes theorem as follows (for simplicity we do not show the random variables):

$$\begin{aligned} P(\text{present}|\text{positive}) &= \frac{P(\text{positive}|\text{present})P(\text{present})}{P(\text{positive}|\text{present})P(\text{present}) + P(\text{positive}|\text{absent})P(\text{absent})} \\ &= \frac{(0.999)(0.00001)}{(0.999)(0.00001) + (0.002)(0.99999)} \quad 4 \\ &= 0.00497. \end{aligned}$$

Surprisingly, we are fairly confident that Sam is not infected with HIV. A probability such as P (HIV = present) is called a prior probability because it is the probability of some event before updating the probability of that event using new information. A probability such as P (HIV = present | ELISA = positive) is called a posterior probability because it is the probability of an event after its prior probability has been updated based on new information. In the previous example, the reason the posterior probability is small, even though the test is fairly accurate, is that the prior probability is extremely low.

As another example, suppose Mary and her husband have been trying to have a baby, and she suspects she is pregnant. She takes a pregnancy test that has a true-positive rate of 0.99 and a false-positive rate of 0.02. Suppose further that 20% of all women who take this pregnancy test are indeed pregnant. Using Bayes theorem, we then have

$$\begin{aligned} P(\text{present}|\text{positive}) &= \frac{P(\text{positive}|\text{present})P(\text{present})}{P(\text{positive}|\text{present})P(\text{present}) + P(\text{positive}|\text{absent})P(\text{absent})} \\ &= \frac{(0.99)(0.2)}{(0.99)(0.2) + (0.02)(0.8)} \quad 5 \\ &= 0.92523. \end{aligned}$$

Even though Mary's test was less accurate than Sam's test, she probably is pregnant, whereas he probably is not infected with HIV. This is due to the prior information. There was a significant prior probability (0.2) that Mary was pregnant, because only women who suspect they are pregnant on other grounds take pregnancy tests. Sam, however, took his test because he wanted to get married. We had no prior information indicating he could be infected with HIV.

Figure 1 summarizes the information used in the application of Bayes theorem in Equation 4. That figure is a 2-variable Bayesian network. It represents the variables HIV and ELISA by nodes in a directed acyclic graph (DAG). Pictorially, a node is a circle representing a variable or feature. A directed graph contains nodes and arrows (called edges) between the nodes. A DAG is a directed graph in which there is no sequence of edges leading from a node back to itself. The edges in a Bayesian network usually represent causal influences. Because the presence of HIV has a causal effect on whether the test result is positive, there is an edge from HIV to ELISA. Besides showing a DAG representing the causal relationships, Figure 1 shows the prior probability distribution of HIV and the conditional probability distribution of ELISA given each value of its parent HIV.

In general, a Bayesian network consists of a DAG, whose edges represent relationships among variables that are often

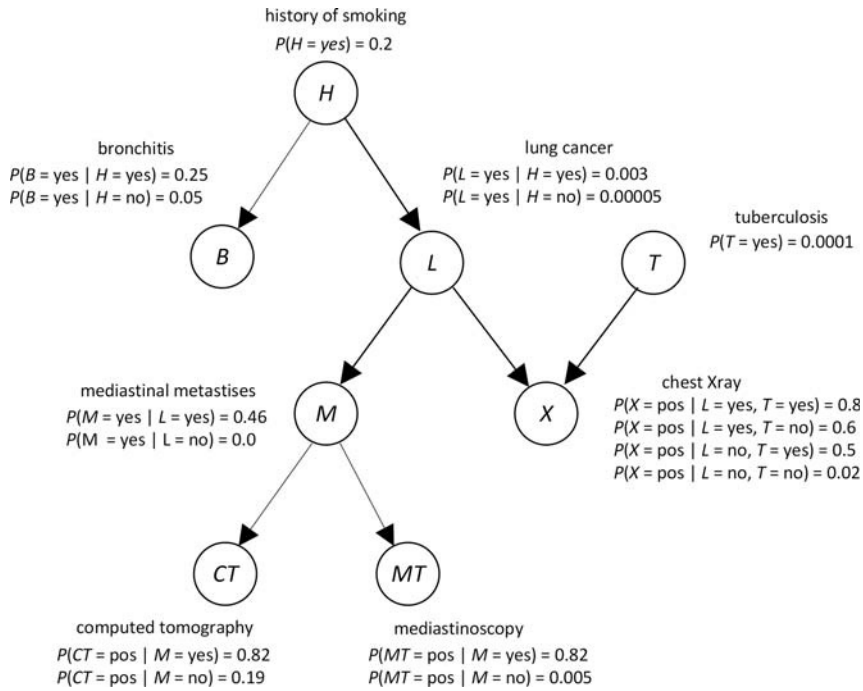


FIGURE 2. A Bayesian network representing relationships among variables related to respiratory diseases.

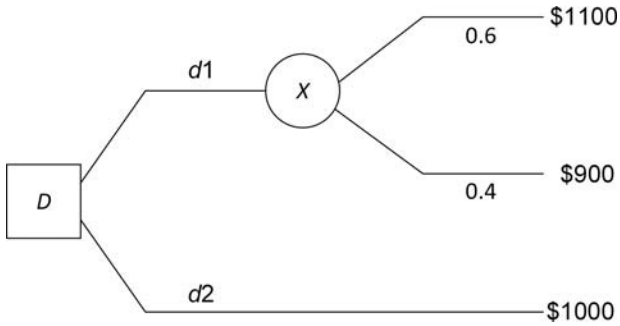


FIGURE 3. A simple decision tree representing the decision whether to buy stock X.

(but not always) causal; the prior probability distribution of every variable that is a root in the DAG; and the conditional probability distribution of every nonroot variable given each set of values of its parents. A variable is root if there are no edges directed at it. We use the terms *node* and *variable* interchangeably when discussing Bayesian networks.

Figure 2 shows a Bayesian network modeling relationships among variables related to respiratory diseases. The node H, which represents "history of smoking," is a root. Because it is a root, the Bayesian network contains its prior probability distribution, which is the probability of an individual having a history of smoking given that we only know the individual is from the population we are investigating. Assuming 20% of individuals in the population have smoked, we assign $P(H = \text{yes}) = 0.2$, and $P(H = \text{no}) = 0.8$. The node L, which represents "lung cancer," is not a root, so the Bayesian network contains its conditional probability distribution given each value of its parent H. Assuming 0.3% of smokers get lung cancer, we assign $P(L = \text{yes} \mid H = \text{yes}) = 0.003$. Assuming 0.005% of nonsmokers get lung cancer, we assign $P(L = \text{yes} \mid H = \text{no}) = 0.00005$. The other conditional probability distributions are developed in a similar fashion.

Using a Bayesian network, we can determine probabilities of interest with a Bayesian network inference algorithm,[9] which repeatedly performs computations similar to those in the application of Bayes Theorem in Equation 4. For example, using the Bayesian network in Figure 1, if a patient has a smoking history (H = yes), a positive chest X-ray (X = pos), and a positive computer tomogram (CT = pos), we can determine the probability of the patient having lung cancer (L = yes). That is, we can compute $P(L = \text{yes} \mid H = \text{yes}, X = \text{pos}, CT = \text{pos})$, which turns out to be 0.185. The prior probability of lung cancer in this model is 0.0064. So, the evidence has increased the probability of lung cancer substantially.

Recommending Decisions

Decision analysis is the discipline that formally analyzes decision alternatives and recommends the alternative that maximizes the expected utility of the outcome to the decision maker. A *utility* is a numerical rating assigned to every possible outcome that can occur as a result of the decision. In decisions concerning money, the utility of the outcome is usually the monetary value of the money realized. So, we maximize expected utility by maximizing expected value. As an example, suppose you have US $1000 and are considering buying stock X, whose current price is US $10 per share. Your time horizon is 1 month, and you feel there is about a 0.6 probability X will be at US $11 per share in 1 month, and there is a 0.4 probability it will be at US $9 per share. Your decision alternatives are $d1$, which is to buy X, and $d2$, which is to do nothing. Figure 3 shows a decision tree representing this decision. In decision analysis, we compute the expected value (utility) of each alternative:

$$E(d1) = 0.6(\$1100) + 0.4(\$900) = \$1020$$

$$E(d2) = \$1000.$$

If you are an expected value maximizer when money is concerned, you would choose $d1$. In general, it is reasonable to be an expected value maximizer with amounts of money that are small relative to your total wealth because, in the long run, if you are good at assessing probabilities, you will realize more money. However, if the amount of money is large compared with your wealth, then your attitude toward risk aversion might cause you to make the safer decision. For example, suppose the investment above concerns US $1 000 000. In this case, you might choose to not invest the US $1 000 000 in the stock because you would not want to risk losing US $100 000. Your attitude toward risk aversion can be formally modeled in decision analysis by using a concave bounded utility function that maps dollar amounts to utilities. See Neapolitan and Jiang[16] for the details.

Influence Diagrams

Often, a problem is too complex to represent it using a decision tree because the size of the decision tree model grows exponentially with the size of the problem. An influence diagram is a Bayesian network augmented with decision nodes and can represent all the same problems as a decision tree. Its size grows linearly with the size of the problem. Figure 4 shows the previous example represented with an influence diagram.

An *influence* diagram contains 3 kinds of nodes: chance (or uncertainty) nodes representing random variables; decision

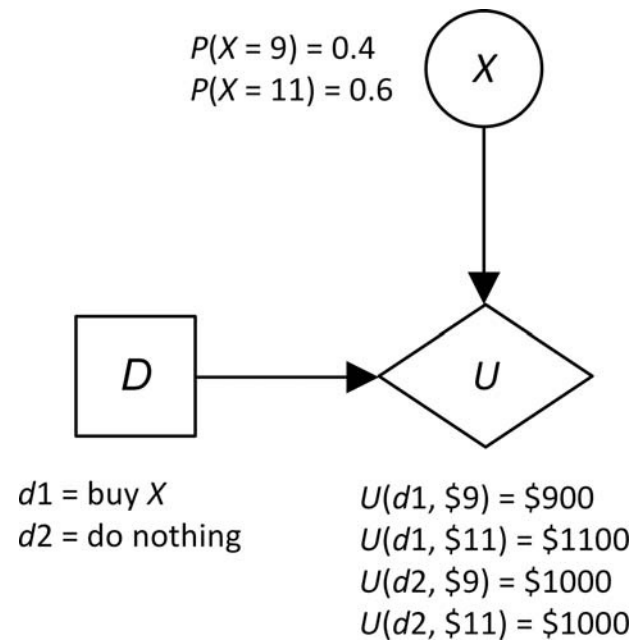
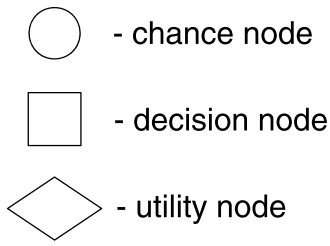
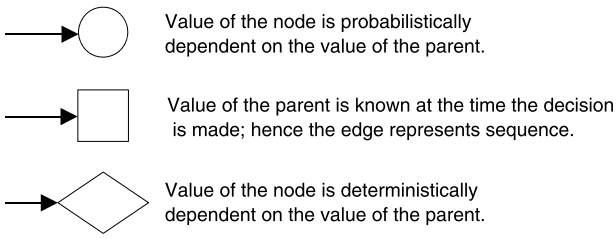


FIGURE 4. An influence diagram modeling the problem determined by the decision tree in Figure 3.

nodes representing decisions to be made; utility nodes, which are random variables whose possible values are the utilities of the outcomes. We depict these nodes as follows:



The edges in an influence diagram have the following meaning:



The chance nodes in an influence diagram constitute a Bayesian network. So an influence diagram is actually a Bayesian network augmented with decision nodes and a utility node. There must be an ordering of the decision nodes in an influence diagram based on the order in which the decisions are made. The order is specified using the edges between the decision nodes. An influence diagram is solved by determining the decision alternative of the first decision that maximizes expected utility. Specialized Bayesian network inference algorithms do this task.[9]

The influence diagram in Figure 4 is the simplest such diagram because it has only 1 chance node, namely, X. So the Bayesian network in that influence diagram contains only X, and we specify the prior probability distribution of X. There is 1 decision node D, and its alternatives are $d1$, which is to buy X, and $d2$ which is to do nothing. The utility node U is dependent both on the future value of X and the decision D. So, there are edges from X and D to U. If we make decision $d1$ and X is at US \$9, then the investment will be worth US \$900. So that is the value of $U(d1,\$9)$. If we make decision $d2$ and X is at \$11, then the investment will be worth \$1100. So that is the value of $U(d1,\$11)$. If we make the decision $d2$, the investment is worth US \$1000 regardless of the future value of X.

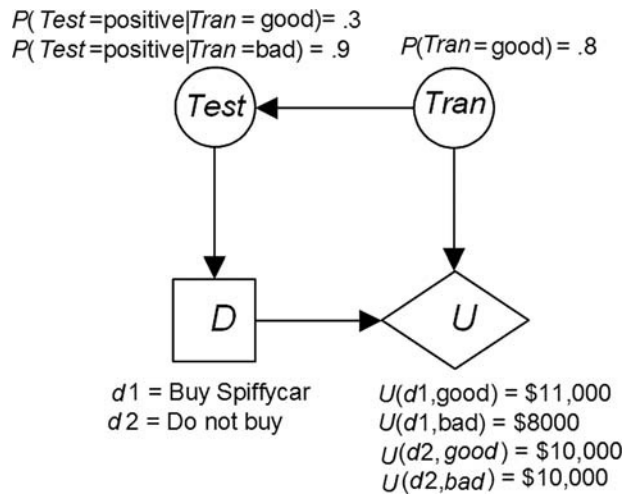


FIGURE 5. An influence diagram representing the decision concerning buying the Spiffycar.

Next, we present a slightly more complex influence diagram. Suppose Sam has the opportunity to buy a 1996 Spiffycar automobile for \$10 000, and he had a prospect that would be willing to pay \$11 000 for the auto if it were in excellent mechanical shape. Suppose further that if the transmission is bad, Sam will have to spend \$3000 to repair it before he could sell the vehicle. So he would end up with only \$8000 if he bought the vehicle and its transmission was bad. Finally, suppose Sam has a friend who could run a test on the transmission, and we have the following:

$$P(\text{Test} = \text{positive}|\text{Tran} = \text{good}) = 0.3$$

$$P(\text{Test} = \text{positive}|\text{Tran} = \text{bad}) = 0.9$$

$$P(\text{Tran} = \text{good}) = 0.8.$$

Figure 5 shows an influence diagram representing this problem. The Bayesian network in this influence diagram contains 2 nodes, Tran and Test. There is an edge from Tran to Test because the value of the test is probabilistically dependent on the state of the transmission. There is an edge from Test to D because the outcome of the test will be known at the time the decision is made. That is, D follows Test in sequence. Finally, the utility U depends only on the value of Tran and the decision D. It does not depend on the outcome of the Test. So there are arrows from Tran and D to U. If Sam makes decision $d1$ and Tran is good, the utility of the outcome will be \$11 000. On the other hand, if Sam makes decision $d1$ and Tran is bad, the utility of the outcome will be \$8000. However, if Sam makes decision $d2$, the utility of the outcome is \$10 000 regardless of whether Tran is good or bad because he has decided not to buy the car.

As mentioned previously, specialized Bayesian network inference algorithms are used to solve influence diagrams. In this case, if the test is positive, the algorithm would determine that

$$\text{EU}(d1) = \$9714,$$

where EU denotes "expected utility." On the other hand, if the test is negative, the algorithm would determine that

$$\text{EU}(d1) = \$10\,897.$$

Regardless of the test outcome, we have that

$$\text{EU}(d2) = \$10\,000.$$

So the decision would be to buy the car if the test came back negative and not to buy it if the test came back positive.

When the probabilities in an influence diagram are obtained from data, they are only estimates of assumed objective relative frequencies. So, our recommended decision might not be the one obtained using these relative frequencies. Neapolitan[17] develops a method for computing the probability that the recommended decision is the one which would be obtained using the objective relative frequencies. This probability is called the *confidence* in the decision.

We have only touched on decision analysis and influence diagrams. For a more thorough introduction, see Neapolitan and Jiang.[16]

Quality-Adjusted Life Expectancy

In medical decision making, the outcomes are often dying and living. In the simplest medical decision model, the utility assigned to being dead is 0, and the utility assigned to 1 year of life is 1. So, we maximize expected utility by maximizing how long the decision maker can expect to live. That is, we make the decision that maximizes life expectancy. However, living in disease states and living with treatments that have unpleasant side effects are not the same as living in perfect health. So, we often adjust for quality of life when comparing sick years and treatment years to well years. As an example, suppose Andrea is considering a kidney transplant. One option for her is simply to stay on dialysis. However, living on dialysis is not equivalent to living in perfect health. So, we ask Andrea to determine what 1 year of life on dialysis is worth relative to 1 well year of life. Let us say she says it is worth 0.6 "well" years. Then for Andrea

1 year on dialysis is equivalent to 0 .6 well years.

The value 0.6 is called the time trade-off quality adjustment or quality-adjusted life year (QALY) for dialysis. Another way to look at it is that Andrea would give up 0.4 years of life to avoid being on dialysis for 0.6 years. So, the utility assigned to death is 0, the utility assigned to a well year is 1, and the utility assigned to a year on dialysis is 0.6. Note that the QALY is patient specific. Another individual might feel that 1 year on dialysis is equivalent to 0.5 well years. When we compute life expectancy using a time trade-off quality adjustment, we call it quality-adjusted life expectancy (QALE). We ordinarily use QALYs instead of simply life years as the utilities in a decision model concerning a treatment or surgery decision, and we make the decision that maximizes QALE. An example is provided next.

Kidney Transplant Decision

A recently developed decision support tool for the kidney transplant decision is the KDRI (we take the liberty of using this in place of the kidney Donor Profile Index for an illustrative case). We briefly describe that index and problems using this metric to make a decision regarding acceptance of a potential donor kidney, and then we show how an influence diagram decision support tool can better inform the clinician and the patient as to the choice that produces the greatest expected benefit based on the probabilities and utilities of outcomes.

Kidney Donor Risk Index

The study that developed the KDRI analyzed 69 440 kidney transplant recipients, who received deceased donor transplants.[7] The study determined the following 14 independent donor and transplant-specific predictor variables: donor age, race, hypertension, diabetes, serum creatinine, cerebrovascular cause of death, height, weight, donation after cardiac death, hepatitis C virus status, human leukocyte antigen-B and -DR mismatch, cold ischemia time, en-bloc transplant, and double transplant. The outcome variable was graft failure, defined as return to dialysis, retransplant, or death. Cox regression was used to model survival prediction. For a given transplant decision, the KDRI produces a risk index for the rate of graft failure relative to that of a healthy 40-year-old donor. The risk index for a healthy 40-year-old donor is set to 1. If the KDRI is, for example, 1.28 then the estimated increase in graft failure risk is 28%.

There are a several difficulties with the KDRI:

1. Cox regression analysis was used to predict survival. However, several difficulties have been noted with the model. First, its proportional hazards assumption is not necessarily justified in all cases.[18,19] Second, the purpose of a Cox model is more to identify covariates than to predict survival. Both a Bayesian network method[20] and a random forest method[21] have been shown to outperform the Cox model at survival prediction.
2. The KDRI does not model the interactions among variables to affect survival outcome. The biomedical community has shown an increased interest in modeling interactions, motivated partly by the efforts to learn how genes interact epistatically to affect disease.[22] However, interactions can be occurring amongst any set of variables. In particular, Zeng et al[23] showed that tumor histology interacts with menopausal status to affect breast cancer death survival, but neither variables is correlated with survival by itself. Certainly, variables can also be interacting to affect graft failure. For example, height and weight might interact. That is, the risk for a 5 ft 6 in. 200 lb donor might be greater than the risk for a 6 ft 2 in. 200 lb donor.
3. The KDRI does not model recipient variables, such as age, height, and so on. However, these variables might also interact with donor variables. Though the estimated posttransplant survival is used in certain situations, no metric has been used to look at the interaction of these 2 sets of parameters. That said, it is quite possible that rather than a simple additive relationship existing between the 2, there may in fact be synergisms and interactions that are not easily calculated.
4. The KDRI only informs us of relative risk. It does not tell the patient what can be expected if the kidney is accepted. In particular, it does not provide a measure of the expected quality of life if the kidney is accepted versus the expected quality of life if the patient stays on dialysis.

An Influence Diagram for the Kidney Transplant Decision

All 4 problems just identified can be resolved by developing an influence diagram using a data set such as the one used in the KDRI study. However, this would be a major research project. Therefore, we just illustrate a schema for such an influence diagram by considering only 1 variable, namely, whether the patient has a donor specific human leukocyte antigen (DSA) antibody to the potential donor organ.

We model the decision of whether to accept an incompatible kidney from a deceased donor or to wait for a compatible kidney to become available. The incompatible kidney has a higher risk of failing. If a kidney transplant has good graft function, both the likelihood of survival and the quality of life are better than if the patient stays on dialysis. However, if the kidney fails, both likelihood of survival and quality of life might be better staying on dialysis.

We provide a simple model of this problem in which we assume a kidney transplant only occurs at time now (year 0), exactly 1 year later (end of year 1), exactly 2 years later (end of year 2), and so on. We also chose a 3-year time horizon only. In application, the time discretization could be more refined, and the time horizon could be longer. Furthermore, we only model that the patient can make the incompatible donor decision once at time now. With some probability the opportunity for the incompatible donor transplant will be available in the future, and these future decisions can also be modeled. Figure 6 shows an influence diagram representing this problem using the Bayesian network package Netica.[24] The Netica

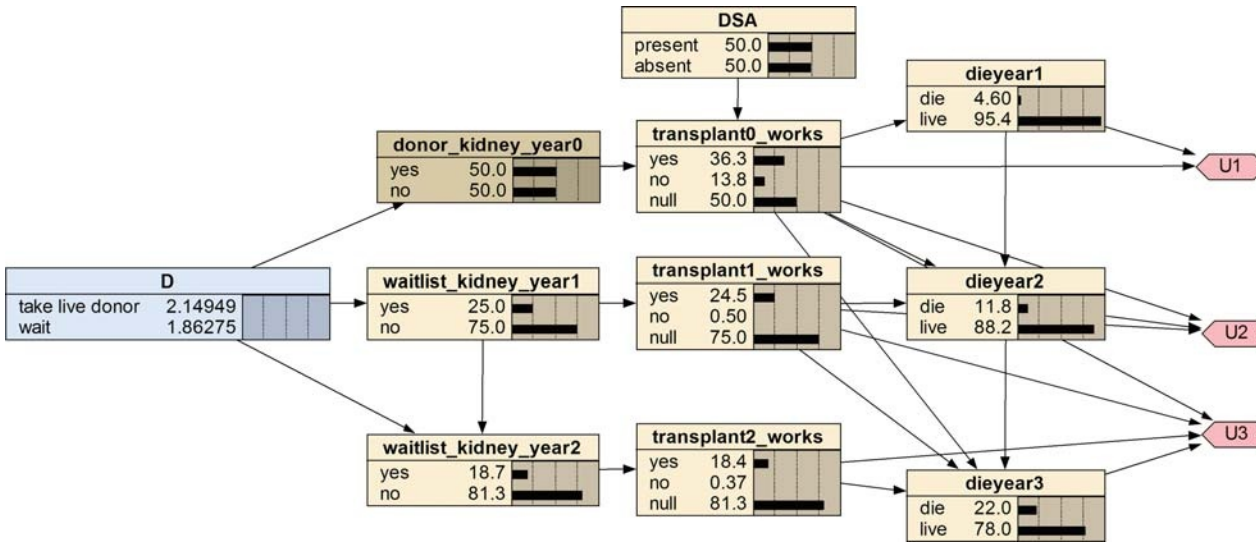


FIGURE 6. An influence diagram modeling the decision whether to accept an incompatible donor kidney.

diagram shows the prior probability of the chance nodes rather than conditional probability distributions, and also the expected utilities of the alternatives for the first decision.

The decision node, which appears on the far left, represents the decision whether to "accept donor" or "wait." The node "donor_kidney_year0" is a deterministic node which has the value "yes" if the decision was to take the donor kidney and the value "no" otherwise. That node affects the node "transplant0_works," which represents whether the transplanted kidney works. Its value is "null" if the value of its parent is "no." That node affects the node "dieyear1" which represents whether the patient dies in the first year, the node "dieyear2" which represents whether the patient dies in the second year, and the node "dieyear3" which represents whether the patient dies in the third year. The node "waitlist_kidney_year1" represents whether the patient receives a compatible kidney in the first year if the decision was to wait. That node affects "transplant1_works" which represents whether the waitlist kidney obtained the first year works. The node "waitlist_kidney_year2" represents whether the patient receives a compatible kidney in the second year if the decision was to wait.

The utility nodes are on the far right. There is 1 node for each year. Each node's value is 1 (year) if the patient lived the year in perfect health, and the value is a QALY if the patient lived the year in less than perfect health. We assigned the quality adjustments based on feasible approximations, not on studies. They are not meant to be used in an actual system. Table 1 shows the utilities for the first utility node.

Let us look at the utilities in Table 1. If the patient dies, the utility is 0. On the other extreme, if the person has the transplant, it works, and the person lives, the utility is 1. If the person has the transplant and it does not work, the QALY has value 0.25. If the person does not have the transplant, the QALY has value 0.5.

Table 2 shows the utilities for the second utility node. The third utility node has similar values. However, we do not show its table because it has 4 parents, and so the table is very large.

The expected utilities of the decision alternatives appear in the decision node. In this case, the expected utility is the QALE. Looking at the decision node, we see that the QALE (based on a 3-year time horizon) of decision "take donor" is 2.4949 and the QALE of "wait" is 1.86275. So, the decision would be to take the donor kidney if we did not know whether a DSA was present. Figure 7 shows the influence diagram with positive DSA. Now the recommended decision is to wait.

CONCLUSIONS

Bayesian networks and influence diagrams are valuable tools for making complex decisions where the trade-off

TABLE 1.

The utilities for the first utility node

U1	dieyear1	transplant0_works
0	die	yes
0	die	no
0	die	null
1	live	yes
0.25	live	no
0.5	live	null

TABLE 2.

The utilities for the second utility node

U2	dieyear2	transplant1_works	transplant0_works
0	die	yes	yes
0	die	yes	no
0	die	yes	null
0	die	no	yes
0	die	no	no
0	die	no	null
0	die	null	yes
0	die	null	no
0	die	null	null
1	live	yes	yes
1	live	yes	no
1	live	yes	null
0.25	live	no	yes
0.25	live	no	no
0.25	live	no	null
1	live	null	yes
0.25	live	null	no
0.5	live	null	null

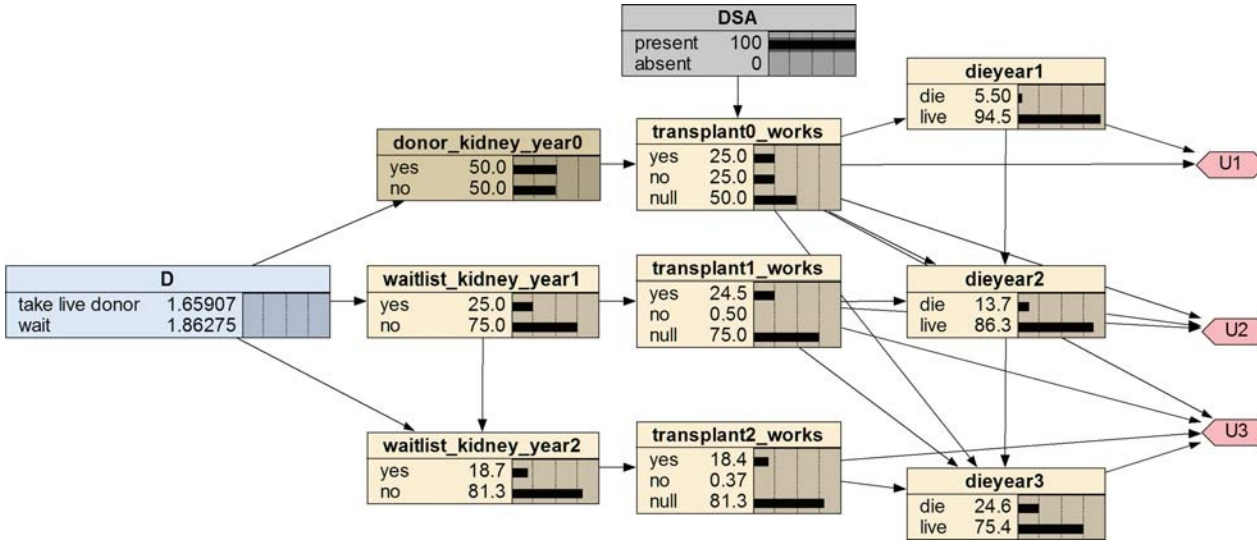


FIGURE 7. The influence diagram in Figure 6 with *DSA* instantiated to *high*.

between risk and benefit is not readily and easily apparent. Decisions in transplant often involve trade-offs between potential benefit and potential harm of treatment or intervention. Though we discussed the KDRI and noted difficulties with it, this issue could easily apply to many other decisions in transplant. For example, consider the decision of whether to treat or not to treat a patient with a protocol biopsy that is suspicious for acute T cell–mediated rejection (Banff 1A). In the absence of further analysis, we might routinely assume a positive test (Banff 1A) result warrants treatment. However, if we assume that (1) the renal biopsy is negative only 80% of the time in the absence of acute rejection (specificity); and (2) that a kidney transplant recipient, who is adherent and has low immunologic risk recipient has a 1% chance of having acute rejection, then a Bayesian analysis reveals that even if the true-positive rate (sensitivity) is 100%, the posterior probability of acute rejection given a positive renal biopsy is only about 0.048. So, the test has little predictive value for such recipients. On the other hand, if a patient is nonadherent, has high immunologic risk with a rising creatinine, then one might assign a 50% priori likelihood to graft failure, and in this case, the Bayesian analysis will reveal that a Banff 1A biopsy result justifies treatment, assuming the true-positive rate is high.

We developed a schema for an influence diagram kidney transplant decision and illustrated how the influence diagram approach can provide the distinct capability of recommending the decision that maximizes the benefit and minimizes the risk of decisions we face everyday in transplant. We used only 1 predictor variable (DSA) that affects the outcome variables in our illustrative system. With a good data set, such as the one used in the KDRI study, we have the opportunity to develop a system that models all relevant predictors and which can provide the clinician and the potential transplant recipient with a valuable decision support tool for many of the complex decisions all stakeholders within transplant must make everyday.

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