Tegaderm CHG IV Securement Dressing for Central Venous and Arterial Catheter Insertion Sites

A decision tree example with probabilistic sensitivity analysis

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2021-01-29

Introduction

This vignette is an example of modelling a decision tree using the `rdecision` package, with probabilistic sensitivity analysis. It is based on the model reported by Jenks *et al* [1] in which a transparent dressing used to secure vascular catheters (Tegaderm CHG) was compared with a standard dressing.

Two methods of evaluating the decision are presented. The first method constructs a decision tree and evaluates the costs associated with traversing each pathway through it. The second method is a direct calculation and summation of costs, without the need to construct a tree. Point estimates and probabilistic sensitivity analysis are conducted for both methods.

Model variables

Thirteen variables were used in the model. The choice of variables, their distributions and their parameters are taken from table 3 of Jenks *et al* [1], with the following corrections:

- For variables with lognormal uncertainty, the manufacturer gave values for the mean m and standard deviation s in log space. However, their standard deviations were quoted as negative values. This was an error, but had no effect on their results, because they sampled values of $\exp(m + sz)$, where z is a sample from a standard normal distribution and is symmetrical about 0. For the variables with log normal uncertainty given below, positive standard deviation parameters, with the same absolute value, have been used as hyperparameters of the log normal distributions. Also note that the *median* value on the natural scale of a random variable distributed as $logN(m, s)$, where μ and σ are the mean and standard deviation on the log scale, is e^{μ}; the mean on the natural scale is slightly larger. For example, the hazard ratio for CRBSI with Tegaderm versus standard dressing was modelled as $logN(-0.911, 0.393)$, which has median 0.402 (the point estimate of the ratio from the literature) and mean 0.434.
- The relative risk for dermatitis was modelled as $logN(1.482, 0.490)$.
- The point estimate cost of CRBSI was £9900, not £9990, although the parameters (198,50) are quoted correctly.

The 13 model variables were constructed as follows:

```
# clinical variables
r.CRBSI <- NormModVar$new(
  'Baseline CRBSI rate', '/1000 catheter days', mu=1.48, sigma=0.074
)
hr.CRBSI <- LogNormModVar$new(
  'Tegaderm CRBSI HR', 'ratio', p1=-0.911, p2=0.393
```

```
)
r.LSI <- NormModVar$new(
  'Baseline LSI rate', '/patient', mu=0.1, sigma=0.01
)
hr.LSI <- LogNormModVar$new(
  'Tegaderm LSI HR', 'ratio', p1=-0.911, p2=0.393
)
r.Dermatitis <- NormModVar$new(
  'Baseline dermatitis risk', '/catheter', mu=0.0026, sigma=0.00026
)
rr.Dermatitis <- LogNormModVar$new(
  'Tegaderm Dermatitis RR', 'ratio',  p1=1.482, p2=0.490
)

# cost variables
c.CRBSI <- GammaModVar$new(
  'CRBSI cost', 'GBP', shape=198.0, scale=50
)
c.Dermatitis <- GammaModVar$new(
  'Dermatitis cost', 'GBP', shape=30, scale=5
)
c.LSI <- GammaModVar$new(
    'LSI cost', 'GBP', shape=50, scale=5
  )
c.Tegaderm <- ConstModVar$new(
  'Tegaderm CHG cost', 'GBP', const=6.21
)
c.Standard <- ConstModVar$new(
  'Standard dressing cost', 'GBP', const=1.34
)
n.cathdays <- NormModVar$new(
  'No. days with catheter', 'days', mu=10, sigma=2
)
n.dressings <- NormModVar$new(
  'No. dressings', 'dressings', mu=3, sigma=0.3
)
```

The decision tree approach

The decision problem may be solved by constructing a decision tree comprising decision nodes, chance nodes and leaf nodes. The general approach is to create expressions involving model variables, construct a tree, and then evaluate the decision for the base case and its uncertainty.

Model variable expressions

Variables in the model may be included in the decision tree via mathematical expressions, which involve model variables and are themselves model variables. Forms of expression involving R's numerical functions and multiple model variables are supported, provided they conform to R syntax. The following code creates the model variable expressions to be used as values in the decision tree edges.

```
# probabilities
p.Dermatitis.S <- ExprModVar$new(
  'P(dermatitis|standard dressing)', 'P',
  rlang::quo(n.dressings*r.Dermatitis)
)
p.Dermatitis.T <- ExprModVar$new(
  'P(dermatitis|Tegaderm)', 'P',
  rlang::quo(n.dressings*r.Dermatitis*rr.Dermatitis)
)
r.LSI.T <- ExprModVar$new(
  'P(LSI|Tegaderm)', 'P', rlang::quo(r.LSI*hr.LSI)
)
p.CRBSI.S <- ExprModVar$new(
  'P(CRBSI|standard dressing)', 'P',  rlang::quo(r.CRBSI*n.cathdays/1000)
)
p.CRBSI.T <- ExprModVar$new(
  'P(CRBSI|Tegaderm)', 'P', rlang::quo(r.CRBSI*n.cathdays*hr.CRBSI/1000)
)
p.NoComp.S <- ExprModVar$new("P(No comp|standard dressing)", "P",
  rlang::quo(1-(p.Dermatitis.S+r.LSI+p.CRBSI.S))
)
p.NoComp.T <- ExprModVar$new("P(No comp|Tegaderm)", "P",
  rlang::quo(1-(p.Dermatitis.T+r.LSI.T+p.CRBSI.T))
)
```

The decision tree

The following code constructs the decision tree based on figure 2 of Jenks *et al* [1]. In the formulation used by `rdecision`, the decision tree is constructed from sets of decision, chance and leaf nodes and from edges (actions and reactions). Leaf nodes are synonymous with pathways in Briggs' terminology [2]). The time horizon is not stated explicitly in the model, and is assumed to be 7 days here. It was implied that the time horizon was ICU stay plus some follow-up, and the costs reflect those incurred in that period, so the assumption of 7 days does not affect the `rdecision` implementation of the model.

```
# create decision tree
th <- as.difftime(7, units="days")
# standard dressing branch
t1 <- LeafNode$new("Dermatitis", interval=th)
t2 <- LeafNode$new("LSI", interval=th)
t3 <- LeafNode$new("CRBSI", interval=th)
t4 <- LeafNode$new("No comp", interval=th)
c1 <- ChanceNode$new()
e1 <- Reaction$new(c1,t1,p=p.Dermatitis.S,cost=c.Dermatitis)
e2 <- Reaction$new(c1,t2,p=r.LSI,cost=c.LSI)
e3 <- Reaction$new(c1,t3,p=p.CRBSI.S,cost=c.CRBSI)
e4 <- Reaction$new(c1,t4,p=p.NoComp.S,cost=0)
# Tegaderm dressing branch
t5 <- LeafNode$new("Dermatitis", interval=th)
t6 <- LeafNode$new("LSI", interval=th)
t7 <- LeafNode$new("CRBSI", interval=th)
t8 <- LeafNode$new("No comp", interval=th)
c2 <- ChanceNode$new()
e5 <- Reaction$new(c2,t5,p=p.Dermatitis.T,cost=c.Dermatitis)
```

```
e6 <- Reaction$new(c2,t6,p=r.LSI.T,cost=c.LSI)
e7 <- Reaction$new(c2,t7,p=p.CRBSI.T,cost=c.CRBSI)
e8 <- Reaction$new(c2,t8,p=p.NoComp.T,cost=0)
# decision node
d1 <- DecisionNode$new("d1")
e9 <- Action$new(d1,c1,label="Standard",cost=c.Standard)
e10 <- Action$new(d1,c2,label="Tegaderm",cost=c.Tegaderm)
# create decision tree
V <- list(d1,c1,c2,t1,t2,t3,t4,t5,t6,t7,t8)
E <- list(e1,e2,e3,e4,e5,e6,e7,e8,e9,e10)
DT <- DecisionTree$new(V,E)
```

In the manufacturer's model, the uncertainties in the probabilities associated with the polytomous chance nodes were modelled as independent variables. This is not recommended because there is a chance that a particular run of the PSA will yield probabilities that are outside the range [0,1]. Representing the uncertain probabilities with draws from a Dirichlet distribution is preferred. Creating a `ChanceNode` with ModVars is permitted, but results in a warning being issued.

Summary of the model

The model variables and their operands associated with a node and (optionally) its descendants can be tabulated using the method `tabulate_modvars`. This returns a data frame describing each variable, its description, units and uncertainty distribution. Variables inheriting from type `ModVar` will be included in the tabulation; regular numeric values will not be listed. For extensive models, variables associated with separate branches of a tree can be tabulated separately by calling the method for different head nodes.

The operands of model variables which are expressions of other model variables can be included in the tabulation via the `include.operands` parameter. This is recursive, allowing the complete structure of a model, *i.e.* its model variables and the way in which they are combined, to be tabulated. In the Tegaderm model, the complete structure is as follows:

Description	Distribution
Dermatitis cost	Ga(30,5)
P(dermatitis|standard dressing)	n.dressings * r.Dermatitis
No. dressings	N(3,0.3)
Baseline dermatitis risk	N(0.0026,0.00026)
LSI cost	Ga(50,5)
Baseline LSI rate	N(0.1,0.01)
CRBSI cost	Ga(198,50)
P(CRBSI|standard dressing)	r.CRBSI * n.cathdays/1000
Baseline CRBSI rate	N(1.48,0.074)
No. days with catheter	N(10,2)
P(No comp|standard dressing)	1 - (p.Dermatitis.S + r.LSI + p.CRBSI.S)
P(dermatitis|Tegaderm)	n.dressings * r.Dermatitis * rr.Dermatitis
Tegaderm Dermatitis RR	LN1(1.482,0.49)
P(LSI|Tegaderm)	r.LSI * hr.LSI
Tegaderm LSI HR	LN1(-0.911,0.393)
P(CRBSI|Tegaderm)	r.CRBSI * n.cathdays * hr.CRBSI/1000
Tegaderm CRBSI HR	LN1(-0.911,0.393)
P(No comp|Tegaderm)	1 - (p.Dermatitis.T + r.LSI.T + p.CRBSI.T)
Standard dressing cost	Const(1.34)
Tegaderm CHG cost	Const(6.21)

Point estimates and distributions of model variables

The point estimates, units and distributional properties are obtained from the same call, in the remaining columns. Rows with `Qhat` indicate that the quantiles have been estimated from simulation.

Description	Units	Mean	Q2.5	Q97.5	Qhat
Dermatitis cost	GBP	150.000	NA	NA	NA
P(dermatitis|standard dressing)	P	0.008	NA	NA	NA
No. dressings	dressings	3.000	NA	NA	NA
Baseline dermatitis risk	/catheter	0.003	NA	NA	NA
LSI cost	GBP	250.000	NA	NA	NA
Baseline LSI rate	/patient	0.100	NA	NA	NA
CRBSI cost	GBP	9900.000	NA	NA	NA
P(CRBSI|standard dressing)	P	0.015	NA	NA	NA
Baseline CRBSI rate	/1000 catheter days	1.480	NA	NA	NA
No. days with catheter	days	10.000	NA	NA	NA
P(No comp|standard dressing)	P	0.877	NA	NA	NA
P(dermatitis|Tegaderm)	P	0.039	NA	NA	NA
Tegaderm Dermatitis RR	ratio	4.963	NA	NA	NA
P(LSI|Tegaderm)	P	0.043	NA	NA	NA
Tegaderm LSI HR	ratio	0.434	NA	NA	NA
P(CRBSI|Tegaderm)	P	0.006	NA	NA	NA
Tegaderm CRBSI HR	ratio	0.434	NA	NA	NA
P(No comp|Tegaderm)	P	0.911	NA	NA	NA
Standard dressing cost	GBP	1.340	NA	NA	NA
Tegaderm CHG cost	GBP	6.210	NA	NA	NA

Running the model

The following code runs a single model scenario, using the `evaluatePathways` method of a decision node to evaluate each pathway from the decision node. In the model there are eight possible root-to-leaf paths, each of which begins with the decision node and ends with a leaf node. For example, pathway `Dermatitis (Standard Dressing)` involves a traversal of nodes `d`, `chance.S`, and `leaf.S.Dermatitis`. The method `evaluateChoices` is similar, but aggregates the results by choice. The results of the scenario model, using the code from the previous section, yields the following table. This model did not consider utility, and the columns associated with utility are removed.

References

1 Jenks M, Craig JA, Green W *et al.* Tegaderm CHG IV securement dressing for central venous and arterial catheter insertion sites: A NICE Medical Technology Guidance. *Applied Health Economics and Health Policy* 2016;**14**:135–49.

2 Briggs A, Claxton K, Sculpher M. *Decision modelling for health economic evaluation.* Oxford, UK:: Oxford University Press 2006.