

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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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* (2016) in which a transparent dressing used to secure vascular catheters (Tegaderm CHG) was compared with a standard dressing.

Creating the model

Model variables

The following code creates the variables to be used in the model. The choice of variables, their distributions and their parameters are taken from table 3 of Jenks *et al* (2016).

```
# clinical variables
rate.CRBSI <- NormalModelVariable$new(
  'Baseline CRBSI rate',
  'per 1000 catheter days',
  mu=1.48, sigma=0.074
)
rate.LSI <- NormalModelVariable$new(
  'Baseline LSI rate',
  'per patient',
  mu=0.1, sigma=0.01
)
rate.Dermatitis <- NormalModelVariable$new(
  'Baseline dermatitis risk',
  'per catheter',
  mu = 0.0026, sigma=0.00026
)

# cost variables
cost.CRBSI <- GammaModelVariable$new('Cost of CRBSI', 'GBP', alpha=198, beta=50)
cost.Dermatitis <- GammaModelVariable$new('Cost of dermatitis', 'GBP', alpha=30, beta=5)
cost.LSI <- GammaModelVariable$new('Cost of LSI', 'GBP', alpha=50, beta=5)
cost.Tegaderm <- ConstModelVariable$new('Cost of Tegaderm CHG', 'GBP', const=6.21)
cost.Standard <- ConstModelVariable$new('Cost of standard dressing', 'GBP', const=1.34)
n.cathdays <- NormalModelVariable$new('No. of days with catheter', NA, mu=10, sigma=2)
n.dressings <- NormalModelVariable$new('No. of dressings', NA, mu=3, sigma=0.3)
```

Model variable expressions

Variables in the model may be included in the decision tree via model variable expressions, which are mathematical expressions which involve model variables. The most simple form of model variable expression involving a model variable `X` is simply `quote(X)`. More complex forms of expression involving R's numerical functions and multiple model variables are supported, provided the expressions conform to R syntax.

The following code creates the model variable expressions to be used as values in the decision tree nodes.

```
# probabilities
p.Dermatitis.S <- ModelVariableExpression$new(
  quote(rate.Dermatitis),
  'Probability of dermatitis with standard dressing'
)
p.LSI.S <- ModelVariableExpression$new(
  quote(rate.LSI),
  'Probability of LSI with standard dressing'
)
p.CRBSI.S <- ModelVariableExpression$new(
  quote(rate.CRBSI*n.cathdays/1000),
  'Probability of CRBSI with standard dressing'
)

# costs
cost.Dermatitis.MVE <- ModelVariableExpression$new(
  quote(cost.Dermatitis),
  'Cost of dermatitis'
)
cost.LSI.MVE <- ModelVariableExpression$new(
  quote(cost.LSI),
  'Cost of LSI'
)
cost.CRBSI.MVE <- ModelVariableExpression$new(
  quote(cost.CRBSI),
  'Cost of CRBSI'
)
cost.S <- ModelVariableExpression$new(
  quote(n.dressings*cost.Standard)
)
cost.T <- ModelVariableExpression$new(
  quote(n.dressings*cost.Tegaderm)
)
```

Constructing the decision tree

The following code constructs the decision tree, node by node, based on figure 2 of Jenks *et al* (2016). In the formulation used by `rdecision`, each node is a potentially recursive structure which is allowed to have zero or more child nodes; any child nodes must have already been declared before their parent node is declared. This implies that a tree should be constructed from right to left, starting with leaf nodes which have no children (leaf nodes are synonymous with pathways in Briggs' terminology (2006)). The final node to be constructed is the node representing the decision problem.

```
# standard dressing branch
leaf.S.Dermatitis <- LeafNode$new('Dermatitis (Standard Dressing)')
```

```

leaf.S.LSI <- LeafNode$new('Local site infection (Standard Dressing)')
leaf.S.CRBSI <- LeafNode$new('CRBSI (Standard Dressing)')
leaf.S.NoComp <- LeafNode$new('No complication (Standard Dressing)')

chance.S <- ChanceNode$new(
  children = list(leaf.S.Dermatitis, leaf.S.LSI, leaf.S.CRBSI, leaf.S.NoComp),
  p = c(p.Dermatitis.S, p.LSI.S, p.CRBSI.S, as.numeric(NA)),
  edgelabels = c('Dermatitis', 'Local site infection', 'CRBSI', 'No complication'),
  costs = c(cost.Dermatitis.MVE, cost.LSI.MVE, cost.CRBSI.MVE, 0)
)

# Tegaderm dressing branch
leaf.T.Dermatitis <- LeafNode$new('Dermatitis (Tegaderm CHG)')
leaf.T.LSI <- LeafNode$new('Local site infection (Tegaderm CHG)')
leaf.T.CRBSI <- LeafNode$new('CRBSI (Tegaderm CHG)')
leaf.T.NoComp <- LeafNode$new('No complication (Tegaderm CHG)')

chance.T <- ChanceNode$new(
  children = list(leaf.T.Dermatitis, leaf.T.LSI, leaf.T.CRBSI, leaf.T.NoComp),
  p = c(0.25, 0.25, 0.25, 0.25),
  edgelabels = c('Dermatitis', 'Local site infection', 'CRBSI', 'No complication'),
  costs = c(cost.Dermatitis.MVE, cost.LSI.MVE, cost.CRBSI.MVE, 0)
)

# decision node
d <- DecisionNode$new(
  children = list(chance.S, chance.T),
  edgelabels = c('Standard Dressing', 'Tegaderm CHG'),
  costs = c(cost.S, cost.T)
)

```

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 `ModelVariableExpressions` is permitted, but results in a warning being issued.

Running the model

The following code runs a single model scenario, using low-level functions to evaluate each pathway and decision option. The `path.apply` function applies a user-provided function to each node of every root-to-leaf path in the model. 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 following code extracts and calculates various features associated with each root-to-leaf node traversal, and puts them into a table. The extra parameter `expected=T` ensures that the expected values of the model variables are returned, rather than a sample from their distributions.

```

RES <- data.frame(
  'Choice' = unlist(path.apply(d, FUN=pathway.choice)),
  'Pathway' = unlist(path.apply(d, FUN=pathway.name)),
  'Probability' = unlist(path.apply(d, FUN=pathway.probability, expected=F)),

```

```

'Cost' = unlist(path.apply(d, FUN=pathway.cost, expected=F)),
'ExpectedCost' = NA
)
#> num [1:4] 0.00231 0.10536 0.01506 NA
#> num [1:4] 0.00239 0.10773 0.01396 NA
#> num [1:4] 0.0025 0.0937 0.0147 NA
#> num [1:4] 0.00273 0.08121 0.01669 NA
#> num [1:4] 0.25 0.25 0.25 0.25
#> num [1:4] 0.25 0.25 0.25 0.25
#> num [1:4] 0.25 0.25 0.25 0.25
#> num [1:4] 0.25 0.25 0.25 0.25
RES$ExpectedCost <- round(RES$Probability*RES$Cost,2)

```

Model results

Base case

The results of the scenario model, using the code from the previous section, yields the following result:

Choice	Pathway	Probability	Cost	ExpectedCost
Standard Dressing	Dermatitis (Standard Dressing)	0.0023051	121.964499	0.28
Standard Dressing	Local site infection (Standard Dressing)	0.0023861	273.975356	0.65
Standard Dressing	CRBSI (Standard Dressing)	0.0025010	8813.278875	22.04
Standard Dressing	No complication (Standard Dressing)	0.0027267	4.187455	0.01
Tegaderm CHG	Dermatitis (Tegaderm CHG)	0.2500000	194.202997	48.55
Tegaderm CHG	Local site infection (Tegaderm CHG)	0.2500000	235.852747	58.96
Tegaderm CHG	CRBSI (Tegaderm CHG)	0.2500000	10169.701575	2542.43
Tegaderm CHG	No complication (Tegaderm CHG)	0.2500000	19.056208	4.76

There are, as expected, eight root-to-leaf pathways, which `path.apply` has worked out itself from the model structure. The total probability, expected cost for each choice can be calculated from the table as follows:

```

SUM <- aggregate(
  RES[,c('Probability', 'ExpectedCost')],
  by = list(RES$Choice),
  FUN = sum
)
names(SUM) <- c('Choice', 'Probability', 'Expected Cost')

```

which gives the following result, which is consistent with the result reported by Jenks *et al* (2016).

Choice	Probability	Expected Cost
Standard Dressing	0.0099189	22.98
Tegaderm CHG	1.0000000	2654.70

References

Briggs, Andrew, Karl Claxton, and Mark Sculpher. 2006. *Decision Modelling for Health Economic Evaluation*. Oxford, UK: Oxford University Press.

Jenks, Michelle, Joyce Craig, William Green, Neil Hewitt, Mick Arber, and Andrew J. Sims. 2016. “Tegaderm CHG IV Securement Dressing for Central Venous and Arterial Catheter Insertion Sites: A NICE Medical Technology Guidance.” *Applied Health Economics and Health Policy*.