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 4 of Jenks *et al* (2016).

```
# clinical variables
r.CRBSI <- GammaModelVariable$new(
  'Baseline CRBSI rate',
  '/1000 catheter days',
  alpha=1.48*100, beta=1/100
)
hr.CRBSI <- LogNormalModelVariable$new(
  'Tegaderm CRBSI HR',
  'ratio',
  mu=log(0.402), sigma=0.393
)
r.LSI <- GammaModelVariable$new(
  'Baseline LSI rate',
  '/1000 catheter days',
  alpha=1.4, beta=0.1
)
hr.LSI <- LogNormalModelVariable$new(
  'Tegaderm LSI HR',
  'ratio',
  mu=log(0.402), sigma=0.393
)
r.Dermatitis <- BetaModelVariable$new(
  'Baseline dermatitis probability',
  'probability',
```

```
  alpha=1, beta=475
)
rr.Dermatitis <- LogNormalModelVariable$new(
  'Tegaderm Dermatitis RR',
  'ratio',
  mu=log(1), sigma=0.5
)

# cost variables
c.CRBSI <- GammaModelVariable$new('CRBSI cost', 'GBP', alpha=9990/3000, beta=3000)
c.Dermatitis <- GammaModelVariable$new('Dermatitis cost', 'GBP', alpha=2, beta=3)
c.LSI <- GammaModelVariable$new('LSI cost', 'GBP', alpha=100/30, beta=30)
c.Tegaderm <- ConstModelVariable$new('Tegaderm CHG cost', 'GBP', const=6.26)
c.Standard <- ConstModelVariable$new('Standard dressing cost', 'GBP', const=1.54)
n.cathdays <- GammaModelVariable$new('No. days with catheter', 'days', alpha=10/5, beta=5)
n.dressings <- GammaModelVariable$new('No. dressings', 'dressings', alpha=3/2, beta=2)
```

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 `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$new(
  quote(r.Dermatitis),
  'Probability of dermatitis with standard dressing'
)
p.Dermatitis.T <- ModelVariableExpression$new(
  quote(r.Dermatitis*rr.Dermatitis),
  'Probability of dermatitis with Tegaderm'
)
p.LSI.S <- ModelVariableExpression$new(
 quote(r.LSI),
 'Probability of LSI with standard dressing'
)
p.LSI.T <- ModelVariableExpression$new(
 quote(r.LSI*hr.LSI),
 'Probability of LSI with Tegaderm'
)
p.CRBSI.S <- ModelVariableExpression$new(
  quote(r.CRBSI*n.cathdays/1000),
  'Probability of CRBSI with standard dressing'
)
p.CRBSI.T <- ModelVariableExpression$new(
  quote(r.CRBSI*n.cathdays*hr.CRBSI/1000),
  'Probability of CRBSI with standard dressing'
)

# costs
```

```
c.Dermatitis.MVE <- ModelVariableExpression$new(
  quote(c.Dermatitis),
  'Cost of dermatitis'
)
c.LSI.MVE <- ModelVariableExpression$new(
  quote(c.LSI),
  'Cost of LSI'
)
c.CRBSI.MVE <- ModelVariableExpression$new(
  quote(c.CRBSI),
  'Cost of CRBSI'
)
c.S <- ModelVariableExpression$new(
  quote(n.dressings*c.Standard)
)
c.T <- ModelVariableExpression$new(
  quote(n.dressings*c.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),
  edgelabels = c('Dermatitis', 'Local site infection', 'CRBSI', 'No complication'),
  costs = list(c.Dermatitis.MVE, c.LSI.MVE, c.CRBSI.MVE, 0),
  p = list(p.Dermatitis.S, p.LSI.S, p.CRBSI.S, as.numeric(NA)),
  ptype = 'MVE'
)

# 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),
  edgelabels = c('Dermatitis', 'Local site infection', 'CRBSI', 'No complication'),
  costs = list(c.Dermatitis.MVE, c.LSI.MVE, c.CRBSI.MVE, 0),
  p = list(p.Dermatitis.T, p.LSI.T, p.CRBSI.T, as.numeric(NA)),
```

```
  ptype='MVE'
)

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

Documenting the model

Package `rdecision` includes tools for automated documentation of the model structure and inputs.

Model inputs

The model variables associated with a node and its descendants can be tabulated using the method `tabulateModelVariables`. The method returns a data frame describing each variable, its description, units and uncertainty distribution. Variables inheriting from type `ModelVariable` 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. Selected columns are omitted from the

```
local({
  DF <- d$tabulateModelVariables()
  DF$Variable <- NULL
  DF$SD <- NULL
  knitr::kable(DF, row.names=F, format.args=list(scientific=F), digits=3)
})
```

Description	Units	Distribution	Mean	Q2.5	Q97.5
No. dressings	dressings	Ga(1.5,2)	3.000	0.216	9.348
Standard dressing cost	GBP	Constant	1.540	1.540	1.540
Tegaderm CHG cost	GBP	Constant	6.260	6.260	6.260
Baseline dermatitis probability	probability	Be(1,475)	0.002	0.000	0.008
Baseline LSI rate	/1000 catheter days	Ga(1.4,0.1)	0.140	0.009	0.449
Baseline CRBSI rate	/1000 catheter days	Ga(148,0.01)	1.480	1.251	1.728
No. days with catheter	days	Ga(2,5)	10.000	1.211	27.858
Dermatitis cost	GBP	Ga(2,3)	6.000	0.727	16.715
LSI cost	GBP	Ga(3.333,30)	100.000	23.017	232.451
CRBSI cost	GBP	Ga(3.33,3000)	9990.000	2297.146	23229.563
Tegaderm Dermatitis RR	ratio	logN(0,0.5)	1.133	0.375	2.664
Tegaderm LSI HR	ratio	logN(-0.911,0.393)	0.434	0.186	0.868
Tegaderm CRBSI HR	ratio	logN(-0.911,0.393)	0.434	0.186	0.868

Running the model

The following code runs a single model scenario, using the `evaluate` method of a decision node to evaluate each pathway and decision option. 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`. This model did not consider utility, and the columns associated with utility are removed.

```
RES <- d$evaluate(expected=T)
RES$Utility <- NULL
RES$ExpectedUtility <- NULL
```

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)	0.0021008	10.62	0.02
Standard Dressing	Local site infection (Standard Dressing)	0.1400000	104.62	14.65
Standard Dressing	CRBSI (Standard Dressing)	0.0148000	9994.62	147.92
Standard Dressing	No complication (Standard Dressing)	0.8430992	4.62	3.90
Tegaderm CHG	Dermatitis (Tegaderm CHG)	0.0023806	24.78	0.06
Tegaderm CHG	Local site infection (Tegaderm CHG)	0.0607984	118.78	7.22
Tegaderm CHG	CRBSI (Tegaderm CHG)	0.0064273	10008.78	64.33
Tegaderm CHG	No complication (Tegaderm CHG)	0.9303938	18.78	17.47

There are, as expected, eight root-to-leaf pathways, which `path.apply` has worked out itself from the model structure. The total probability and expected cost for each choice can be calculated from the table as follows which gives a result consistent with that reported by Jenks *et al* (2016).

```
local({
  SUM <- aggregate(
    RES[,c('Probability', 'ExpectedCost')],
    by = list(RES$Choice),
    FUN = sum
  )
  names(SUM) <- c('Choice', 'Probability', 'Expected Cost')
  knitr::kable(SUM)
})
```

Choice	Probability	Expected Cost
Standard Dressing	1	166.49
Tegaderm CHG	1	89.08

Probabilistic senstivity analysis

When they are created, each `ModelVariable` returns its expected value when its method `value()` is called. Calling the method `sample()` of a model variable causes it to sample from its uncertainty distribution, and return the sampled value when method `value()` is next called. The same sampled value will be returned until `sample()` is called again. Calling `sample(expected=T)` causes `value()` to return the expected value of the variable.

Probabilistic sensitivity analysis is supported through the use of sampling model variables. In practice, because the model variables are contained within model variable expressions embedded in the model, decision nodes expose a method called `sample()`. This causes each model variable associated with the decision node and its descendants to be sampled. The code needed to run N samples of the model, and the results of the first 10 samples are as follows:

```
local({
  N <- 10000
  RES <<- data.frame(
    Run = 1:N,
    Tegaderm = numeric(length=N),
    Standard = numeric(length=N)
  )
  for (i in 1:N) {
    RUN <- d$evaluate(expected=F)
    RES$Tegaderm[i] <<- sum(RUN$ExpectedCost[RUN$Choice=='Tegaderm CHG'])
    RES$Standard[i] <<- sum(RUN$ExpectedCost[RUN$Choice=='Standard Dressing'])
  }
  RES$Difference <<- RES$Tegaderm - RES$Standard
  knitr::kable(head(RES, n=10))
})
#> Warning in edge$setP(pedge[i]): Edge$setP: Conditional probability argument to
#> Edge adjusted to range [0,1]

#> Warning in edge$setP(pedge[i]): Edge$setP: Conditional probability argument to
#> Edge adjusted to range [0,1]

#> Warning in edge$setP(pedge[i]): Edge$setP: Conditional probability argument to
#> Edge adjusted to range [0,1]

#> Warning in edge$setP(pedge[i]): Edge$setP: Conditional probability argument to
#> Edge adjusted to range [0,1]
```

Run	Tegaderm	Standard	Difference
1	71.81	20.70	51.11
2	79.22	49.44	29.78
3	402.26	110.84	291.42
4	85.09	88.42	-3.33
5	66.33	277.51	-211.18
6	35.46	133.18	-97.72
7	66.45	97.19	-30.74
8	24.07	187.33	-163.26
9	48.59	33.55	15.04
10	103.08	91.75	11.33

From PSA, the median cost of treatment with Tegaderm was 89.33, the median cost of treatment with standard dressings was 167.51 and the median cost saving was -78.18. The 95% confidence interval for cost saving was -495 to 172.6. Overall, 70.48% of runs found that Tegaderm was cost saving. These results replicate those reported by the manufucturer.

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.*