

A dip into R for decision modelling

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Poll: What software do you mostly use for cost-effectiveness analysis?

Live Content Slide

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Poll: Do you think R is better for cost-effectiveness analysis and modelling than Excel?



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Overview

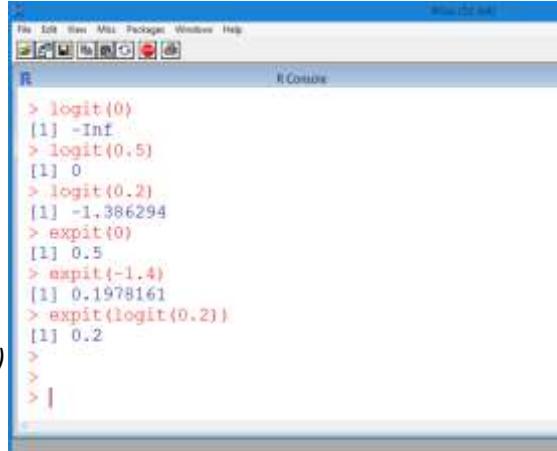
- Heard the wonderful things you can do in R.
- Itching to get your hands dirty?
- We'll now talk through the specifics of programming a (probabilistic) decision tree in R.
- The most boring presentation of ISPOR? We'll see...



Simple functions – logit and its inverse

```
# Logistic link function
logit<-function(x)
{
  return(log(x/(1-x)))
}

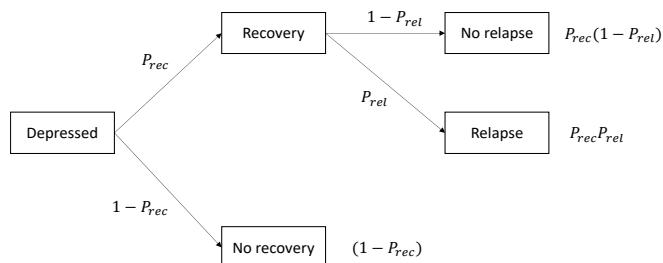
# Inverse of logit
expit<-function(x)
{
  return(1/(1+exp(-x)))
}
```



R Console

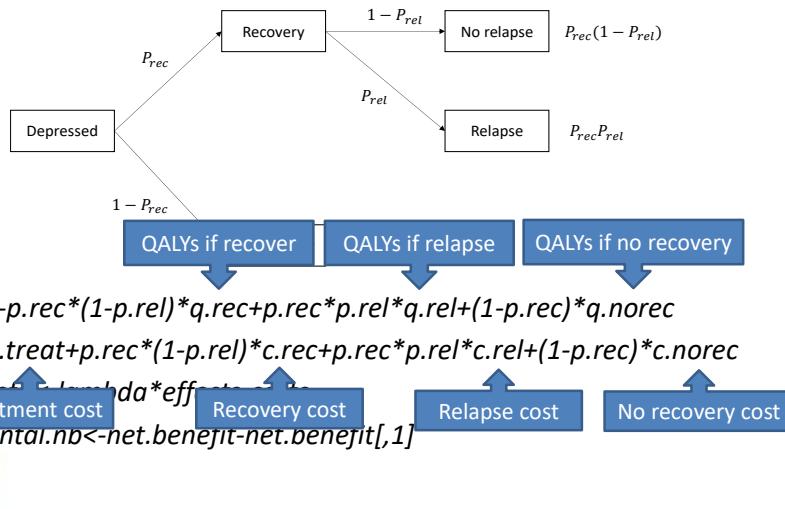
```
> logit(0)
[1] -Inf
> logit(0.5)
[1] 0
> logit(0.2)
[1] -1.386294
> expit(0)
[1] 0.5
> expit(-1.4)
[1] 0.1978161
> expit(logit(0.2))
[1] 0.2
>
>
> |
```

Simple decision tree in R

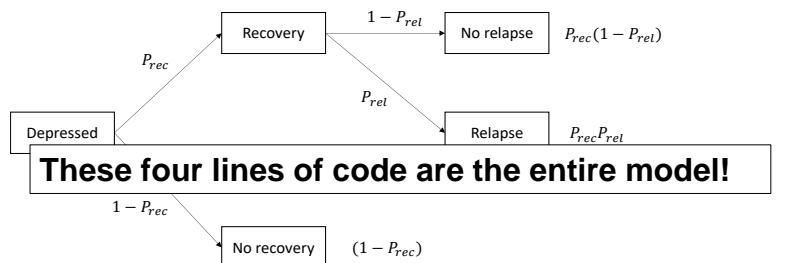


- Consider this simple decision tree with artificial input parameters.
- Probabilities of recovery and relapse for no treatment (option 1), cognitive behavioural therapy (option 2), and antidepressants (option 3).
- This toy model is available on GitHub:
<https://github.com/Bogdasayen/Depression-toy-decision-tree-in-R>

Implementing a decision tree in R

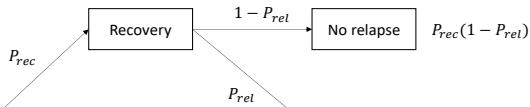


Implementing a decision tree in R



And now we make it probabilistic...

Making it probabilistic (model code)



See any difference?

R performs the same calculations whether the p.rec and other variables are vectors or scalars

No recovery $(1 - P_{rec})$

```

effects<-p.rec*(1-p.rel)*q.rec+p.rec*p.rel*q.rel+(1-p.rec)*q.norec
costs<-c.treat+p.rec*(1-p.rel)*c.rec+p.rec*p.rel*c.rel+(1-p.rec)*c.norec
net.benefit<-lambda*effects-costs
incremental.nb<-net.benefit-net.benefit[,1]
  
```



Making it probabilistic (Costs, Utilities)

Outcome	Costs	QALYS
Recovery, no relapse	$C_{rec} = N(\mu = 1000, \sigma = 50)$	$Q_{rec} = N(\mu = 26, \sigma = 2)$
Recovery, relapse	$C_{rel} = N(\mu = 2000, \sigma = 100)$	$Q_{rel} = N(\mu = 23, \sigma = 3)$
No recovery	$C_{no\ rec} = N(\mu = 2500, \sigma = 125)$	$Q_{no\ rec} = N(\mu = 20, \sigma = 4)$

```

# Costs for recovery, relapse, and no recovery
c.rec<-rnorm(n=n.samples, mean=1000, sd=50)
c.rel<-rnorm(n=n.samples, mean=2000, sd=100)
c.norec<-rnorm(n=n.samples, mean=2500, sd=125)
  
```

```

# QALYs for recovery, relapse, and no recovery
q.rec<-rnorm(n=n.samples, mean=26, sd=2)
q.rel<-rnorm(n=n.samples, mean=23, sd=3)
q.norec<-rnorm(n=n.samples, mean=20, sd=4)
  
```



Making it probabilistic (Treatment effects)

- Log odds ratios follow multivariate normal

Recovery:
$$\begin{pmatrix} lor_{2,rec} \\ lor_{3,rec} \end{pmatrix} \sim MVN \left(\begin{pmatrix} 0.99 \\ 1.33 \end{pmatrix}, \begin{pmatrix} 0.22 & 0.15 \\ 0.15 & 0.20 \end{pmatrix} \right)$$

Relapse:
$$\begin{pmatrix} lor_{2,rel} \\ lor_{3,rel} \end{pmatrix} \sim MVN \left(\begin{pmatrix} -1.48 \\ -0.40 \end{pmatrix}, \begin{pmatrix} 0.14 & 0.05 \\ 0.05 & 0.11 \end{pmatrix} \right)$$

- As it's a statistical language, the multivariate normal is implemented simply in R:

```
lor.rec<-mvrnorm(n=n.samples,mu=c(0.99,1.33),  
sigma=matrix(c(0.22,0.15,0.15,0.20),nrow=2))  
lor.rel<-mvrnorm(n=n.samples,mu=c(-1.48,-0.40),  
sigma=matrix(c(0.14,0.05,0.05,0.11),nrow=2))
```



Instead use MCMC via R2OpenBUGS

- Link directly with network meta-analysis code in OpenBUGS (or JAGS/STAN etc.)

```
library(R2OpenBUGS)
```

- Load some BUGS model file

```
source("fixed.effects.binary.R")
```

- Set simulation parameters

```
n.chains<-2; num.sims<-10000*n.chains; burn.in<-50000*n.chains
```

- Call R2OpenBUGS key function

```
bugs.object<-
```

```
bugs(data=bugs.data.recovery,inits=NA,model=fixed.effects.binary...)
```

- Then get parameter samples from bugs.object\$sims.array



Instead MCMC via R2OpenBUGS

- Or load precalculated log odds ratios for recovery (similarly for relapse)
`mcmc.recovery<-read.csv(file="lor.recovery.bugs.csv")`
- Can use just the first n.samples of the matrix
`lor.rec<-mcmc.recovery[1:n.samples,]`

Making it probabilistic (Reference probabilities)

Parameter	No Treatment (Option 1)
P_{rec}	$P_{1,rec} = Beta(\alpha = 6, \beta = 200)$
P_{rel}	$P_{1,rel} = Beta(\alpha = 2, \beta = 100)$

- The beta distribution is another of many implemented in base R.
- Note however the idiosyncratic naming convention of the parameters.
- α is *shape1* and β is *shape2*.

```
p.rec[,1]<-rbeta(n=n.samples, shape1=6, shape2=200)
p.rel[,1]<-rbeta(n=n.samples, shape1=2, shape2=100)
```

Making it probabilistic (Comparator probabilities)

Parameter	CBT (Option 2)	Antidepressant (Option 3)
P_{rec}	$P_{2,rec} = \text{expit}(\text{logit}(P_{1,rec}) + lor_{2,rec})$	$P_{3,rec} = \text{expit}(\text{logit}(P_{1,rec}) + lor_{3,rec})$
P_{rel}	$P_{2,rel} = \text{expit}(\text{logit}(P_{1,rel}) + lor_{2,rel})$	$P_{3,rel} = \text{expit}(\text{logit}(P_{1,rel}) + lor_{3,rel})$

- We can use a loop over the number of treatments $n.treat$

```
for(i in 2:n.treat){
  p.rec[,i]<-expit(logit(p.rec[,1])+lor.rec[,i-1])
  p.rel[,i]<-expit(logit(p.rel[,1])+lor.rel[,i-1])
}
```

Making it probabilistic - vectorise

Parameter	CBT (Option 2)	Antidepressant (Option 3)
P_{rec}	$P_{2,rec} = \text{expit}(\text{logit}(P_{1,rec}) + lor_{2,rec})$	$P_{3,rec} = \text{expit}(\text{logit}(P_{1,rec}) + lor_{3,rec})$
P_{rel}	$P_{2,rel} = \text{expit}(\text{logit}(P_{1,rel}) + lor_{2,rel})$	$P_{3,rel} = \text{expit}(\text{logit}(P_{1,rel}) + lor_{3,rel})$

- Or we can vectorise, which is much faster than a loop

```
p.rec[,c(2:n.treat)]<-expit(logit(p.rec[,1])+lor.rec[,c(2:n.treat)-1])
p.rel[,c(2:n.treat)]<-expit(logit(p.rel[,1])+lor.rel[,c(2:n.treat)-1])
```

- The expit and logit functions work on vectors and matrices.
- Can set $n.treat$ to any number without having to duplicate code.

Formatting results

- Use `paste("string1", "string2")` function for string concatenation
- Use `round(x,digits=3)` for numeric formatting

```
format.results<-function(x,digits=2)
{
  paste(round(mean(x),digits=digits),
        ("",round(quantile(x,probs=0.025),digits=digits),
        ",round(quantile(x,probs=0.975),digits=digits),"",sep=""))
}
>
>
> c.rec<-rnorm(n=n.samples, mean=1000, sd=50)
> format.results(c.rec)
[1] "999.38 (901.73, 1095.85)"
>
```

Decision tree results

- Build a results matrix

```
results.matrix<-matrix(NA, nrow=4,ncol=n.treat)
```

- Name the rows and columns

```
rownames(results.matrix)<-c("Total costs","Total QALYs", "Net Benefit", "Incremental NB")
```

```
colnames(results.matrix)<-t.names
```

- Then calculate summaries

```
for(i.treat in 1:n.treat)
```

```
{
```

```
  results.matrix["Total costs",i.treat]<-format.results(x=costs[,i.treat])
  results.matrix["Total QALYs",i.treat]<-format.results(x=effects[,i.treat])
  results.matrix["Net Benefit",i.treat]<-format.results(x=net.benefit[,i.treat])
  results.matrix["Incremental NB",i.treat]<-format.results(x=incremental.nb[,i.treat])
```

```
}
```

Exporting the results matrix to Excel

- Export as a csv

```
write.csv(results.matrix, file="depression.results.csv")
```

- Or as an Excel file

```
library(xlsx)
```

```
write.xlsx(results.matrix, file="depression.results.xlsx", sheetName="CEA results")
```

	No treatment	CBT	Antidepressant
Total costs	2458.08 (2216.38, 2692.91)	2678.9 (2424.37, 2937.03)	2366.58 (2087.97, 2621.49)
Total QALYs	20.09 (12.87, 27.59)	20.41 (13.54, 27.56)	20.59 (14.02, 27.52)
So you can link back to Excel if you really can't resist.			
Net Benefit	549117.1)	548404.61)	548049.21)
Incremental NB	0 (0, 0)	6162.68 (-1978.38, 26095.58)	9996.67 (-2660.86, 36001.2)

And next?

- The model is available for you to try:

<https://github.com/Bogdasayen/Depression-toy-decision-tree-in-R>

- A full Markov cost-effectiveness model is also available:

<https://github.com/Bogdasayen/DOACs-AF-Economic-model>

- Bristol University will run a 2-day introductory course on R for Economic Evaluation.

- Internal pilot in 2019, open externally in 2020.

- Devin will now show you what can be done once R is mastered...



Thank you!

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