

An overview of a suite of functions for CEA in R using continuous-time multi-state modelling

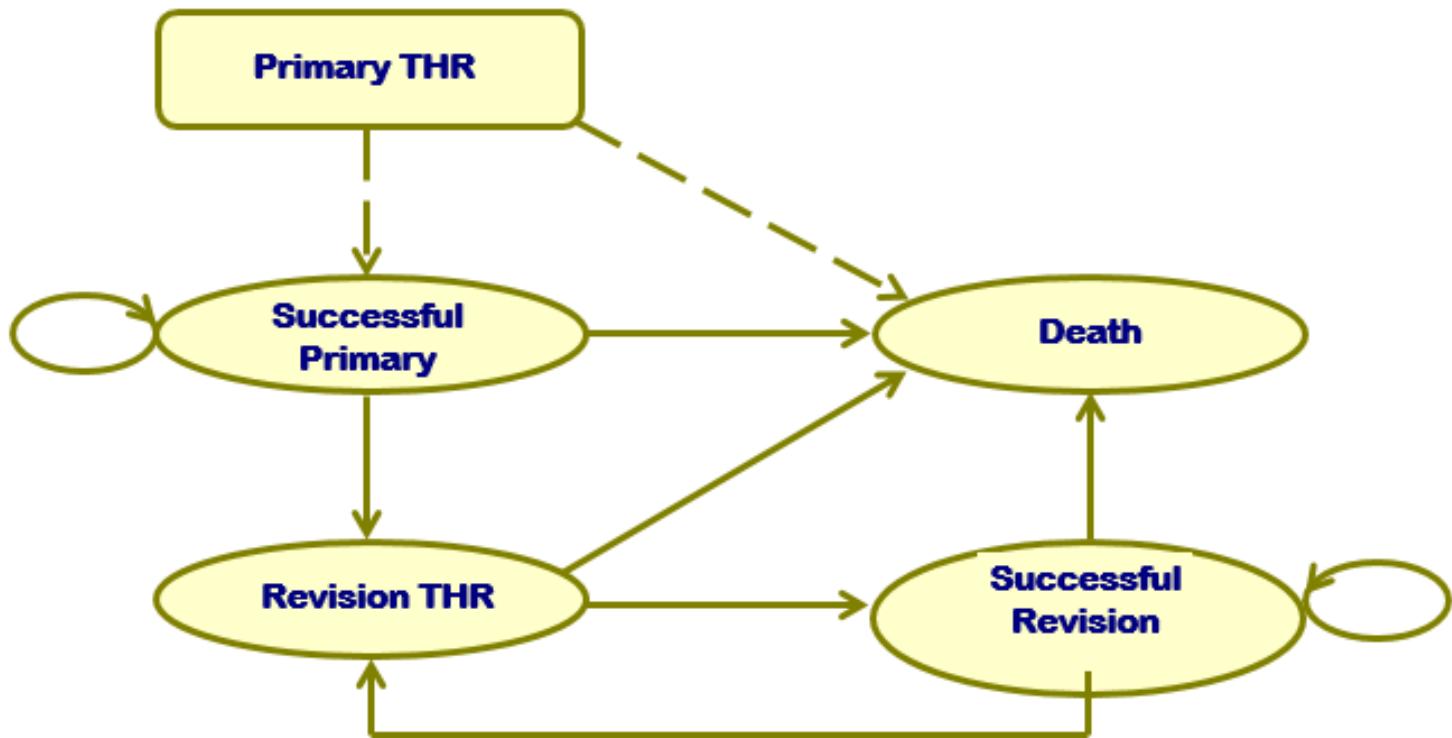
Dr Claire Williams

R for CEA Workshop, UCL
11th July 2018

Motivation

- Excel-based Markov modelling course gave the incentive to use R as an alternative
- Particular approach is based on `mstate` package in R
 - `mstate` uses IPD to build Cox models for each transition
 - `mstate` was adapted to use parametric distributions for the hazards: exponential, Weibull, Gompertz, log normal, log-logistic, generalised gamma
 - original motivation: extrapolation
 - another advantage: don't necessarily need IPD – just need to supply a cumulative hazard

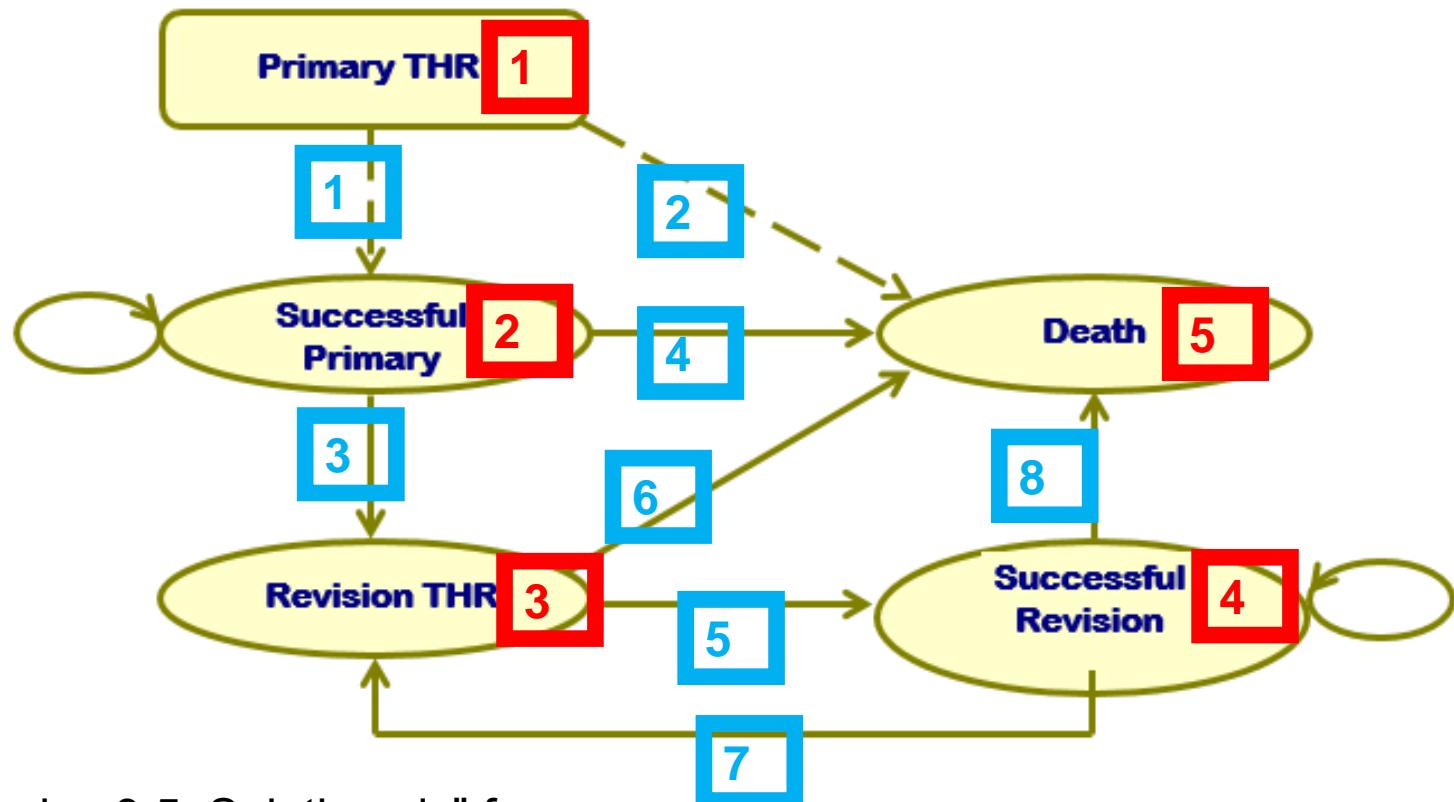
Hip fracture Markov model example



Source: “Exercise 3.5: Solution.xls” from

<https://www.gla.ac.uk/hehta/continuingprofessionaldevelopment/advancedmodellingmethods/#/downloads>

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State transition diagram R code

```
tmat <- transMat(x = list(c(2, 5), c(3,5),c(4,5),  
c(3,5), c()), names=c("Primary", "PriSuc",  
"Revision", "RevSuc","Death"))
```

tmat

to

from	Primary	PriSuc	Revision	RevSuc	Death
Primary	NA	1	NA	NA	2
PriSuc	NA	NA	3	NA	4
Revision	NA	NA	NA	5	6
RevSuc	NA	NA	7	NA	8
Death	NA	NA	NA	NA	NA

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Alternative approach to relaxing the Markov property

Markov property - future states depend only on the present state and not on how it arrived in the present state

- Markov property can be formally tested by including in the model a covariate that represents history e.g. time in previous state
- If covariate is found to have a statistically significant effect there is evidence that the Markov property doesn't hold

Modelling progression → death time in previous state included as a covariate

Call:

```
coxph(formula = Surv(Tstart, Tstop, status) ~ treat +  
       prog_ty,  
       data = msmcancer3, method = "breslow")  
n= 254, number of events= 50
```

	coef	exp(coef)	se(coef)	z	Pr(> z)
treat	0.4416	1.5552	0.2938	1.503	0.13280
prog_ty	-0.8832	0.4135	0.3332	-2.651	0.00804

Markov and semi-Markov models

Markov models

- time measured from initial state regardless of state
- inherent Markov property
- predictions use Markov exact prediction formulae

Semi-Markov models

- time set back to zero every time patient enters a new state (clock-reset model)
- time depends on history so not Markov
- predictions use simulation sampling through available paths in the model

IPD – based functions: Markov or semi-Markov models

- modelparam
- Markov semiMarkov
- visualMarkov visualsemiMarkov
- meanLY
- PSAprob
- PSAmeanLY PSAQALY
- CEplane
- CEAC

modelparam function

```
modelparam(Markov=FALSE, covs="treat", trans  
num=3, dist="wei", data=msmcancer)
```

Covariate	W.mean	Coef	Exp (Coef)	se (Coef)	Wald	p
treat	0.389	0.237	1.267	0.300	0.430	
log(scale)		1.368		0.218		0.000
log(shape)		0.143		0.116		0.218
Events		45				
Total time at risk		192.69				
Max. log. likelihood		-109.46				
LR test statistic		0.62				
Degrees of freedom		1				
Overall p-value		0.432542				

Markov and semiMarkov functions

```
Markov(ntrans=3, ncovs=c(1,1,2),  
covs=rbind("covariate1", "covariate1",  
c("covariate1", "covariate2")) ,  
coveval=rbind(0,0,c(0,1)) ,  
dist=cbind("wei", "wei", "wei") ,  
dist2=cbind(NA, NA, NA) ,  
timeseq=seq(0,4,1/12) ,  
timeseq_ext=seq(49/12,15,1/12) ,  
data=msmcancer, trans=tmat)
```

visualMarkov and visualsemiMarkov functions

```
visualMarkov(nobjects=6,  
             objects=rbind(weiexactRFC, expexactRFC, gomexactRFC,  
             loglexactRFC, lognexactRFC, gamexactRFC),  
             objects2=rbind(weiexactRFC[[2]], expexactRFC[[2]],  
             gomexactRFC[[2]], loglexactRFC[[2]], lognexactRFC[[2]],  
             gamexactRFC[[2]]), state=1, instate=TRUE, absorb=1,  
             initialstate=TRUE, predfrom=2,  
             tteach=c(181, 181, 181, 181, 181, 181),  
             ylab = "Probability of being progression-free",  
             xlab="Years since start of study", ylim=c(0,1), xlim=c(0,15),  
             lwd=2, col=rep("black", 6),  
             lty=c("51", "dotted", "21", "longdash", "twodash", "16")) ,
```

continued on next slide

visualMarkov and visualsemiMarkov functions

```
obsdata=RFCdata, CI=FALSE, observed="KM",
KMtime=RFCdata$progdeath_ty, KMstatus=RFCdata$progdeath,
ncr=2, legendpos="topright", legendncol=1, legendcex=1,
legendcurves=c("Kaplan-Meier", "Exponential", "Lognormal",
"Loglogistic", "Weibull", "Generalised gamma", "Gompertz"),
legendlty=c("solid", "dotted", "twodash", "longdash", "51", "16",
"21"),
legendbty="n", legendlwd=2, legendcol="black",
main="Probability of being progression-free",
cex.main=1.25)
```

meanLY function

```
meanLY(Markov=FALSE, object, state=1, instate=TRUE,  
discounted=TRUE, dis1yr.onwards=TRUE, rate=0.035)
```

	RFC	FC	Incremental
Mean Life Years	5.82	5.60	0.21
Mean Life Years Progression-free	3.30	2.56	0.74
Mean Life Years in Progression	2.52	3.04	-0.53
Mean QALYs	4.15	3.87	0.28
Mean QALYs Progression-free	2.64	2.05	0.59
Mean QALYs in Progression	1.51	1.83	-0.32

incorporating costs

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Mean QALYs Progression-free	2.64	2.05	0.59
Mean QALYs in Progression	1.51	1.83	-0.32
Mean Total Cost	£25,917	£15,508	£10,408
Cost per Life Year Gained			£48,772
Cost per QALY Gained			£37,665

PSAprob function

```
PSAprob(ntrans=3, ncovs=c(1,1,2),  
covs=rbind("treat", "treat", c("treat", "lemedian")) ,  
coveval=rbind(0,0,c(0,0)) ,  
dist=cbind("wei", "wei", "wei") ,  
dist2=cbind(NA, NA, NA) ,  
timeseq=seq(0,4,1/12) ,  
timeseq_ext=seq(49/12,15,1/12) ,  
data=msmcancer, trans=tmat,  
Markov=FALSE,  
nruns=1000, seedno=12345, M=100)
```

PSAmeanLY and PSAQALY functions

```
PSAmeanLY(object=PSASMSARFC, state=1, instate=TRUE,  
discounted=TRUE, rate=0.035) )
```

```
set.seed(12345)  
utility1=rbeta(1000,800,200)
```

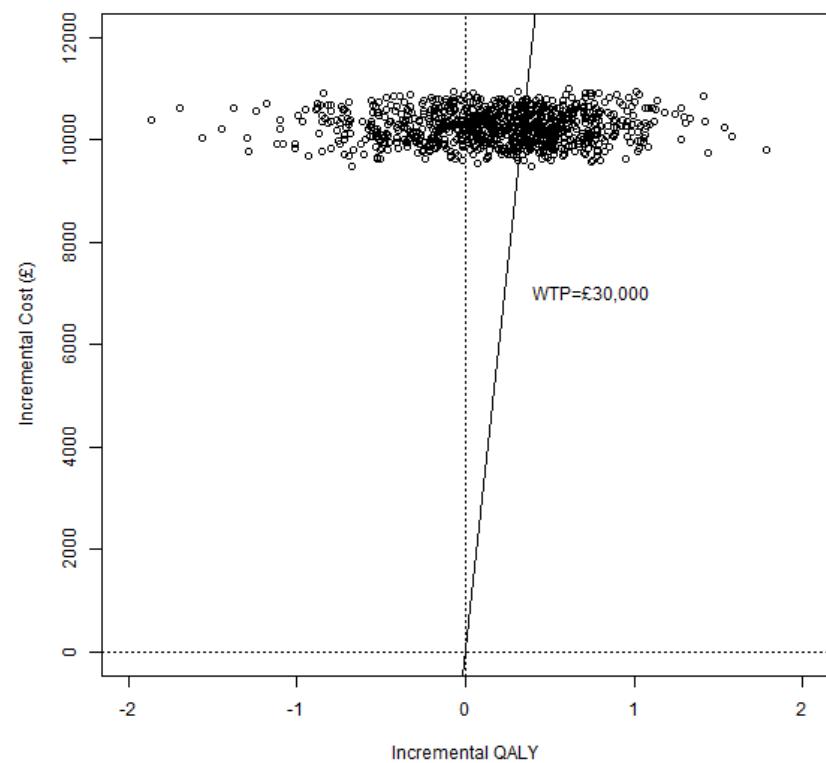
```
PSARFCQALYPFSdis<- PSAQALY(object=PSASMSARFC,  
utility=utility1, state=1, discounted=TRUE,  
dislyronwards=TRUE, rate=0.035)
```

```
mean(PSARFCQALYPFSdis)
```

then incorporate costs as probabilistic

CEplane function

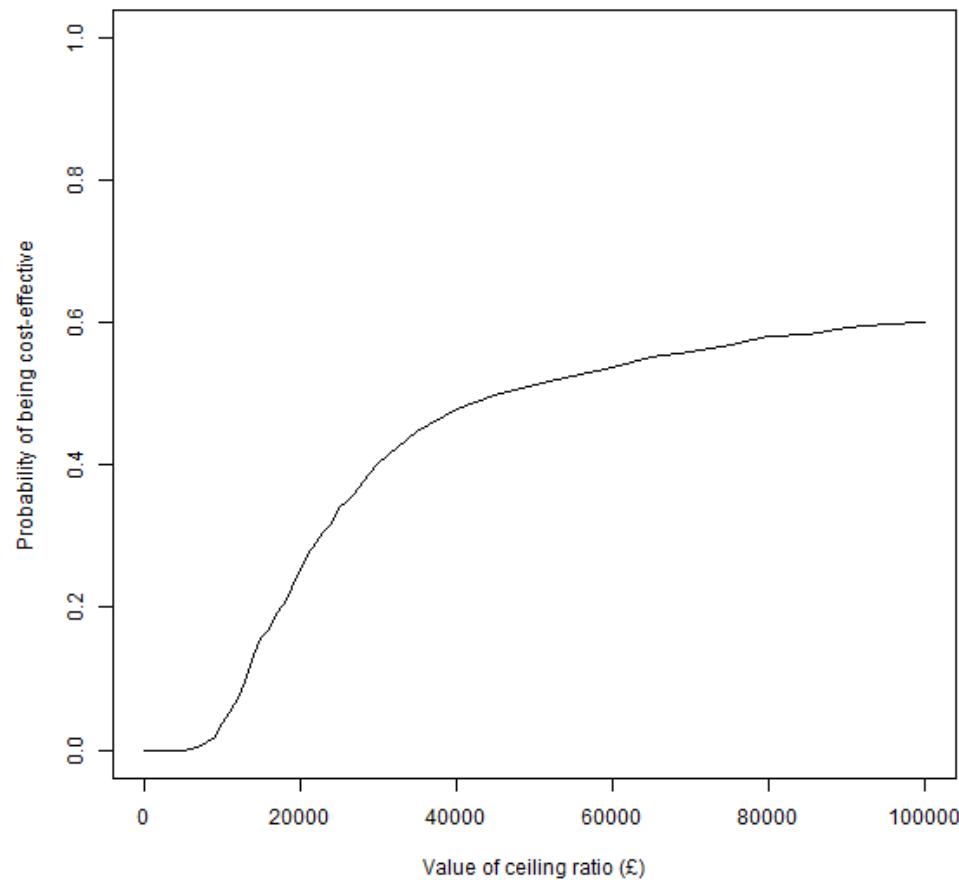
```
CEplane(x=incQALY, y=incCost, xlower=-2,  
xupper=2, ylower=0, yupper=20000, ICER=30000,  
text="ICER= £30,000")
```



CEAC function

```
CEAC(cRatiosim=c(seq(0,1000,100),  
seq(1500,5000,500),seq(6000,30000,1000),  
seq(35000,100000,5000)),nruns=1000,nruns2=1000  
, xlower=0, xupper=100000, ylower=0, yupper=1,  
QALY1=QALY_RFC_dis, QALY2=QALY_FC_dis,  
cost1=total_cost_RFC_dis,  
cost2=total_cost_FC_dis,  
secondcurve=FALSE, QALY1_2=QALY_RFC_dis,  
QALY2_2=QALY_FC_dis,  
cost1_2=total_cost_RFC_dis,  
cost2_2=total_cost_FC_dis))
```

CEAC



functions that can be used without IPD

Markov_noipd and semiMarkov_noipd

- allow previous model output and background mortality rates to be used to inform transition assumptions
- somewhat limited at the moment

Excel hip fracture model has been coded in R

- If interested please email me for my code:

claire.williams@bristol.ac.uk

Not included but discussed by others

- Previous speakers already discussed Vol analysis in R
- Boby and Iryna demonstrated shiny to create a more user-friendly front-end
- Looking forward: encourage more use of R for health economic modelling

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Reference

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doi:[10.1177/0272989X16651869](https://doi.org/10.1177/0272989X16651869)