

# Cohort State-Transition Models in R: A Tutorial - Part I

## Appendix

Fernando Alarid-Escudero, PhD\*      Eline Krijkamp, MSc<sup>†</sup>      Eva A. Enns, PhD<sup>‡</sup>      Alan Yang, MSc<sup>§</sup>  
Myriam G.M. Hunink, PhD<sup>¶</sup>      Petros Pechlivanoglou, PhD<sup>||</sup>      Hawre Jalal, MD, PhD\*\*

2021-04-13

### Cohort tutorial model components

**Table I**

This table contains an overview of the key model components used in the code for the Sick-Sicker example from the DARTH manuscript: “An Introductory Tutorial to Cohort State-Transition Models in R”. The first column gives the mathematical notation for some of the model components that are used in the equations in the manuscript. The second column gives a description of the model component with the R name in the third column. The forth gives the data structure, e.g. scalar, list, vector, matrix etc, with the according dimensions of this data structure in the fifth column. The final column indicated the type of data that is stored in the data structure, e.g. numeric (5,2,6.3,7.4), category (A,B,C), integer (5,6,7), logical (TRUE, FALSE).

Element	Description	R name	Data structure	Dimensions	Data type
$n_t$	Time horizon	<code>n_t</code>	scalar		numeric
$v_s$	Names of the health states	<code>v_n</code>	vector	<code>n_states</code> x 1	character
$n_s$	Number of health states	<code>n_states</code>	scalar		numeric

\*Division of Public Administration, Center for Research and Teaching in Economics (CIDE), Aguascalientes, AGS, Mexico

<sup>†</sup>Department of Epidemiology and Department of Radiology, Erasmus University Medical Center, Rotterdam, The Netherlands

<sup>‡</sup>Division of Health Policy and Management, University of Minnesota School of Public Health, Minneapolis, MN, USA

<sup>§</sup>The Hospital for Sick Children, Toronto

<sup>¶</sup>Center for Health Decision Sciences, Harvard T.H. Chan School of Public Health, Boston, USA

<sup>||</sup>The Hospital for Sick Children, Toronto and University of Toronto, Toronto, Ontario, Canada

\*\*University of Pittsburgh, Pittsburgh, PA, USA

Element	Description	R name	Data structure	Dimensions	Data type
$v_{str}$	Names of the strategies	<code>v_names_str</code>	scalar		character
$n_{str}$	Number of strategies	<code>n_str</code>	scalar		character
$\mathbf{d_c}$	Discount rate for costs	<code>d_c</code>	scalar		numeric
$\mathbf{d_e}$	Discount rate for effects	<code>d_e</code>	scalar		numeric
	Discount weights for costs	<code>v_dwc</code>	vector	$(\mathbf{n\_t} \times 1) + 1$	numeric
	Discount weights for effects	<code>v_dwe</code>	vector	$(\mathbf{n\_t} \times 1) + 1$	numeric
$age_0$	Age at baseline	<code>n_age_init</code>	scalar		numeric
$age$	Maximum age of follow up	<code>n_age_max</code>	scalar		numeric
$M$	Cohort trace	<code>m_M</code>	matrix	$(\mathbf{n\_t} + 1) \times \mathbf{n\_states}$	numeric
$m_0$	Initial state vector	<code>v_s_init</code>	vector	$1 \times \mathbf{n\_states}$	numeric
$m_t$	State vector in cycle t	<code>v_mt</code>	vector	$1 \times \mathbf{n\_states}$	numeric
<b>Transition probabilities</b>					
$p_{[H,S1]}$	From Healthy to Sick conditional on surviving	<code>p_HS1</code>	scalar		numeric
$p_{[S1,H]}$	From Sick to Healthy conditional on surviving	<code>p_S1H</code>	scalar		numeric
$p_{[S1,S2]}$	From Sick to Sicker conditional on surviving	<code>p_S1S2</code>	scalar		numeric
$r_{[H,D]}$	Constant rate of dying when Healthy (all-cause mortality rate)	<code>r_HD</code>	scalar		numeric
$hr_{[S1,H]}$	Hazard ratio of death in Sick vs Healthy	<code>hr_S1</code>	scalar		numeric
$hr_{[S2,H]}$	Hazard ratio of death in Sicker vs Healthy	<code>hr_S2</code>	scalar		numeric
$hr_{[S1,S2]_{trtB}}$	Hazard ratio of becoming Sicker when Sick under treatment B	<code>hr_S1S2_trtB</code>	scalar		numeric
$P$	Time-independent transition probability matrix	<code>m_P</code>	matrix	$\mathbf{n\_states} \times \mathbf{n\_states}$	numeric
<b>Annual costs</b>					
	Healthy individuals	<code>c_H</code>	scalar		numeric
	Sick individuals in Sick	<code>c_S1</code>	scalar		numeric
	Sick individuals in Sicker	<code>c_S2</code>	scalar		numeric
	Dead individuals	<code>c_D</code>	scalar		numeric
	Additional costs treatment A	<code>c_trtA</code>	scalar		numeric
	Additional costs treatment B	<code>c_trtB</code>	scalar		numeric
<b>Utility weights</b>					
	Healthy individuals	<code>u_H</code>	scalar		numeric
	Sick individuals in Sick	<code>u_S1</code>	scalar		numeric
	Sick individuals in Sicker	<code>u_S2</code>	scalar		numeric
	Dead individuals	<code>u_D</code>	scalar		numeric

Element	Description	R name	Data structure	Dimensions	Data type
	Treated with treatment A	<code>u_trtA</code>	scalar		numeric
<b>A</b>	<b>Outcome structures</b>				
	Transition dynamics array	<code>a_A</code>	array	<code>n_states</code> x <code>n_states</code> x ( <code>n_t</code> + 1)	numeric
	Expected QALYs per cycle under a strategy	<code>v_qaly</code>	vector	1 x ( <code>n_t</code> + 1)	numeric
	Expected costs per cycle under a strategy	<code>v_cost</code>	vector	1 x ( <code>n_t</code> + 1)	numeric
	Total expected discounted QALYs for a strategy	<code>n_tot_qaly</code>	scalar		numeric
	Total expected discounted costs for a strategy	<code>n_tot_cost</code>	scalar		numeric
	Summary of the model outcomes	<code>df_cea</code>	data frame		
	Summary of the model outcomes	<code>table_cea</code>	table		

**Table II: Input parameters for probabilistic analysis**

Parameter	Distribution	Distribution values	Parameter mean	Parameter standard error
Number of simulation	<code>n_sim</code>	1000		
- Constant rate of dying when Healthy (all-cause mortality)	<i>Lognormal</i>	$\log(\mu) = \log(0.002)$ , $\log(\sigma) = 0.01$	0.002	0.00002
Annual transition probabilities				
- Disease onset (Healthy to Sick)	<i>Beta</i>	$\alpha = 30$ , $\beta = 170$	0.15	0.026
- Recovery (Sick to Healthy)	<i>Beta</i>	$\alpha = 60$ , $\beta = 60$	0.5	0.045
- Disease progression (Sick to Sicker) in the age-dependent model	<i>Beta</i>	$\alpha = 84$ , $\beta = 716$	0.106	0.011
Risks of disease and treatment				
- Hazard ratio of death in Sick vs Healthy	<i>Lognormal</i>	$\log(\mu) = \log(3)$ , $\log(\sigma) = 0.01$	3	0.03
- Hazard ratio of death in Sicker vs Healthy	<i>Lognormal</i>	$\log(\mu) = \log(10)$ , $\log(\sigma) = 0.2$	10	0.2
- Hazard ratio of Sick to Sicker under treatment B	<i>Lognormal</i>	$\log(\mu) = \log(0.6)$ , $\log(\sigma) = 0.2$	0.60	0.013
Annual costs				
- Healthy individuals	<i>Gamma</i>	<i>Shape</i> = 100 , <i>Scale</i> = 20	2000	200

Parameter	Distribution	Distribution values	Parameter mean	Parameter standard error
- Sick individuals in Sick	<i>Gamma</i>	<i>Shape</i> = 177.8, <i>Scale</i> = 22.5	4000	300
- Sick individuals in Sicker	<i>Gamma</i>	<i>Shape</i> = 225 , <i>Scale</i> = 66.7	15000	1000
- Cost of treatment A for individuals in Sick or Sicker	<i>Gamma</i>	<i>Shape</i> = 73.5, <i>Scale</i> = 163.3	12000	1400
- Cost of treatment B for individuals in Sick or Sicker	<i>Gamma</i>	<i>Shape</i> = 86.2, <i>Scale</i> = 150.8	13050	1430
Utility weights				
- Healthy individuals	<i>Beta</i>	$\alpha = 200, \beta = 3$	0.985	0.008
- Sick individuals in Sick	<i>Beta</i>	$\alpha = 130, \beta = 45$	0.74	0.033
- Sick individuals in Sicker	<i>Beta</i>	$\alpha = 230, \beta = 230$	0.5	0.023
- Individuals treated with treatment A	<i>Beta</i>	$\alpha = 300, \beta = 15$	0.95	0.012