

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

Appendix

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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	n_t	scalar		numeric
v_s	Names of the health states	v_n	vector	n_states x 1	character
n_s	Number of health states	n_states	scalar		numeric

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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
Transition probabilities					
$p_{[H,S1]}$	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
Annual costs					
	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
Utility weights					
	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
A	Outcome structures				
	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		
Annual transition probabilities				
- Disease onset (H to S1)	<i>Beta</i>	$\alpha = 30, \beta = 170$	0.15	0.025
- Recovery (S1 to H)	<i>Beta</i>	$\alpha = 60, \beta = 60$	0.5	0.045
- Disease progression (S1 to S2)	<i>Beta</i>	$\alpha = 84, \beta = 716$	0.105	0.01
in the age-dependent model				
- Weibull scale parameter (S1 to S2) in the model with tunnel states	<i>Lognormal</i>	$\log(\mu) = \log(0.08), \log(\sigma) = 0.02$	0.08	0.002
- Weibull shape parameter (S1 to S2) in the model with tunnel states	<i>Lognormal</i>	$\log(\mu) = \log(1.1), \log(\sigma) = 0.02$	1.1	0.02
Annual mortality				
- Hazard ratio of death in S1 vs H	<i>Lognormal</i>	$\log(\mu) = \log(3), \log(\sigma) = 0.01$	3	0.03
- Hazard ratio of death in S2 vs H	<i>Lognormal</i>	$\log(\mu) = \log(10), \log(\sigma) = 0.2$	10	1
- Log odds ratio of S1 to S2	<i>Normal</i>	$\mu = \log(0.6), \sigma = 0.1$	-0.51	0.1
Annual costs				

Parameter	Distribution	Distribution values	Parameter mean	Parameter standard error
- Healthy individuals	<i>Gamma</i>	shape = 100 , Scale = 20	2000	200
- Sick individuals in S1	<i>Gamma</i>	shape = 177.8, Scale = 22.5	4000	300
- Sick individuals in S2	<i>Gamma</i>	shape = 225 , Scale = 66.7	15000	1000
- Cost of treatment A for individuals in S1 or S2	<i>Gamma</i>	shape = 576 , Scale = 20.8	12000	500
- Cost of treatment B for individuals in S1 or S2	<i>Gamma</i>	shape = 676 , Scale = 19.2	13000	500
Utility weights				
- Healthy individuals	<i>Beta</i>	$\alpha = 200, \beta = 3$	0.985	0.008
- Sick individuals in S1	<i>Beta</i>	$\alpha = 130, \beta = 45$	0.74	0.033
- Sick individuals in S2	<i>Beta</i>	$\alpha = 230, \beta = 230$	0.5	0.023
Intervention effect				
- Utility for treated individuals in S1	<i>Beta</i>	$\alpha = 300, \beta = 15$	0.95	0.012
Transition rewards				
- Disutility (H to S1)	<i>Beta</i>	$\alpha = 11, \beta = 1088$	0.01	0.003
- Increase in cost (H to S1)	<i>Gamma</i>	$\alpha = 25, \beta = 40$	1000	200
- Increase in cost (D)	<i>Gamma</i>	$\alpha = 100, \beta = 20$	2000	200