An Introductory Tutorial on Cohort State-Transition Models in R Using a Cost-Effectiveness Analysis Example

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).

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Element	Description	R name	Data structure	Dimensions	Data type
n_t	Time horizon	`n_cycles`	scalar		numeric
	Cycle length	`cycle_length`	scalar		numeric
v_s	Names of the health states	`v_names_states`	vector	`n_states` x 1	character
n_s	Number of health states	`n_states`	scalar		numeric
v_{str}	Names of the strategies	`v_names_str`	scalar		character
n_{str}	Number of strategies	`n_str`	scalar		character
$\mathbf{d_c}$	Discount rate for costs	`d_c`	scalar		numeric
$\mathbf{d_e}$	Discount rate for effects	`d_e`	scalar		numeric
	Discount weights for costs	`v_dwc`	vector	(`n_t` x 1) + 1	numeric
	Discount weights for effects	`v_dwe`	vector	(`n_t` x 1) + 1	numeric
	Sequence of cycle numbers	`v_cycles`	vector	(`n_t` x 1) + 1	numeric
wcc	Within-cycle correction weights using Simpson's 1/3 rule	`v_wcc`	vector	(`n_t` x 1) + 1	numeric
age_0	Age at baseline	`n_age_init`	scalar		numeric
age	Maximum age of follow up	`n_age_max`	scalar		numeric
M	Cohort trace	`m_M`	matrix	(`n_t` + 1) x `n_states`	numeric
m_0	Initial state vector	`v_m_init`	vector	1 x `n_states`	numeric
m_t	State vector in cycle t	`v_mt`	vector	1 x `n_states`	numeric
	Transition probabilities and rates				
$p_{[H,S1]}$	From Healthy to Sick conditional on surviving	`p_HS1`	scalar		numeric
$p_{[S1,H]}$	From Sick to Healthy conditional on surviving	`p_S1H`	scalar		numeric
$p_{[S1,S2]}$	From Sick to Sicker conditional on surviving	`p_S1S2`	scalar		numeric
$p_{[S1,S2]_{trtB}}$	From Sicker to Sick under treatment B conditional on surviving	`p_S1S2_trtB`	scalar		numeric
$r_{[H,D]}$	Constant rate of dying when Healthy (all-cause mortality rate)	`r_HD`	scalar		numeric
$r_{[S1,S2]}$	Constant rate of becoming Sicker when Sick	`r_S1S2`	scalar		numeric
$r_{[S1,S2]_{trtB}}$	Constant rate of becoming Sicker when Sick for treatment B	`r_S1S2_trtB`	scalar		numeric
$hr_{[S1,H]}$	Hazard ratio of death in Sick vs Healthy	`hr_S1`	scalar		numeric
$hr_{[S2,H]}$	Hazard ratio of death in Sicker vs Healthy	`hr_S2`	scalar		numeric
$hr_{[S1,S2]_{trtB}}$	Hazard ratio of becoming Sicker when Sick under treatment B	`hr_S1S2_trtB`	scalar		numeric
P	Time-independent transition probability matrix* * `_trtX` is used to specify for which strategy the transition probability matrix is	`m_P`	matrix	`n_states` x `n_states`	numeric

Element	Description	R name	Data structure	Dimensions	Data type
	Annual costs				
	Healthy individuals	`c_H`	scalar		numeric
	Sick individuals in Sick	`c_S1`	scalar		numeric
	Sick individuals in Sicker	`c_S2`	scalar		numeric
	Dead individuals	`c_D`	scalar		numeric
	Additional costs treatment A	`c_trtA`	scalar		numeric
	Additional costs treatment B	`c_trtB`	scalar		numeric
	Vector of state costs for a strategy A	`v_c_str`	vector	1 x `n_states`	numeric
	Utility weights				
	Healthy individuals	`u_H`	scalar		numeric
	Sick individuals in Sick	`u_S1`	scalar		numeric
	Sick individuals in Sicker	`u_S2`	scalar		numeric
	Dead individuals	`u_D`	scalar		numeric
	Treated with treatment A	`u_trtA`	scalar		numeric
	Vector of state utilities for a strategy	`v_u_str`	vector	1 x `n_states`	numeric
	Outcome structures				
	Expected QALYs per cycle under a strategy	`v_qaly_str`	vector	1 x (`n_t` + 1)	numeric
	Expected costs per cycle under a strategy	`v_cost_str`	vector	1 x (`n_t` + 1)	numeric
	Total expected discounted QALYs for a strategy	`n_tot_qaly_str`	scalar		numeric
	Total expected discounted costs for a strategy	`n_tot_cost_str`	scalar		numeric
	Summary matrix with costs and QALYS per strategy	`m_outcomes`	table	`n_states` x 2	
	Summary of the model outcomes	`df_cea`	data frame		
	Summary of the model outcomes	`table_cea`	table		
	Probabilistic analysis structures				
	Number of PSA iterations	`n_sim`	scalar		numeric
	Data frame with PSA input values for each iteration	`df_psa_input`	table		
	Data frame to store the accumulated cost per strategy for each PSA iteration	`df_c`	table	`n_sim` x `n_states`	numeric
	Data frame to store the accumulated effects per strategy for each PSA iteration	`df_e`	table	`n_sim` x `n_states`	numeric

Element	Description	R name	Data structure	Dimensions	Data type
	For more details about the PSA structures read the vignettes of `dampack`				

Table II: Input parameters for probabilistic analysis

Parameter	Distribution	Distribution values	Parameter mean	Parameter standard error
Number of simulation	`n_sim`	1000		
- Constant rate of dying when Healthy (all-cause mortality)	*Lognormal*	$log(\mu) = log(0.002)$, $log(\sigma) = 0.01$	0.002	0.00002
Annual transition probabilities				
- Disease onset (Healthy to Sick)	*Beta*	$\alpha = 30$, $\beta = 170$	0.15	0.026
- Recovery (Sick to Healthy)	*Beta*	$\alpha = 60$, $\beta = 60$	0.5	0.045
- Disease progression (Sick to Sicker) in the age-dependent model	*Beta*	$\alpha = 84$, $\beta = 716$	0.106	0.011
Risks of disease and treatment				
- Hazard ratio of death in Sick vs Healthy	*Lognormal*	$log(\mu) = log(3)$, $log(\sigma) = 0.01$	3	0.03
- Hazard ratio of death in Sicker vs Healthy	*Lognormal*	$log(\mu) = log(10)$, $log(\sigma) = 0.2$	10	0.2
- Hazard ratio of Sick to Sicker under treatment B	*Lognormal*	$log(\mu) = log(0.6)$, $log(\sigma) = 0.2$	0.60	0.013
Annual costs				
- Healthy individuals	*Gamma*	$Shape = 100$, $Scale = 20$	2000	200
- Sick individuals in Sick	*Gamma*	$Shape = 177.8$, $Scale = 22.5$	4000	300
- Sick individuals in Sicker	*Gamma*	$Shape = 225$, $Scale = 66.7$	15000	1000
- Cost of treatment A for individuals in Sick or Sicker	*Gamma*	$Shape = 73.5$, $Scale = 163.3$	12000	1400
- Cost of treatment B for individuals in Sick or Sicker	*Gamma*	$Shape = 86.2$, $Scale = 150.8$	13050	1430
Utility weights				
- Healthy individuals	*Beta*	$\alpha = 200$, $\beta = 3$	0.985	0.008

Parameter	Distribution	Distribution values	Parameter mean	Parameter standard error
- Sick individuals in Sick	*Beta*	$\alpha = 130$, $\beta = 45$	0.74	0.033
- Sick individuals in Sicker	*Beta*	$\alpha = 230$, $\beta = 230$	0.5	0.023
- Individuals treated with treatment A	*Beta*	$\alpha = 300$, $\beta = 15$	0.95	0.012