Cohort tutorial

Appendix

DARTH workgroup

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Cohort tutorial model components

Table I: Input parameters

This table contains an overview of the key model components used in the code for the Sick-Sicker example from the DARTH manuscript: "Implementation of cohort state-transition models in R". The first column gives the mathematical notation for some of the model components that are used in the euqations in the manuscript. The second column gives a describtion 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), categoric (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	categorical
n_s	Number of health states	`n_states`	scalar		numeric
v_{str}	Names of the strategies	`v_names_str`	scalar		categorical
n_{str}	Number of strategies	`n_str`	scalar		numeric
$\mathbf{d_c}$	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
$\mathbf{v_{hcc}}$	half-cycle correction	`v_hcc`	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_s_init`	vector	1 x `n_states`	numeric

Element	Description	R name	Data structure	Dimensions	Data type
	Transition probabilities				
$p_{[H,S1]}$	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
$p_{[H,D]}$	Annual all-cause mortality	`p_HD`	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
$or_{[S1,S2]}$	Odds ratio of becoming Sicker when Sick under New treatment 2	`or_S1S2`	scalar		numeric
γ	Weibell parameters gamma	`n_gamma`	scalar		numeric
λ	Weibell parameters lambda	`n_lambda`	scalar		numeric
P	Transition probability matrix	`m_P`	matrix	`n_states` x `n_states`	numeric
$p_{[S1,S2,t]}$	Time dependent transition probability from sick to sicker	`v_p_S1S2_tunnels`	vector	`n_t` x 1	numeric
$r_{[H,D,t]}$	Age-specific background mortality rates	`v_r_mort_by_age`	vector	(`n_age_max` + 1) x 1	numeric
$p_{[H,D,t]}$	Age-specific mortality risk in the Healthy state	`v_p_HDage`	vector	`n_t` x 1	numeric
$p_{[S1,D,t]}$	Age-specific mortality risk in the Sick state	`v_p_S1Dage`	vector	`n_t` x 1	numeric
$p_{[S2,D,t]}$	Age-specific mortality risk in the Sicker state	`v_p_S2Dage`	vector	`n_t` x 1	numeric
	Annual costs				
	Healthy individuals	`c_H`	scalar		numeric
	Sick individuals in the Sick state	`c_S1`	scalar		numeric
	Sick individuals in the Sicker state	`c_S2`	scalar		numeric
	Dead individuals	`c_D`	scalar		numeric
	Additional costs of New treatment 1	`c_trt1`	scalar		numeric
	Additional costs of New treatment 2	`c_trt2`	scalar		numeric
	Utility weights				
	Healthy individuals	`u_H`	scalar		numeric

Element	Description	R name	Data structure	Dimensions	Data type
	Sick individuals in the Sick state	u_S1	scalar		numeric
	Sick individuals in the Sicker state	u_S2	scalar		numeric
	Dead individuals	u_D	scalar		numeric
	Being treated	u_trt1	scalar		numeric
	Transition weights				
	Utility decrement of healthy individuals when transitioning to the Sick state	du_HS1	scalar		numeric
	Cost of healthy individuals when transitioning to the Sick state	ic_HS1	scalar		numeric
	Cost of dying	ic_D	scalar		numeric
$\mathbf{P}$	Age-dependent transition probability array	a_P	array	n_states x n_states x n_t	numeric
$\mathbf{A}$	Transition dynamics array	a_A	array	n_states x n_states x (n_t + 1)	numeric
	Number of tunnel states	n_tunnel_size	scalar		numeric
	Tunnel names of the Sick state	v_Sick_tunnel	vector	1 x n_t	numeric
	Number of states including tunnel states	n_states_tunnels	scalar		numeric
	State names including tunnel states	v_n_tunnels	vector	1 x n_states_tunnels	categorical
	Initial state vector for the model with tunnels	v_s_init_tunnels	vector	1 x n_states_tunnels	numeric
	Transition dynamics array for the model with tunnels	a_A_tunnels	array	n_states_tunnels x n_states_tunnels x (n_t + 1)	numeric
	Transition probability array for the model with tunnels	a_P_tunnels	array	n_states_tunnels x n_states_tunnels x n_t	numeric
$\mathbf{R_u}$	Transition rewards for effects	a_R_u	array	n_states x n_states x (n_t + 1)	numeric
$\mathbf{R_c}$	Transition rewards for costs	a_R_c	array	n_states x n_states x (n_t + 1)	numeric
$\mathbf{Y_u}$	Expected effects per states per cycle	a_Y_u	array	n_states x n_states x (n_t + 1)	numeric
$\mathbf{R_c}$	Expected costs per state per cycle	a_Y_c	array	n_states x n_states x (n_t + 1)	numeric
	Expected QALYs per cycle	v_qaly	vector	1 x (n_t + 1)	numeric
	Expected costs per cycle	v_cost	vector	1 x (n_t + 1)	numeric

Element	Description	R name	Data structure	Dimensions	Data type
	Total expected discounted QALYs for all strategies	`v_tot_qaly`	vector	1 x `n_str`	numeric
	Total expected discounted costs for all strategies	`v_tot_cost`	vector	1 x `n_str`	numeric
	Summary of the model outcomes	`df_cea`	data frame		
	Summary of the model outcomes - reformatted	`table_cea`	table		

Table II: Input parameters for probabilistic analysis

Parameter	**Distribution**	**Distribution values**	**Parameter mean**	**Parameter standard deviation**
Number of simulation	`n_sim`	1000		
Annual transition probabilities				
- Disease onset (H to S1)	Beta	$\alpha = 30.45,\ \beta = 172.55$	0.15	0.03
- Recovery (S1 to H)	Beta	$\alpha = 49.50,\ \beta = 49.50$	0.50	0.05
- Disease progression (S1 to S2) in the age-dependent model	Beta	$\alpha = 98.57,\ \beta = 840.18$	0.105	0.01
Annual mortality				
- Hazard ratio of death in S1 vs H	Lognormal	$\log(\mu) = \log(3),\ \log(\sigma) = log(1.18)$	3	0.5
- Hazard ratio of death in S2 vs H	Lognormal	$\log(\mu) = \log(10),\ \log(\sigma) = \log(1.1)$	10	1
- Log odds ratio of S1 to S2	Normal	$\mu = \log(0.6),\ \sigma = 0.1$	-0.51	1
Annual costs				
- Healthy individuals	Gamma	shape = 100, scale = 20	2000	200
- Sick individuals in S1	Gamma	shape = 177.78, scale = 22.5	4000	300
- Sick individuals in S2	Gamma	shape = 225, scale = 66.67	15000	1000
- Cost of treatment A for individuals in S1 or S2	Gamma	shape = 225, scale = 53.33	12000	800
- Cost of treatment B for individuals in S1 or S2	Gamma	shape = 208.64, scale = 62.31	13000	900

Parameter	Distribution	Distribution values	Parameter mean	Parameter standard deviation
Utility weights				
- Healthy individuals	Beta	$\alpha = 12.81,\ \beta = 0.01$	0.999	0.008
- Sick individuals in S1	Beta	$\alpha = 130,\ \beta = 45$		
- Sick individuals in S2	Beta	$\alpha = 230,\ \beta = 230$		
Intervention effect				
- Utility for treated individuals in S1	Beta	$\alpha = 300,\ \beta = 15$		