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

Element	Description	R name	Data structure	Dimensions	Data type
m_0	Initial state vector	`v_s_init`	vector	1 x `n_states`	numeric
	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				

Element	Description	R name	Data structure	Dimensions	Data type
	Healthy individuals	`u_H`	scalar		numeric
	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

Element	Description	R name	Data structure	Dimensions	Data type
	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
	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 error
Number of simulation	`n_sim`	1000		
Annual transition probabilities				
- Disease onset (H to S1)	Beta	$\alpha = 30,\ \beta = 170$	0.15	0.025
- Recovery (S1 to H)	Beta	$\alpha = 60,\ \beta = 60$	0.5	0.045
- Disease progression (S1 to S2) in the age-dependent model	Beta	$\alpha = 84,\ \beta = 716$	0.105	0.01
- Weibull scale parameter (S1 to S2) in the model with tunnel states	Lognormal	$\log(\mu) = \log(0.08),\ \log(\sigma) = 0.02$	0.08	0.002
- Weibull shape parameter (S1 to S2) in the model with tunnel states	Lognormal	$\log(\mu) = \log(1.1),\ \log(\sigma) = 0.02$	1.1	0.02
Annual mortality				
- Hazard ratio of death in S1 vs H	Lognormal	$\log(\mu) = \log(3),\ \log(\sigma) = 0.01$	3	0.03
- Hazard ratio of death in S2 vs H	Lognormal	$\log(\mu) = \log(10),\ \log(\sigma) = 0.02$	10	1
- Log odds ratio of S1 to S2	Normal	$\mu = \log(0.6),\ \sigma = 0.1$	-0.51	0.1
Annual costs				
- Healthy individuals	Gamma	shape = 100, scale = 20	2000	200
- Sick individuals in S1	Gamma	shape = 177.8, scale = 22.5	4000	300
- Sick individuals in S2	Gamma	shape = 225, scale = 66.7	15000	1000
- Cost of treatment A for individuals in S1 or S2	Gamma	shape = 576, scale = 20.8	12000	500
- Cost of treatment B for individuals in S1 or S2	Gamma	shape = 676, scale = 19.2	13000	500
Utility weights				
- Healthy individuals	Beta	$\alpha = 200,\ \beta = 3$	0.985	0.008
- Sick individuals in S1	Beta	$\alpha = 130,\ \beta = 45$	0.74	0.033
- Sick individuals in S2	Beta	$\alpha = 230,\ \beta = 230$	0.5	0.023
Intervention effect				
- Utility for treated individuals in S1	Beta	$\alpha = 300,\ \beta = 15$	0.95	0.012
Transition rewards				
- Disutility (H to S1)	Beta	$\alpha = 11,\ \beta = 1088$	0.01	0.003
- Increase in cost (H to S1)	Gamma	$\alpha = 25,\ \beta = 40$	1000	200
- Increase in cost (D)	Gamma	$\alpha = 100,\ \beta = 20$	2000	200