

Cost-Effectiveness and Decision Modeling in R

Basic Markov Model Exercise

The DARTH workgroup

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- Jalal H, Pechlivanoglou P, Krijkamp E, Alarid-Escudero F, Enns E, Hunink MG. An Overview of R in Health Decision Sciences. *Med Decis Making*. 2017; 37(3): 735-746. <https://journals.sagepub.com/doi/abs/10.1177/0272989X16686559>
- Krijkamp EM, Alarid-Escudero F, Enns EA, Jalal HJ, Hunink MGM, Pechlivanoglou P. Microsimulation modeling for health decision sciences using R: A tutorial. *Med Decis Making*. 2018;38(3):400-22. <https://journals.sagepub.com/doi/abs/10.1177/0272989X18754513>
- Krijkamp EM, Alarid-Escudero F, Enns E, Pechlivanoglou P, Hunink MM, Jalal H. A Multidimensional Array Representation of State-Transition Model Dynamics. *BioRxiv* 670612 2019. <https://www.biorxiv.org/content/10.1101/670612v1>

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Exercise I: Construct a Markov Model of the Sick-Sicker Disease

In this exercise, we will model a hypothetical disease that affects individuals with an average age of 25 years and results in increased mortality, increased healthcare costs, and reduced quality of life. The disease has two levels; affected individuals initially become sick but can subsequently progress and become sicker. Two alternative strategies exist for this hypothetical disease: a no-treatment and a treatment strategy. Under the treatment strategy, individuals in the sick and sicker states are treated until they recover (only if sick; individuals in the sicker state cannot recover) or die. The cost of the treatment is additive to the baseline healthcare costs of being sick or sicker. The treatment improves quality of life for those individuals who are sick but has no impact on the quality of life of those who are sicker. Unfortunately, it is not possible to reliably differentiate between people in the sick and sicker states, so treatment cannot be targeted to only those in the sick state. You are asked to evaluate the cost-effectiveness of the treatment.

To model this disease, we will rely on a state-transition cohort model, called the Sick-Sicker model, first described by Enns et al. The Sick-Sicker model consists of four health states: Healthy (H), two disease states, Sick (S1) and Sicker (S2), and Dead (D) (Figure 1). All individuals start in the Healthy state. Over time, healthy individuals may develop the disease and can progress to S1. Individuals in S1 can recover (return to state H), progress further to S2 or die. Individuals in S2 cannot recover (i.e. cannot transition to either S1 or H). Individuals in H have a baseline probability of death; individuals in S1 and S2 experience increased mortality compared to those in the H state, given in terms of hazard ratios. These ratios are used to calculate the probabilities of dying when in S1 and S2.

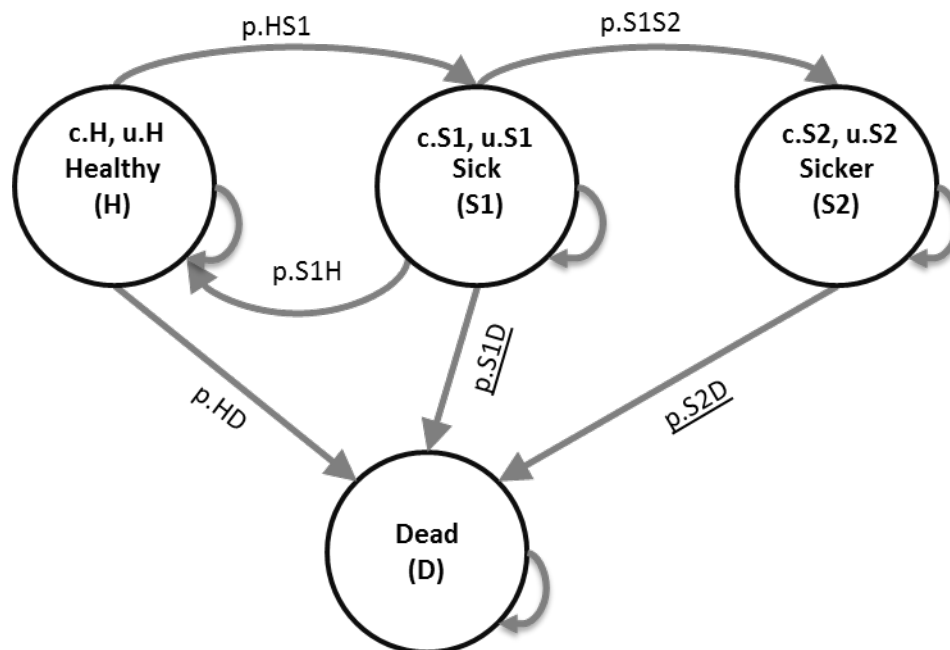


Figure 1: Schematic representation of the Sick-Sicker model

Tasks

1. Build the Markov model in R for no treatment and treatment strategies.
2. Plot the survival curve for the cohort under no treatment.
3. Estimate the cost-effectiveness of treatment vs no-treatment.
4. Create a cost-effectiveness table with all results of interest.

Table I: Input parameters

Parameter	R name	Value
Time horizon	n_t	30 years
Cycle length		1 year
Names of health states	v_n	H, S1, S2, D
Annual discount rate (costs/QALYs)	d_r	3%
Annual transition probabilities		
- Disease onset (H to S1)	p_HS1	0.15
- Recovery (S1 to H)	p_S1H	0.5
- Disease progression (S1 to S2) in the time-homogeneous model	p_S1S2	0.105
Annual mortality		
- All-cause mortality (H to D)	p_HD	0.005
- Hazard ratio of death in S1 vs H	hr_S1	3
- Hazard ratio of death in S2 vs H	hr_S2	10
Annual costs		
- Healthy individuals	c_H	\$2,000
- Sick individuals in S1	c_S1	\$4,000
- Sick individuals in S2	c_S2	\$15,000
- Dead individuals	c_D	\$0
- Additional costs of sick individuals treated in S1 or S2	c_trt	\$12,000
Utility weights		
- Healthy individuals	u_H	1.00
- Sick individuals in S1	u_S1	0.75
- Sick individuals in S2	u_S2	0.50
- Dead individuals	u_D	0.00
Intervention effect		
- Utility for treated individuals in S1	u_trt	0.95

*Note: To calculate the probability of dying from S1 and S2, use the hazard ratios provided. To do so, first convert the probability of dying from healthy, p_{HD} , to a rate; then multiply this rate by the appropriate hazard ratio; finally, convert this rate back to a probability. Recall that you can convert between rates and probabilities using the following formulas: $r = -\log(1 - p)$ and $p = 1 - e^{(-rt)}$