

Introduction to Decision Modeling Using R

Basic Markov Model Exercise

The DARTH workgroup

Developed by the Decision Analysis in R for Technologies in Health (DARTH) workgroup:

Fernando Alarid-Escudero, PhD (1)

Eva A. Enns, MS, PhD (2)

M.G. Myriam Hunink, MD, PhD (3,4)

Hawre J. Jalal, MD, PhD (5)

Eline M. Krijkamp, MSc (3)

Petros Pechlivanoglou, PhD (6,7)

Alan Yang, MSc (7)

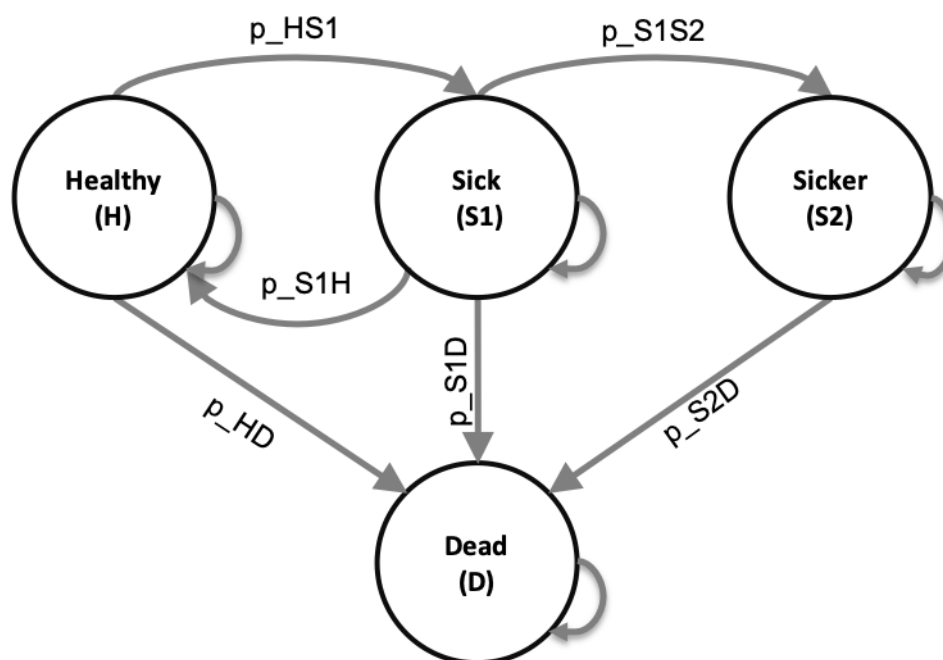
In collaboration of:

1. Division of Public Administration, Center for Research and Teaching in Economics (CIDE), Aguascalientes, Mexico
2. University of Minnesota School of Public Health, Minneapolis, MN, USA
3. Erasmus MC, Rotterdam, The Netherlands
4. Harvard T.H. Chan School of Public Health, Boston, USA
5. University of Pittsburgh Graduate School of Public Health, Pittsburgh, PA, USA
6. University of Toronto, Toronto ON, Canada
7. The Hospital for Sick Children, Toronto ON, Canada

Please cite our publications when using this code:

- 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>
- Alarid-Escudero F, Krijkamp EM, Enns EA, Yang A, Hunink MGM, Pechlivanoglou P, Jalal H. Cohort State-Transition Models in R: A Tutorial. *arXiv:200107824v2*. 2020:1-48. <http://arxiv.org/abs/2001.07824>
- 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. *Med Decis Making*. Online First <https://doi.org/10.1177/0272989X19893973>

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.



2

Tasks

Using the template `markov_sick-sicker_template.Rmd`, please do the following.

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