Adapting the model to your needs

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R for Health Technology Assessment

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You may need to model:

a. A different cycle length (monthly, daily, etc.)
b. A different number of states
c. A different discount rate (3.5%, 5%, etc)
d. A different treatment effectiveness measure (RR, OR, etc.)
e. Just two strategies: new treatment vs. standard of care (rare diseases)
f. A different initial state vector

Please, do not worry about:

- ❖ Adding all-cause mortality rates per age.
- ❖ Adding time-dependent variables (treatment effectiveness, health utilities, etc.)
- ❖ Running probabilistic sensitivity analysis

for Health Technology Assessment

NEXT WORKSHOP
REGISTRATIONS OPEN SOON..

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a. A different cycle lengths (monthly, daily, etc.)

```
67 # Model input ----
68 ## General setup ----
69 cycle_length <- 1       # cycle length equal to one year (use 1/12 for monthly)
70 n_age_init <- 25        # age at baseline
71 n_age_max  <- 100       # maximum age of follow up
72 n_cycles <- (n_age_max - n_age_init)/cycle_length # time horizon, number of cycles
```

```
244 #* Vector of state utilities under strategy SoC
245 v_u_SoC    <- c(H  = u_H,
246                 S1 = u_S1,
247                 S2 = u_S2,
248                 D  = u_D) * cycle_length
249 #* Vector of state costs under strategy SoC
250 v_c_SoC    <- c(H  = c_H,
251                 S1 = c_S1,
252                 S2 = c_S2,
253                 D  = c_D) * cycle_length
```

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b. A different number of states

```
67  # Model input ----
68  ## General setup ----
69  cycle_length <- 1       # cycle length equal to one year (use 1/12 for monthly)
70  n_age_init <- 25        # age at baseline
71  n_age_max  <- 100       # maximum age of follow up
72  n_cycles <- (n_age_max - n_age_init)/cycle_length # time horizon, number of cycles
73  v_names_states <- c("H",  # the 4 health states of the model:
74                      "S1", # Healthy (H), Sick (S1), Sicker (S2), Dead (D)
75                      "S2",
76                      "D")
77
78  n_states <- length(v_names_states)     # number of health states
79
80  ### Discounting factors ----
```

b. A different number of states

```r
### Fill in matrix ----
#* From H
m_P["H", "H"]   <- (1 - p_HD) * (1 - p_HS1)
m_P["H", "S1"]  <- (1 - p_HD) * p_HS1
m_P["H", "D"]   <- p_HD
#* From S1
m_P["S1", "H"]  <- (1 - p_S1D) * p_S1H
m_P["S1", "S1"] <- (1 - p_S1D) * (1 - (p_S1H + p_S1S2))
m_P["S1", "S2"] <- (1 - p_S1D) * p_S1S2
m_P["S1", "D"]  <- p_S1D
#* From S2
m_P["S2", "S2"] <- 1 - p_S2D
m_P["S2", "D"]  <- p_S2D
#* From D
m_P["D", "D"]   <- 1
```

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b. A different number of states

```
#### Costs ----
c_H    <- 2000  # annual cost of being Healthy
c_S1   <- 4000  # annual cost of being Sick
c_S2   <- 15000 # annual cost of being Sicker
c_D    <- 0     # annual cost of being dead
c_trtA <- 12000 # annual cost of receiving treatment A
c_trtB <- 13000 # annual cost of receiving treatment B
#### Utilities ----
u_H    <- 1     # annual utility of being Healthy
u_S1   <- 0.75  # annual utility of being Sick
u_S2   <- 0.5   # annual utility of being Sicker
u_D    <- 0     # annual utility of being dead
u_trtA <- 0.95  # annual utility when receiving treatment A
```

b. A different number of states

```
206 ### Check that transition probabilities are [0, 1] ----
207 check_transition_probability(m_P,      verbose = TRUE)  # m_P >= 0 && m_P <= 1
208 check_transition_probability(m_P_strA, verbose = TRUE)  # m_P_strA >= 0 && m_P_strA <= 1
209 check_transition_probability(m_P_strB, verbose = TRUE)  # m_P_strB >= 0 && m_P_strB <= 1
210 check_transition_probability(m_P_strAB, verbose = TRUE) # m_P_strAB >= 0 && m_P_strAB <= 1
211 ### Check that all rows sum to 1 ----
212 check_sum_of_transition_array(m_P,      n_states = n_states, n_cycles = n_cycles, verbose = TRUE)  # rowSums(m_P) == 1
213 check_sum_of_transition_array(m_P_strA, n_states = n_states, n_cycles = n_cycles, verbose = TRUE)  # rowSums(m_P_strA) == 1
214 check_sum_of_transition_array(m_P_strB, n_states = n_states, n_cycles = n_cycles, verbose = TRUE)  # rowSums(m_P_strB) == 1
215 check_sum_of_transition_array(m_P_strAB, n_states = n_states, n_cycles = n_cycles, verbose = TRUE) # rowSums(m_P_strAB) == 1
```

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c. A different discount rate

```
80 ### Discounting factors ----
81 d_c <- 0.03 # annual discount rate for costs
82 d_e <- 0.03 # annual discount rate for QALYs
83
```

```
121 ### Discount weight for costs and effects ----
122 v_dwc  <- 1 / ((1 + (d_e * cycle_length)) ^ (0:n_cycles))
123 v_dwe  <- 1 / ((1 + (d_c * cycle_length)) ^ (0:n_cycles))
```

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d. A different treatment effectiveness measure (RR, OR, etc.)

PharmacoEconomics (2020) 38:1153–1164
https://doi.org/10.1007/s40273-020-00937-z

PRACTICAL APPLICATION

Estimating Transition Probabilities from Published Evidence: A Tutorial for Decision Modelers

Risha Gidwani[1,2,3] · Louise B. Russell[4,5]

Table 1 Common forms of published data and their definitions

Statistic	Evaluates	Range
Probability/risk	$\frac{\#\text{of events that occurred in a time period}}{\#\text{of people followed for that time period}}$	0–1
Rate	$\frac{\#\text{of events that occurred in a time period}}{\text{Total time period experienced by all subjects followed}}$	0 to ∞
Relative risk	$\frac{\text{Probability of outcome in exposed}}{\text{Probability of outcome in unexposed}}$	0 to ∞
Odds	$\frac{\text{Probability of outcome}}{1 - \text{Probability of outcome}}$	0 to ∞
Odds ratio	$\frac{\text{Odds of outcome in exposed}}{\text{Odds of outcome in unexposed}}$	0 to ∞

5 Converting Probabilities to the Model's Cycle Length

Once the evidence is in the form of probabilities, it may need to be converted to the model's cycle length. For example, a trial may report outcomes at 2 years' follow-up, while the model has an annual cycle length. For a model node with only two branches, that is, two possible state transitions, the relationship between probabilities and rates provides a simple way to derive probabilities that match the model's cycle length. Recall that a probability is the number of events in a time period divided by the total number of people followed for that time period, and ranges from 0 to 1.0. A rate is the number of events divided by the total time at risk experienced by all people followed, and ranges from 0 to infinity. Thus, probabilities and rates for the same event are differentiated by their denominators: the calculation of a rate takes into account the time spent at risk, while the calculation of a probability does not [26]. See Appendix for a detailed example and the assumptions involved in the formula.

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e. Just two strategies: new treatment vs. standard of care (rare diseases)

```r
### Strategies ----
v_names_str <- c("Standard of care",      # store the strategy names
                 "Strategy A",
                 "Strategy B",
                 "Strategy AB")
n_str       <- length(v_names_str)        # number of strategies

```

```r
### Initialize cohort trace for strategies A, B, and AB ----
#* Structure and initial states are the same as for SoC
m_M_strA  <- m_M # Strategy A
[redacted] m_M # Strategy B
[redacted] m_M # Strategy AB
```

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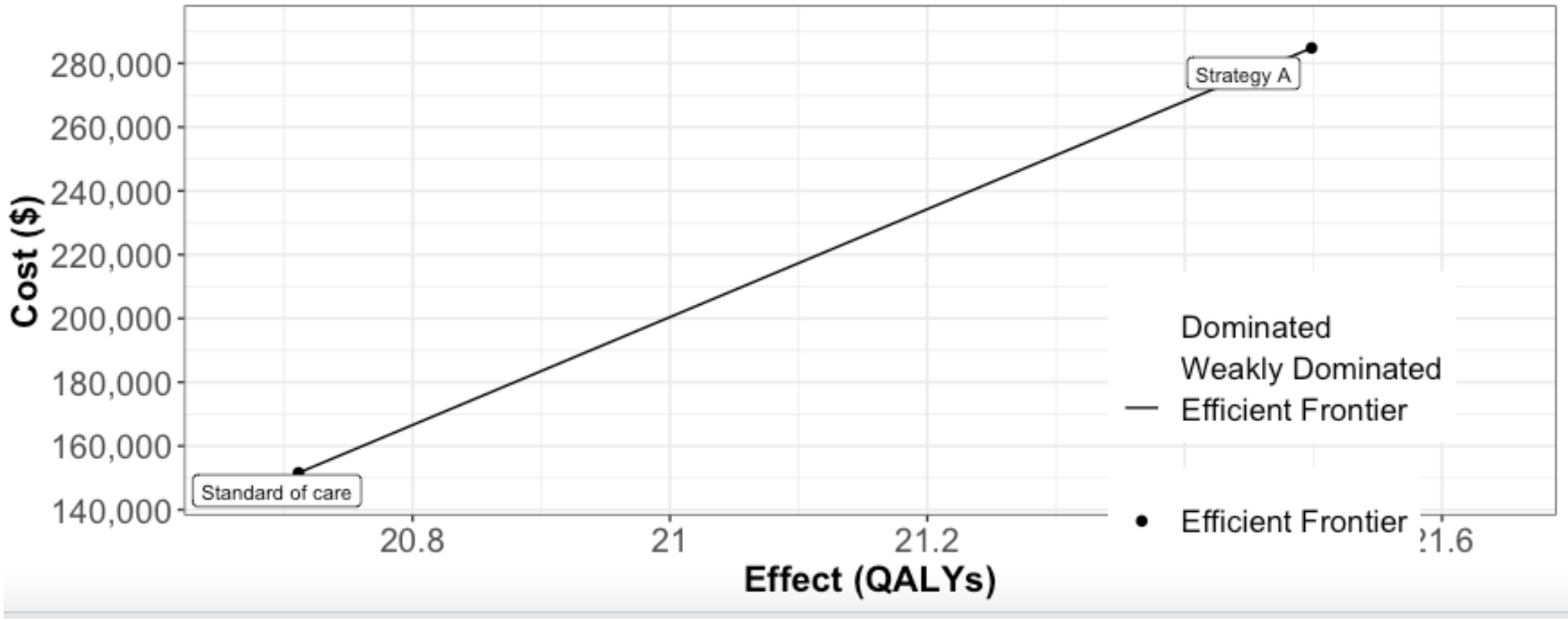
e. Just two strategies: new treatment vs. standard of care (rare diseases)



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f. A different initial state vector

```
139 ## Initial state vector ----
140 #* All starting healthy
141 v_m_init <- c(H = 1, S1 = 0, S2 = 0, D = 0) # initial state vector
142 v_m_init
143
```

```
    H S1 S2  D
0   1  0  0  0
1  NA NA NA NA
2  NA NA NA NA
3  NA NA NA NA
4  NA NA NA NA
5  NA NA NA NA
6  NA NA NA NA
7  NA NA NA NA
8  NA NA NA NA
9  NA NA NA NA
10 NA NA NA NA
11 NA NA NA NA
```

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f. A different initial state vector

```
139 ## Initial state vector ----
140 #* All starting healthy
141 v_m_init <- c(H = 0.7, S1 = 0.2, S2 = 0.1, D = 0) # initial state vector
142 v_m_init
143
```

```
     H  S1  S2  D
0  0.7 0.2 0.1  0
1   NA  NA  NA NA
2   NA  NA  NA NA
3   NA  NA  NA NA
4   NA  NA  NA NA
5   NA  NA  NA NA
6   NA  NA  NA NA
```

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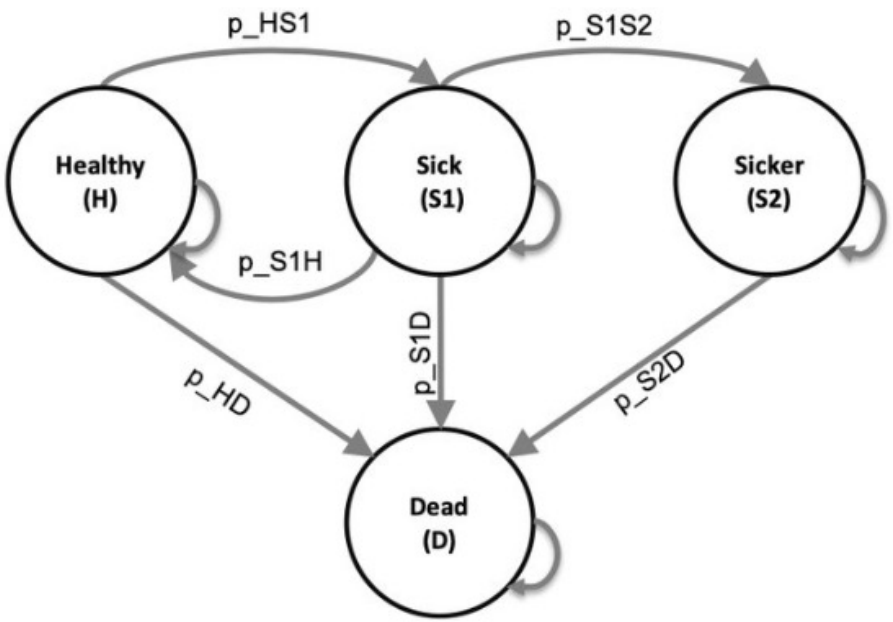
Final exercise

- Add to the original ”Sick-Sicker” model a new state: the “Sickest (S3)” state.

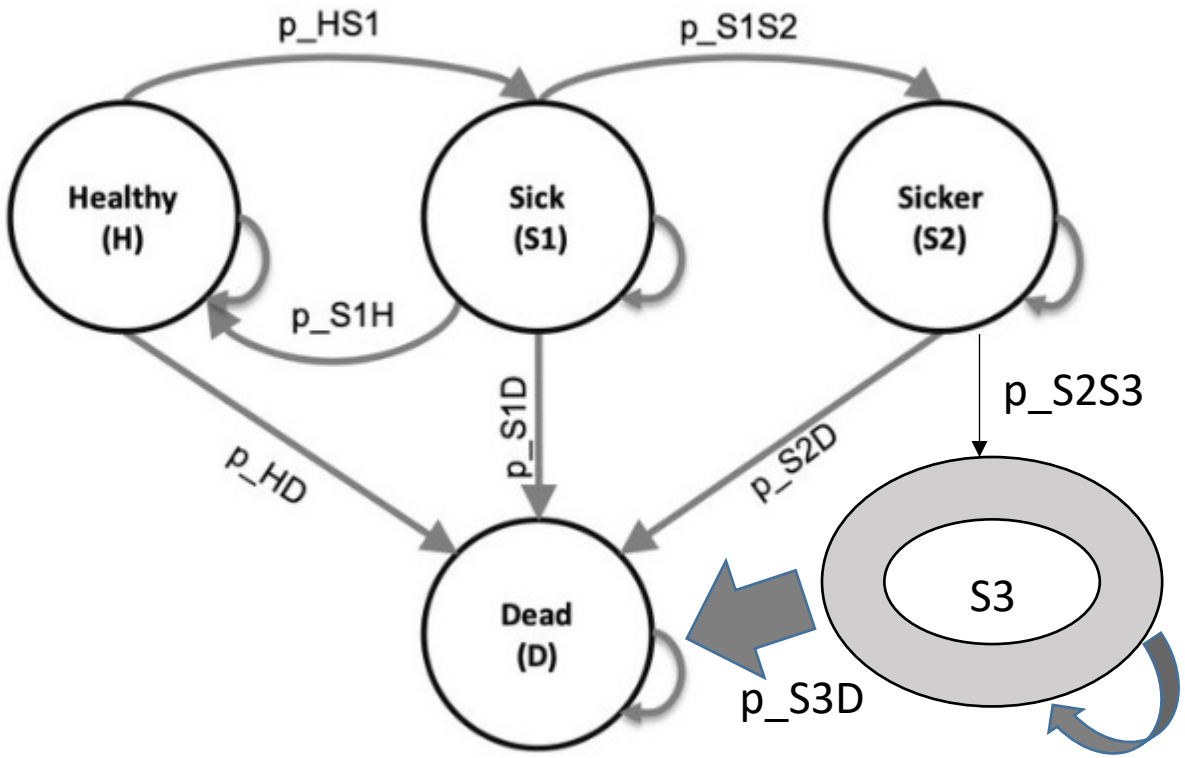


Figure

Caption

Figure 1: State-transition diagram of the Sick-Sicker cohort state-transition model. The circles represent the health states, and the arrows represent the possible transition probabilities. The labels next to the arrows represent the variable names for these transitions.

Final exercise



Figure

Caption

Figure 1: State-transition diagram of the Sick-Sicker cohort state-transition model. The circles represent the health states, and the arrows represent the possible transition probabilities. The labels next to the arrows represent the variable names for these transitions.

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Final exercise

- Annual cost of being “Sickest (S3)” = 20000
- Annual utility value of being “Sickest (S3)” = 0.4
- Annual probability (from S2 to S3) = 0.05
- Annual probability (from S3 to Death) = 0.03

Note: we will assume that Treatment A and Treatment B won't be given to patients during the "Sickest (S3)" state

THANKS

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