hesim: Health Economic Simulation Modeling and Decision Analysis

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Abstract

Health economic models simulate the costs and effects of health technologies for use in health technology assessment (HTA) to inform efficient use of scarce resources. Models have historically been developed using spreadsheet software (e.g., Microsoft Excel) and while use of R is growing, general purpose modeling software is still limited. **hesim** helps fill this gap by facilitating parameterization, simulation, and analysis of economic models in an integrated manner. Supported model types include cohort discrete time state transition models (cDTSTMs), individual continuous time state transition models (iCTSTMs), and partitioned survival models (PSMs), encompassing Markov (time-homogeneous and time-inhomogeneous) and semi-Markov processes. A modular design based on **R6** and S3 classes allows users to combine separate submodels for disease progression, costs, and quality-adjusted life years (QALYs) in a flexible way. Probabilistic sensitivity analysis (PSA) is used to propagate uncertainty in model parameters to model outputs. Simulation code is written in C++ so complex simulations such as those combining PSA and individual simulation can be run much more quickly than previously possible. Decision analysis within a cost-effectiveness framework is performed using simulated costs and QALYs from a PSA.

Keywords: health economic evaluation, cost-effectiveness analysis, simulation, modeling, R.

1. Introduction

Health technology assessment (HTA) is a systematic approach for comparing competing health technologies to inform the efficient use of health care resources. Publicly funded health systems such as those in Australia, Canada, and the United Kingdom, among others, use HTA to help maximize health gains for the population given a fixed budget. HTA is also commonly used by private payers to guide coverage decisions and the adoption of new technologies (Trosman, Van Bebber, and Phillips 2011). Such assessments usually rely heavily on cost-effectiveness analysis (CEA) so that decisions can be made on the basis of a formal evaluation of costs and effects (Dakin, Devlin, Feng, Rice, O'Neill, and Parkin 2015). CEA is made feasible by development of health economic models that simulate costs and effects over relevant time horizons using the totality of available evidence.

The most commonly used economic models are Markov state transition models (STMs) that simulate transitions between mutually exclusive health states. When the Markov assumption holds so that transition probabilities are either constant over time or depend only on model time, a cohort-level model can be used (Briggs and Sculpher 1998). If the Markov assumption

is relaxed—e.g., with a semi-Markov model so that transition probabilities depend on time in an intermediate health state—then individual-level models are required in most cases (Brennan, Chick, and Davies 2006; Fiocco, Putter, and van Houwelingen 2008). Individual-level models afford considerably more flexibility and allow patient history to be tracked over time.

Decisions informed by economic models and CEA are subject to uncertainty. One source of decision uncertainty stems from uncertainty in the underlying model parameters. Parameter uncertainty is typically quantified using probabilistic sensitivity analysis (PSA), which involves randomly sampling the model parameters from suitable probability distribution and simulating the model for each sampled parameter set (Claxton, Sculpher, McCabe, Briggs, Akehurst, Buxton, Brazier, and O'Hagan 2005). When combined with individual-level simulation, PSA can take an appreciable amount of time to run (O'Hagan, Stevenson, and Madan 2007).

Estimation of model parameters should ideally be performed using statistical models that are aligned with the structure of the economic model. For instance, when patient-level data is available, a multi-state model can be used to parameterize all possible transitions in a STM while accounting for censoring and competing risks (Williams, Lewsey, Briggs, and Mackay 2017). Similarly, in oncology, partitioned survival models (PSMs) can be parameterized from estimates of progression-free survival (PFS) and overall survival (OS). In other cases, parameters might be combined from disparate sources, such as within a single Bayesian model (Baio 2012). When the clinical evidence base is not limited to a single study, a formal evidence synthesis, such as a network-meta analysis (NMA), might even be performed (Dias, Ades, Welton, Jansen, and Sutton 2018).

Despite their computational demands and foundations in statistics, health economic models have historically been developed with specialized commercial software (e.g., TreeAge) or more commonly with a spreadsheet (almost always Microsoft Excel). The limitations of such software relative to programming languages like R have been increasingly emphasized in the literature (Baio and Heath 2017; Incerti, Thom, Baio, and Jansen 2019; Jalal, Pechlivanoglou, Krijkamp, Alarid-Escudero, Enns, and Hunink 2017). It is therefore no surprise that a number of related R packages have recently been developed, such as **BCEA** (Baio, Berardi, and Heath 2017), **SAVI** (Strong, Oakley, and Brennan 2014), **survHE** (Baio 2020), and **heemod** (Filipović-Pierucci, Zarca, and Durand-Zaleski 2017). Still, of the available packages, only **heemod** provides a general purpose framework for developing simulation models and it is limited to cohort Markov models.

hesim is an R package that advances the functionality and performance of the existing software. Multiple model types are supported including cohort discrete time state transition models (DTSTMs), N-state PSMs, and individual-level continuous time state transition models (CTSTMs), encompassing both Markov (time-homogeneous and time-inhomogeneous) and semi-Markov processes. To maximize flexibility and faciliate integration of the statistical methods and economic model, parameters can be estimated either by fitting a model in R or by inputting parameters obtained from external sources. So that individual-level simulation and PSA can be run quickly, **Rcpp** and **data.table** are heavily utilized. After simulating costs and quality-adjusted life-years (QALYs) from a PSA, decision analysis can be performed within a cost-effectiveness framework.

2. Model taxonomy

STMs simulate transitions between mutually exclusive health states. A common assumption is that the STM is a Markov model, meaning that transitions to the next health state can only depend on the present health state. In a time homogeneous Markov model transition probabilities are constant over time, whereas in a time inhomogeneous model they can depend on time since the start of the model. A semi-Markov model relaxes the Markov assumption and allows transitions to depend on time since entering an intermediate state.

Markov and semi-Markov models can be formulated in either continuous or discrete time, at either the cohort or individual level. In health economics, Markov cohort models tend to be formulated in discrete time (i.e., as cDTSTMs), although state probabilities can be computed in continuous time models using the Aalen-Johansen estimator (Aalen and Johansen 1978). While tunnel states can be used to approximate a semi-Markov model using a cohort approach, they can only be simulated in a general fashion using individual level models. Discrete time individual simulation is possible, but we use a continuous time models (i.e., iCTSTMs) because they do not require specification of model cycles and can be run considerably faster.

PSMs are specialized models that can be parameterized using survival curves and are especially useful in oncology where PFS and OS are commonly reported. They are "area under the curve" models, although they can also be formulate as STMs by using the survival curves to construct transition probabilities.

2.1. Cohort Discrete time state transition models

cDTSTMs simulate the probability that a cohort of patients is in each of H health states over time. Time is measured at discrete times with each time point known as a model cycle. A $1 \times H$ state vector that stores the probability of being in each health state at time t is written as $v_t = [v_{1t}, v_{2t}, \ldots, v_{Ht}]$ where $\sum_i v_{ht} = 1$. A transition probability matrix is denoted by p_t where the (r, s)th element represents a transition from state r to state s between times t and $t + 1$. The state vector at time $t + 1$ for each of T model cycles can be computed as,

$$v_{t+1} = v_t p_t, \quad t = 0, \ldots, T. \tag{1}$$

Costs and QALYs are computed by assigning (potentially time-varying) values to each health state. Utility, a measure of preference for a health state that normally ranges from 0 (dead) to 1 (perfect health), is used when computing QALYs (Torrance 1986). Assuming model time is in years, state values for costs are estimated by annualizing costs. In a Markov model, state values, like transition probabilities, can depend on time since the start of the model but not on time since entering an intermediate health state.

Expected values are computed by integrating the "weighted" probability of being in each state, where weights are a function of the discount factor and state values. That is, for a time horizon T, discounted costs and QALYs in health state h are computed as,

$$\int_0^T z_h(t) e^{-rt} P_h(t) dt, \tag{2}$$

where $z_h(t)$ is the predicted cost or utility value at time t, r is the discount rate, and $P_h(t)$ is the probability of being in a given health state.

In a discrete time, the integral is approximated with

$$\sum_{j=1}^{T} f(t_j^*)\Delta t_j \tag{3}$$

where $\Delta t_j = t_j - t_{j-1}$, $t_j^* \in [t_{j-1}, t_j]$, and $f(t_j^*) = z_h(t_j^*)e^{-rt_j^*}P_h(t_j^*)$. Three methods can be used to estimate $f(t_j^*)$. First, a left Riemann sum uses values at the start of each time interval $f(t_j^*) = f(t_{j-1})$. Second, a right Riemann sum uses values at the end of each time interval $f(t_j^*) = f(t_j)$. Finally, the trapezoid rule averages values at the start and end of each interval $f(t_j^*) = \frac{1}{2}\Delta t_j[f(t_{j-1}) + f(t_j)]$.

2.2. Individual Continuous time state transition models

2.3. Partitioned survival models

3. Framework

As shown in Figure 1, a typical analysis proceeds in a 3 steps:

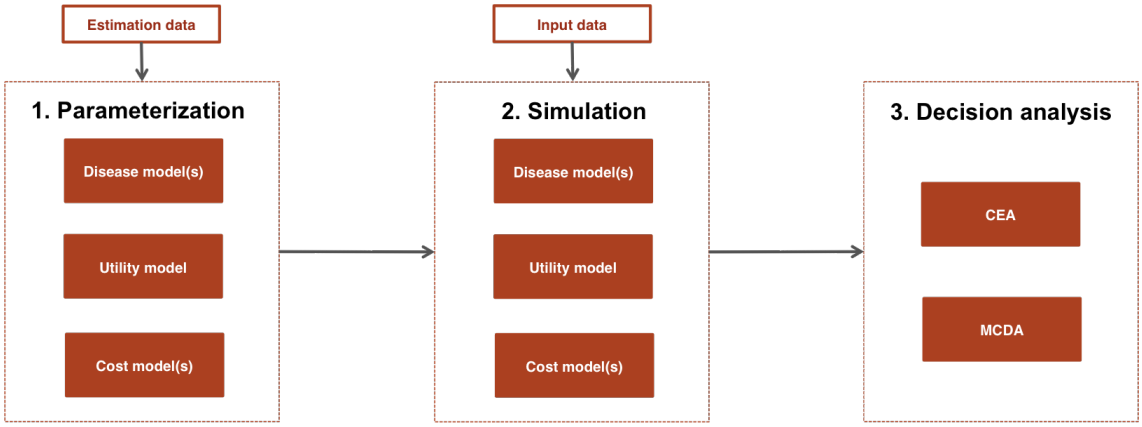

Figure 1: Economic modeling process

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