

Nesting a Decision Tree into a Markov Model Structure: An Alternative Way of Tracking Movement in a Diagnostic Model

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BACKGROUND AND OBJECTIVES

Health economic models can either have a cohort-level or a patient-level approach to estimate costs and benefits [1].

Figure 1: Cohort-level vs patient-level approach



Cohort-level models can take the form of decision-tree and Markov models. A decision tree estimates the probability of various outcomes occurring and then applies costs and benefits to each branch of the tree [1]. A Markov model consists of a set of mutually exclusive health states, with patient movement being estimated through a transition matrix (which estimates the probabilities of patients moving across health states) [1].

The objective was to conceptualise a cohort-level cost-effectiveness model involving multiple screening sessions over a lifetime where, at the point of every screening session, individuals can be redistributed across health states based on their screening results.

This approach was conceptualised as an alternative to a patient-level model, given that only the screening component of the model would have required the need to track each patient individually. By using this proposed alternative approach, fewer resources and time are needed to build the economic model, while not compromising on the validity of the model and its results.

METHODS

A targeted literature review of previous screening models was conducted to assess previous approaches to modelling multiple screening sessions over a lifetime.

A method was conceptualised that involved allocating people into certain health states via a decision tree and then nesting the same decision tree probabilities within Markov model cycles at certain points in the time horizon (in this case, when screening sessions are due).

This method was applied to an economic model using literature-based evidence.

THE CONCEPTUALIZED MODEL

A decision tree was used to capture the first stage of the clinical pathway, with the remainder of the clinical pathway being captured using a Markov model. The screening cohort follows a pre-determined path based on whether the disease was present and at what clinical stage. It was assumed that the time between being invited for a scan to diagnosis was instantaneous.

People entered the model and could either have or not have the disease, with the pathway they follow being determined by the sensitivity/specificity of the screening. Those with a positive screening test were then invited for further diagnostic testing. Those who adhered and attended the testing could either have a positive result and were consequently diagnosed, or a negative result and remained undiagnosed. Those with false negatives (and so incorrectly diagnosed) remain in the health state until either being correctly diagnosed through symptom presentation or the next round of screening. Those who have a false positive test result move into the 'no disease state' and stay here, with a probability of moving into the undiagnosed state in the future.

People who did not adhere to the diagnostic testing moved to the 'undiagnosed' state in the Markov model. People with no disease moved to the 'no disease' state in the Markov model.

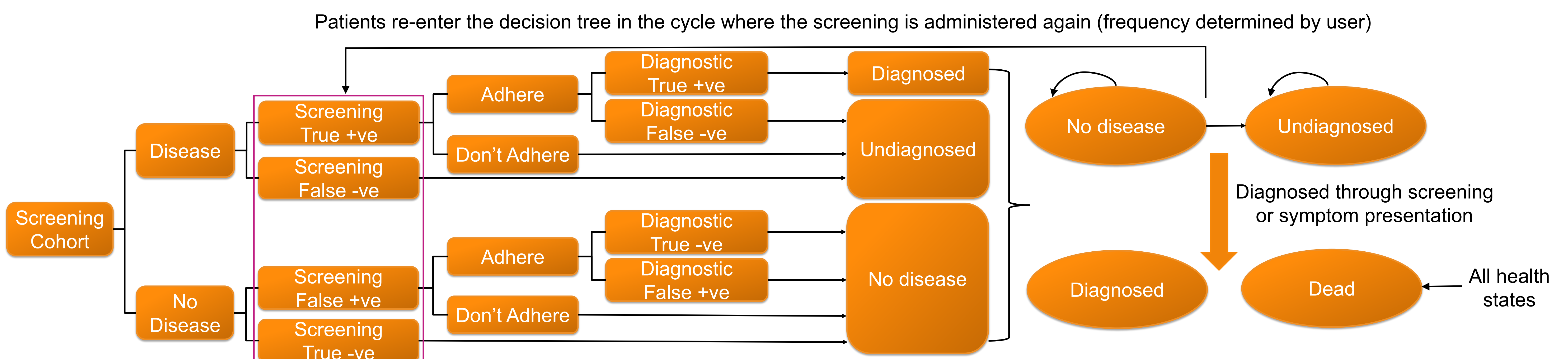
People in the Markov model in the 'no disease' health state have a probability of moving to the 'undiagnosed' health state. People in the 'undiagnosed' health state remain in this state until the screening is re-run (the frequency is determined by the model user) and are redistributed in their new health states based on the results of the screening and the diagnostic test. In between screenings, people could move from 'undiagnosed' to 'diagnosed' health states through symptom presentation. However, once in the 'diagnosed' disease health state people could not move across disease stages and remained in the health state until they died.

CONCLUSIONS

This flexible method can be used when building health economic models to sufficiently track the diagnosis of a naturally progressing disease at the point of screening as well as symptom presentation (for example, diagnosis of cancer). This could also be applied to other types of models where part-way through the time horizon several pathway options become available during one model cycle.

While patient-level models are commonly used across screening modelling, this may not always be the best approach given the resources required to build such a model. This alternative approach has shown that it is possible to employ the concept of patient-level tracking in a cohort-level Markov model.

Figure 2: Model structure



REFERENCES

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