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A dynamic population model for estimating all-cause mortality due to lifetime exposure history

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ABSTRACT

We developed a comprehensive, flexible dynamic model that estimates all-cause mortality for a hypothetical cohort. All model input is user-specified. In the base case, members of the cohort may be exposed to a high risk product as they age. The counterfactual scenario includes exposure to both a high risk and a lower risk product. The model sorts the population into age and exposure categories, and applies the appropriate mortality rates to each category. The model tracks individual exposure histories, and estimates, at the end of each modeled age category, the number of survivors in the two exposure scenarios (base case and counterfactual), and the difference between them. Markov Chain Monte Carlo techniques are used to estimate the variability of the results. Model output was compared against US and Swedish life tables using population-specific tobacco exposure transition probabilities derived from the literature, and it produced similar survival estimates.

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1. Introduction

Statistical models and simulation programs can be used to provide estimates of the health effects expected to result from changes in the distribution of a harmful exposure in a given population. Such changes can occur due to natural trends or to regulatory actions. If the projected changes are due to regulatory action, then modeled results allow direct assessment of the health impacts of alternative policies that might affect the distribution of the exposure in different ways, thus supporting the selection of one policy over another (Levy et al., 2006). Desirable features of such models are the clarity with which the underlying assumptions are stated, and the ability of the model to delineate the relationship between the estimates it produces and the assumptions underlying the model (Garrison 2003; Weinstein et al., 2003).

In this paper, we introduce a new tool, the Dynamic Population Model (DPM). The DPM builds on approaches described by others (Hoogenveen et al., 2008; Kulik et al., 2012; Levy and Friend, 2002; Tengs et al., 2004; Tengs et al., 2005; Tengs et al., 2001) but provides additional flexibility, with all parameters defined by the model user. It improves on the validity of previous models by accounting for age- and time-dependent changes in risks.

Starting with a hypothetical unexposed population and following the population as it ages, the DPM distributes subsets of the cohort into user-defined exposure categories, and applies the correct mortality rate to each category. In the base case, the population has access to only one type of product. In the counterfactual exposure scenario, proportions of the population may use an alternative product with a different risk profile. In this manner, the DPM estimates all-cause mortality in the hypothetical population under different exposure distributions, and compares the numbers of survivors expected under each exposure scenario. The example presented here, and the one upon which the model was built, uses cigarettes and a modified risk tobacco product (MRTP, e.g., smokeless tobacco) associated with lower health risks than cigarettes. It compares the number of survivors in a base case that includes never, current and former cigarette smokers, but no MRTP users, with the number of survivors in a counterfactual scenario that additionally includes never, current and former MRTP users.

2. Methods

2.1. The model

The DPM user defines the size of a hypothetical population. The DPM models a cohort, in which all members of this hypothetical population are the same age and none are exposed at the beginning of the simulation. The time variable is age (categorical). The DPM user specifies at which age to begin and end follow-up, and the age category width. All age categories must have the same width.

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2.2. Transitions between exposure states

The DPM distributes persons into age and exposure categories using age category-specific exposure transition probabilities entered by the DPM user. All cohort members begin as unexposed (to either product), shown in the top left-hand box of Fig. 1. As follow-up of the base case progresses (Fig. 1, top row), individuals either remain as unexposed (curved arrow) or transition to current use of the base case product (top row, second box), shown by the forward arrow. Current users may remain current users (curved arrow) or become former users in the next follow-up interval. Subsequently, former users may restart the base case product and quit again. Rows below the top in Fig. 1 are needed to describe the additional possibility of exposure to the alternative product in the counterfactual scenario. For example, unexposed cohort members (top left-hand box) may remain as unexposed (curved arrow) or transition to use of the alternative product (downward arrow). Current alternative product users may remain current users (curved arrow), switch to the base case product, become concurrent dual users of both products, or quit use of the alternative product in the next follow-up interval. Subsequently, persons can remain in their exposure category (curved arrow) or move into other exposure categories (forward arrow).

The DPM user can define the probability of transitioning from one exposure state to another from available data, or the transition probabilities can be specified to define a particular question of interest. For the example of smoking and MRTP use, assume that the smoking initiation rate among US males aged 13–17 years in a particular year of interest is 11%; then, the probability of transitioning from never tobacco user to smoker in age category 13–17 would be set by the DPM user to 11%. If the DPM user was interested in the effect on population mortality if, among US males aged 13–17, smoking initiation was 5% instead, the DPM user would set the probability of transitioning from never tobacco user to smoker in age category 13–17 to 5%.

The distribution of the cohort into exposure groups is simple enough to be applied in a spreadsheet. However, to obtain variability estimates of the output using Markov chain Monte Carlo techniques, we implemented the DPM in the WinBUGS computer program (version 1.4.3) (Lunn et al., 2000). Transition probabilities can be modeled as fixed (most appropriate for rates defining a specific question of interest) or normally distributed (most appropriate for rates based on estimates from the literature), but are bounded between 0% and 100%. Default means are equal to the respective estimated transition probabilities, and default standard deviation is equal to 1%. The standard deviation can be changed by the DPM user.

2.3. Mortality

A Poisson model embedded within the DPM estimates the number of deaths among persons with a particular exposure history involving only the base case product. The estimates are based on person-years and deaths by age, years of exposure and years since cessation of exposure entered by the user. Only survivors move on to the next age category. Specifically, *r.ne*, the mortality rate among persons who never used the base case (or the alternative) product and *r.bc* and *r.fbc*, the mortality rate among current and

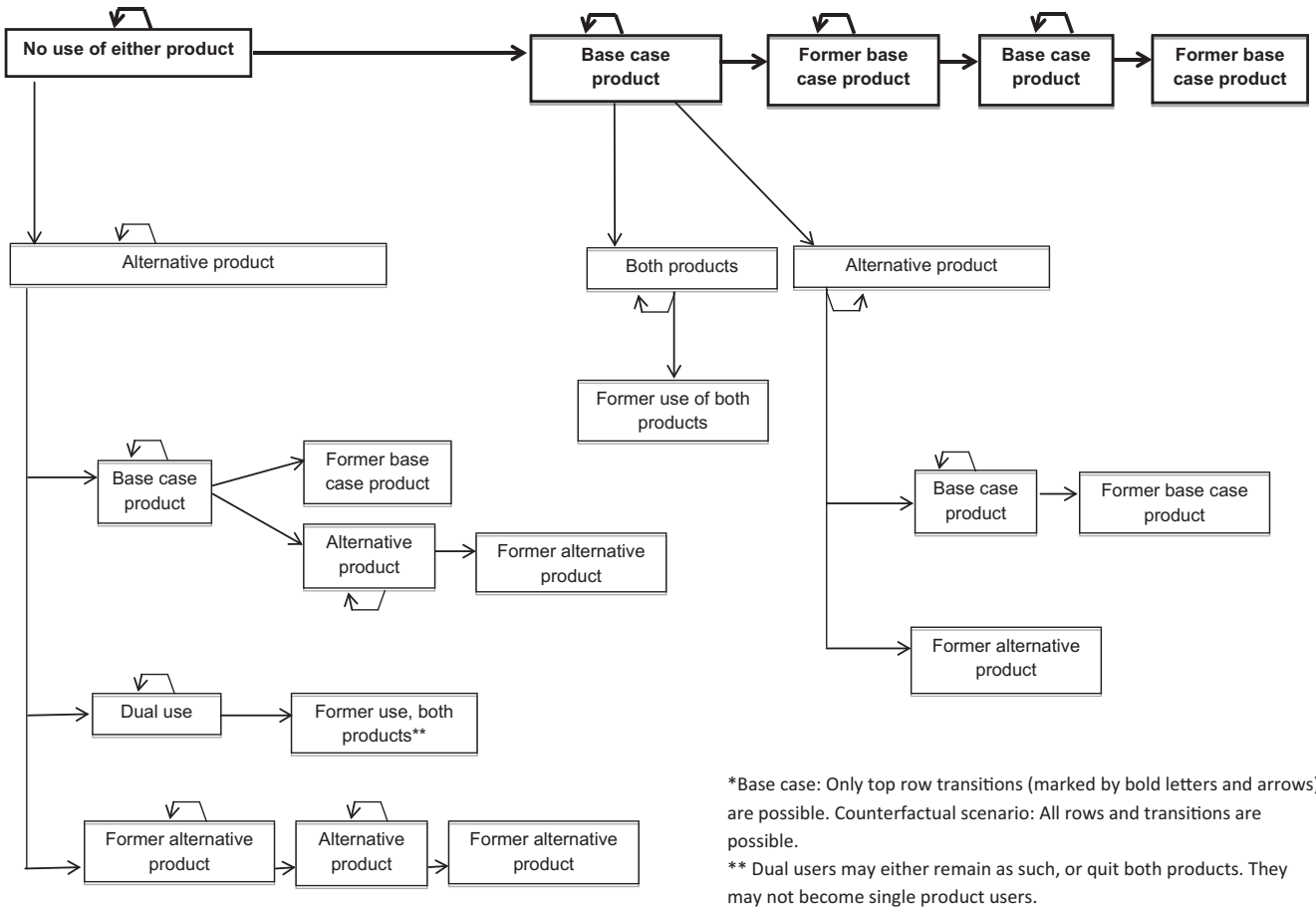

Fig. 1. Schematic representation of the distribution of persons into exposure categories by the Dynamic Population Model. Transitions for base case (top row, only) and counterfactual exposure scenarios (all rows).*

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