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Randomizing the parameters of a Markov chain to model the stroke disease: A technical generalization of established computational methodologies towards improving real applications

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Abstract

Classical Markov models are defined through a stochastic transition matrix, i.e., a matrix whose columns (or rows) are deterministic values representing transition probabilities. However, in practice these quantities could often not be known in a deterministic manner, therefore, it is more realistic to consider them as random variables. Following this approach, this paper is aimed to give a technical generalization of classical Markov methodology in order to improve modelling of stroke disease when dealing with real data. With this goal, we randomize the entries of the transition matrix of a Markov chain with three states (susceptible, reliant and deceased) that has been previously proposed to model the stroke disease. This randomization of the classical Markov model permits the computation of the first probability density function of the solution stochastic process taking advantage of the so-called Random Variable Transformation technique. Afterwards, punctual and probabilistic predictions are computed from the first probability density function. In addition, the probability density functions of the time instants until a certain proportion of the total population remains susceptible, reliant and deceased are also computed. The study is completed showing the usefulness of our computational approach to determine, from a probabilistic point of view, key quantities in medical decision making, such as the cost-effectiveness ratio.

Keywords: Markov process, disease modelling, random variable transformation technique, computing the first probability density function

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1. Introduction

Discrete Markov stochastic processes (s.p.'s) or discrete Markov chains are often applied to model the dynamics of medical events over evenly spaced times, $n = 0, 1, 2, \dots$, usually referred to as periods or cycles. In particular, these kind of s.p.'s have been considered for different purposes. For example, to built and simulate models for chronic illnesses [1, 2], to analyse

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