Letter to the Editor

Application of Hidden Markov Model to Identify Disease Progression Process in Medical Research

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Dear Editor in Chief

Disease progression process means a change of disease stages during the times (1). Identifying how is progress the disease and the number of its stages can be very helpful to increase correct recognition and appropriate prescribing of medications in different disease treatments.
Markov models are a ubiquitous and unique statistical model which can modeling different stages of diseases during time and identify the disease progression process (Fig. 1). The basic assumption of these models is a Markov property, it means that the current stage of the disease must be depend like a chain only on the previous time stage not on other stages that occurred earlier times (2).
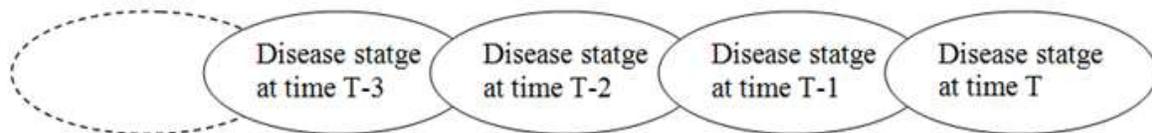

Fig.1: Markov property of disease stages

In most medical records datasets, there is no information about the disease progression and the number of stages that patients have taken during the illness, only test results and demographic information is recorded. Therefore, disease stages and progression process are hidden. In this situation using of another type of Markov models with capability of identifying the number of hidden stages and transition probability among them and as a result modeling of disease progression is recommended. This type of Markov models called Hidden Markov model (HMM, hereafter) (3).

Although this model was introduced in the late the 19th century, depend on computational complexity after extensive advanced in computer sciences using of applied form of this model has changed massively (4). HMM with processing existence information of patients during the time, taking a different number of hidden stages in the range of two to 10 and evaluating model performance, empirically find the best number of hidden stages with the highest accuracy of the model (5).
Patients during their illness may experience different stages of disease, HMM after finding best

number of hidden stages, with estimating transition probability among these stages and estimating initiating disease from each stage can specify the disease progression process and provide appropriate interpretation (6, 7). If the researcher is interested in looking for the stage of disease at any time of follow up patients, HMM can help to find most likely stage at any time by estimating emission probabilities (6).

During the time medical research has undergone massive changes and using statistical models have been more considerate than ever. Todays, different statistical package in different programming language and softwares such as R, Matlab, and Python offered to run the HMM. By applying this valuable model in the medical field not only prescribing appropriate medicine and increasing survival time of patients, but also it leads to saving time and money and as a result, increasing the efficiency of medical diagnosis and therapy systems.

Conflict of interest

The authors declare that there is no conflict of interest.

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