ABSTRACT

In a pure survival study, the response for each patient is survival time. However, survival studies often generate a survival process containing both survival time and a sequence of health measurements for each patient. Obviously, there are associations between survival time and sequential health measurements. The joint modeling is a popular method to deal with this type of survival process in recent decades. The revival modeling, proposed recently, is also designed to deal with such a survival process. In this paper, we review these two methods and apply them to analyze the progression of the prothrombin index and survival time of liver cirrhosis patients. Philosophical considerations of these two models are very distinct. We also compared these two methods at the end.