

Updating the posterior information of joint models for longitudinal and time-to-event data through a sequential approach

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The statistical analysis of the information generated by medical follow-up is a very important challenge in the field of personalised medicine. As the evolutionary course of a patient's disease progresses, its medical follow-up generates more and more information that should be processed immediately in order to review and update its prognosis and treatment. Hence, we focus on this update process through sequential inference methods for joint models of longitudinal and survival data from a Bayesian perspective. More specifically, we propose the use of sequential Monte Carlo methods for static parameter joint models with the intention of reducing computational time in each update of the inferential process. Our proposal is very general and can be easily applied to most popular joint models approaches. We illustrate the use of the presented sequential methodology in a simulated joint model with informative dropout and a joint model with competing risk events for a real scenario involving patients on mechanical ventilation in intensive care units.