

A BAYESIAN APPROACH TO MODEL A MULTI-STATE MARKOV MODEL FROM INTERVAL-CENSORED DATA

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In studies of disease stages and their relation to survival, data are usually obtained at infrequent time points during follow-up. At these points, the clinical status of a patient can be assessed and as a consequence be distinctly categorised using other covariates and in many cases a subjective clinical classification by a medical researcher. In its simplest form these categories can be dead or alive or even extended to, for example, stage I, II, III or IV of HIV/AIDS by using clinical markers. Actual changes of the clinical stages occur normally between two successive follow-up times. A disadvantage of not taking this censoring into consideration in model building, may lead to severe over- or underestimation of the actual time spent in the different stages. The time patients stay in the different stages of a disease can be an indication of the effectiveness of a drug in stemming the spread of the disease. A Markov model is assumed to assess the rate at which patients move from one stage to another, given a set of covariates during follow-ups. A Bayesian approach is followed to model the transition states between actual time points, using a Dirichlet process. This Bayesian approach involves that the probability element corresponding to each patient's contribution to the likelihood is altered according to a Dirichlet process prior. Different approaches in altering the probability contributions are proposed and compared by means of posterior analyses of the transition rates in a non-parametric setting. A paediatric HIV dataset obtained from a large academic hospital in South Africa is used to illustrate the results.