

Development and validation of a dynamic prognostic tool for Prostate Cancer recurrence based on a joint modelling approach

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Joint models for longitudinal and time-to-event data offer a good framework to describe the risk of a clinical event according to the repeated measures of a biomarker. Based on these models, dynamic prognostic tools can be built that may be updated each time a new biomarker data is collected. In Prostate Cancer study, such tool would be of great interest since the biomarker PSA, which is routinely and repeatedly measured on patients treated by a radiation therapy, has been shown to be highly predictive of Prostate Cancer recurrence. However, for now, prognostic models for recurrence of Prostate Cancer only use information collected at the diagnosis. Indeed, the development of dynamic prognostic tools has been limited by the numerical complexity induced by the joint models estimation. In this talk, we propose a dynamic prognostic tool derived from a joint latent class model [2] that avoids the numerical complexity due to the shared random-effects in standard joint modelling.

The main problem when developing a prognostic tool, either dynamic or static, remains in its validation on external data and its comparison with simpler methods. Graf et al. [1] as well as Schemper & Henderson [3] proposed two estimators of the error of prediction for survival data. In this work, we compare these measures on simulated data and provide an empirical measure of their variability. We also show how to use them in the longitudinal context to compare the dynamic prognostic tool we proposed to a proportional hazard model including either baseline covariates or baseline covariates and the last PSA available at the point of prediction. Using data from three large cohorts of patients treated after the diagnosis of Prostate Cancer, we show that the dynamic prognostic tool based on the joint model reduces the error of prediction and offers a powerful tool for individual prediction.

References

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