

Individual dynamic predictions using landmarking and joint modelling: validation of estimators and robustness assessment

Loïc Ferrer^{1,†}, Hein Putter² and Cécile Proust-Lima¹

¹INSERM U1219, Université de Bordeaux, Bordeaux, France

²Leiden University Medical Center, Leiden, the Netherlands

[†]*Email:* loic.ferrer@inserm.fr

Thème privilégié : Mesure de la prédictibilité des modèles

Résumé : After the diagnosis of a disease, one major objective is to predict cumulative probabilities of events such as clinical relapse or death from the individual information collected up to a prediction time, including usually biomarker repeated measures. Several competing estimators have been proposed to calculate these individual dynamic predictions, mainly from two approaches: the joint modelling and the landmarking. These approaches differ by the information used, the model assumptions and the complexity of the computational procedures. It is essential to properly validate the estimators derived from the joint models and the landmark models, quantify their variability and compare them in order to provide key elements for the development and use of individual dynamic predictions in clinical follow-up of patients. Motivated by the prediction of two competing causes of progression of prostate cancer from the history of prostate-specific antigen, we conducted an in-depth simulation study to validate and compare the dynamic predictions derived from these two methods. Specifically, we formally defined the quantity to estimate and its estimators, proposed new techniques to assess the uncertainty around predictions and validated them. We also compared the individual dynamic predictions derived from joint models and landmark models in terms of accuracy of prediction, efficiency and robustness to model assumptions. We show that these prediction tools should be handled with care, in particular by properly specifying models and estimators.