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Title: Bayesian semiparametric modelling of biomarker variability in joint models

## Abstract:

There is growing interest in the role of within-individual variability (WIV) in biomarker trajectories for assessing disease risk and progression. A trajectory-based definition that has attracted recent attention characterises WIV as the curvature-based roughness of the latent biomarker trajectory (TB-WIV). To rigorously evaluate the association between TB-WIV and clinical outcomes and to perform dynamic risk prediction, joint models for longitudinal and time-to-event data (JM) are necessary. However, specifying the longitudinal trajectory is critical in this framework and poses methodological challenges.

In this work, we investigate three Bayesian semiparametric approaches for longitudinal modelling and TB-WIV estimation within the JM framework to improve stability and accuracy over existing approaches. Two key methods are newly introduced: one based on Bayesian penalised splines (P-splines) and another on functional principal component analysis (FPCA). Using extensive simulation studies, we compare their performance under two important TB-WIV definitions against established approaches. Our results demonstrate overall inferential and predictive advantages of the proposed P-spline and FPCA-based approaches while also providing insights that guide method choice and interpretation of inference results. The proposed approaches are applied to data from the UK Cystic Fibrosis Registry, where, for the first time, we identify a significant positive association between lung function TB-WIV and mortality risk in patients with cystic fibrosis and demonstrate improved predictive performance for survival.