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Spatio-temporal P-splines models in Bayesian disease mapping

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In recent years, models incorporating splines have been considered for smoothing mortality or incidence risks in spatio-temporal disease mapping as an alternative to conditional autoregressive (CAR) models. These models have been commonly formulated within a hierarchical Bayesian framework with two main approaches: an Empirical Bayes (EB) and a fully Bayes (FB) approach. The reformulation of the P-splines as generalized linear mixed models (GLMM) has been commonly considered within the EB approach [1, 2], using the well-known penalized quasi-likelihood (PQL) technique for model fitting and inference. From a fully Bayes approach, Markov chain Monte Carlo (McMC) methods have been used to compute the posterior marginal distributions of the splines's regression coefficients [3]. Although these models are very flexible, they can be computationally demanding to analyze spatio-temporal data.

In this work, several models including one, two and three-dimensional P-splines are proposed for smoothing risks in spatio-temporal disease mapping, fitting the models from a fully Bayesian approach using integrated nested Laplace approximations (INLA). Specifically, spatially structured one-dimensional temporal P-splines, as well as temporally structured two-dimensional spatial P-splines are proposed as an alternative to three-dimensional P-splines. Two real cancer data sets will be used to illustrate these models.

References

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