

Predicting Treatment Efficacy via Quantitative MRI: A Bayesian Joint Model

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Abstract

Quantitative magnetic resonance imaging (qMRI) is a host of MRI techniques capable of measuring physiological processes down to the molecular level. Examples include diffusion tensor imaging—measuring the diffusion of water molecules; T_2 -weighted dynamic contrast enhanced MRI—measuring blood volume and blood flow; and MR spectroscopy—measuring metabolite concentrations. Serial measures of qMRI quantities can be used to monitor disease progression and to measure response to treatment. In a recent pilot study, qMRI of diffusion and cerebral blood flow in patients with high-grade glioma tumors (median survival: one year) were obtained at baseline and three weeks into therapy (a combination of radiotherapy and chemotherapy) to determine whether changes in these qMRI measures are predictive of treatment efficacy as measured by one-year survival. Currently, treatment efficacy is assessed radiographically five to six months after treatment begins at which time second line therapies are administered. If treatment efficacy, or lack thereof, could be accurately predicted earlier than this, then second line therapies could be administered earlier, potentially offering patients a longer expected lifetime.

Thus, there is current need for statistical modeling of these complex data to assess whether qMRI measures can accurately predict treatment efficacy. To this end, we present a joint, two-stage Bayesian model of treatment efficacy, as determined by one-year survival status, using qMRI data and then assess its performance. In stage I, we smooth the qMRI data with a multivariate spatio-temporal pairwise difference prior model. We propose four summary statistics—functionals of posterior parameters—from the first stage. In stage II, these statistics enter a generalized non-linear model (GNLM) as predictors of one-year survival status. The covariates enter the systematic component nonlinearly via a multivariate adaptive regression spline basis. The systematic component is then linked to the outcome by way of the probit link function. The number of basis functions is assumed unknown, a priori, and is estimated via reversible jump MCMC. By modeling the spatio-temporal correlation in the images and by allowing a complex and flexible decision boundary provided by the Bayesian GNLM, our model achieves higher overall correct classification rates than do simpler models.