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Bayesian Sparsity-Path-Analysis of Genetic Association Signal using Generalized t Priors

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(Submitted on 1 Jun 2011)

We explore the use of generalized t priors on regression coefficients to help understand the nature of association signal within "hit regions" of genome-wide association studies. The particular generalized t distribution we adopt is a Student distribution on the absolute value of its argument. For low degrees of freedom we show that the generalized t exhibits 'sparsity-prior' properties with some attractive features over other common forms of sparse priors and includes the well known double-exponential distribution as the degrees of freedom tends to infinity. We pay particular attention to graphical representations of posterior statistics obtained from sparsity-path-analysis (SPA) where we sweep over the setting of the scale (shrinkage / precision) parameter in the prior to explore the space of posterior models obtained over a range of complexities, from very sparse models with all coefficient distributions heavily concentrated around zero, to models with diffuse priors and coefficients distributed around their maximum likelihood estimates. The SPA plots are akin to LASSO plots of maximum a posteriori (MAP) estimates but they characterise the complete marginal posterior distributions of the coefficients plotted as a function of the precision of the prior. Generating posterior distributions over a range of prior precisions is computationally challenging but naturally amenable to sequential Monte Carlo (SMC) algorithms indexed on the scale parameter. We show how SMC simulation on graphic-processing-units (GPUs) provides very efficient inference for SPA. We also present a scale-mixture representation of the generalized t prior that leads to an EM algorithm to obtain MAP estimates should only these be required.

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