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Cross-Validatory Model Comparison and Divergent Region Detection using iIS and $iWAIC$ for Disease Mapping

Two statistical problems arise in using Bayesian hierarchical models for disease mapping. The first is to compare goodness of fit of various models, which can be used to test different hypotheses. The second problem is to identify outlier/divergent regions with unusually high or low residual risk of disease. Leave-one-out cross-validatory (LOOCV) model assessment has been used for these two problems. However, actual LOOCV is time-consuming. This paper introduces two methods, namely iIS and $iWAIC$, for approximating LOOCV with only Markov chain samples simulated from a posterior based on a full data set.