Improved inference in Bayesian segmentation using Monte Carlo sampling: Application to hippocampal subfield volumetry

Many segmentation algorithms in medical image analysis use Bayesian modeling to augment local image appearance with prior anatomical knowledge. Such methods often contain a large number of free parameters that are first estimated and then kept fixed during the actual segmentation process. However, a faithful Bayesian analysis would marginalize over such parameters, accounting for their uncertainty by considering all possible values they may take. Here we propose to incorporate this uncertainty into Bayesian segmentation methods in order to improve the inference process. In particular, we approximate the required marginalization over model parameters using computationally efficient Markov chain Monte Carlo techniques. We illustrate the proposed approach using a recently developed Bayesian method for the segmentation of hippocampal subfields in brain MRI scans, showing a significant improvement in an Alzheimer’s disease classification task. As an additional benefit, the technique also allows one to compute informative “error bars” on the volume estimates of individual structures.