

MRI Tissue Classification using High Resolution Bayesian Hidden Markov Normal Mixture Models

In the study of medical imaging one important task is to use MR images to identify the major tissues within a subject's brain. Classification is usually based on a T1-weighted image providing one measurement for voxels in the brain. A simple model views each voxel as homogeneous, belonging entirely to one of the three major tissue types; the measurements are usually modeled as normally distributed with means and variances depending on the tissue types of their voxels. Since nearby voxels tend to be of the same tissue type, a Markov random field model can be used to capture the spatial similarity of voxels.

A more realistic model would take into account the fact that some voxels are not homogeneous; while some may contain only one tissue type, others on the interface will contain two or possibly three different tissue types. Our approach to this problem is to construct a higher resolution image in which each voxel is divided into subvoxels. For each voxel the measured value is the sum of the unobserved measurements for the subvoxels and subvoxels are in turn assumed to be homogeneous and follow the simpler model. To reflect the observation that some tissue types are rarely adjacent, we use what we call the repulsion Potts model instead of the simple Potts model to characterize the spatial structure among subvoxels. A Bayesian hierarchical model is used to conduct MRI tissue classification. Conditional independence is exploited to improve the speed of sampling. The subvoxel approach provides more accurate tissue classification and also allows more effective estimation of the proportion of major tissue types present in each voxel for both the simulated and real data sets.