mritc: A Package for MRI Tissue Classification

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July 2010
Outline

- Basics of MRI Tissue Classification
- Available Methods
- Computational Issues
- Overview of the Package
MRI is a non-invasive method for imaging the inside of objects.

- MRI has many medical applications.
- Different contrast: T1, T2, PD
- Sometimes more than one image type is available.
- Each image is a 3D array of image intensities, one for each voxel (volume picture element).
Brain Tissue Classification

- Major brain tissue types:
  - White matter (WM)
  - Gray Matter (GM)
  - Cerebrospinal fluid (CSF)

There are others, but tissue classification usually focuses on these.

- Some applications:
  - Diagnosis of disease
  - Surgery preparation

- Manual tissue classification is very labor intensive.

- Automated methods try to match quality of manual at lower cost.

- Focus on using intensities in a T1 MR image.

WM = light gray
GM = medium gray
CSF = dark gray
Basic Properties of the Data

- Data consist of image intensities $y_1, \ldots, y_N$ for $N$ voxels in a 3D grid.
- $N$ is large, for example $256 \times 256 \times 192$.
- Intensities are often scaled to $[0, 255]$ and rounded to an integer.
- Tissue types are denoted by $z_i \in \{1, \ldots, k\}$ with $k = 3$ corresponding to three tissue types.
- A density plot of a relatively low noise MR image:
A Simple Mixture Model

- A common model: given the tissue structure $z$, intensities are
  - independent
  - normally distributed,

$$y_i | z_i \sim N(\mu(z_i), \sigma^2(z_i))$$

- Mean and variance depend on the tissue type.
- Assuming tissue types are independent leads to a simple normal mixture model

$$f(y) = \prod_{i=1}^{N} \sum_{z_i=1}^{k} \phi_{\mu(z_i), \sigma^2(z_i)}(y_i)p(z_i = k)$$

- Parameters are easily estimated by the EM algorithm.
- Tissue types can be assigned using the Bayes classifier.
Incorporating Spatial Information

- Adjacent voxels are likely to contain the same tissue type.
- A more realistic model accounts for this spatial homogeneity in $z$.
- The Potts model family provides simple models for spatial homogeneity:

$$p(z) = C(\beta)^{-1} \exp \left\{ \sum_i \alpha_i(z_i) + \beta \sum_{i \sim j} w_{ij} f(z_i, z_j) \right\}$$

- This is an example of a Markov random field model.
The hidden Markov normal mixture model

\[ p(y|z, \mu, \sigma^2)p(z) \]

can be fitted by

- Iterated Conditional Modes (ICM) algorithm—alternately maximizing each parameter conditional on all others being fixed.
Alternatively, we can

- specify a prior distributions $p(\mu, \sigma^2)$ on $\mu, \sigma^2$
- use MCMC to compute characteristics of the posterior distribution

$$p(\mu, \sigma^2, z|y)$$

Assume $\mu, \sigma^2, z$ are independent and

- $\mu$ i.i.d. normal distribution
- $\sigma^2$ i.i.d inverse Gamma distribution

Then the full conditionals satisfy

- $\mu$ independent normal
- $\sigma^2$ independent inverse Gamma
- $z$ Potts model with external field

$$\alpha_i(z_i) = \log f(y_i|\mu(z_i), \sigma(z_i))$$
Partial Volume Effect

- Partial volume effect—some voxels contain more than one tissue type.
- One approach is to introduce intermediate classes: CG (CSF/GM) and GW (GM/WM).
- This helps reduce confounding in estimation.
- A number of studies have used this approach.
- Normal mixture model with dependent means and variances (GPV) performs well.
  - The means and variances of CG and GW are equal to weighted average of corresponding pure tissues
  - The densities of voxels from CG and GW are equal to mean densities based on the distribution of weights
A Higher Resolution Spatial Model

We have adopted a different approach:

- Each voxel is divided in half in the $x$, $y$, $z$ directions, producing 8 subvoxels.

- Each subvoxel is viewed as containing only one tissue type.

- The observed voxel intensity $y_i$ is

$$y_i = v_{i1} + \ldots + v_{i8}$$

where $v_{i1}, \ldots, v_{i8}$ are the unobserved subvoxel intensities.
A Higher Resolution Spatial Model
The Subvoxel-level Model

- Conditional on the tissue types, the $v_{ij}$ are independent normals
- A spatial model is used at the subvoxel level
- To capture the fact that CSF and WM rarely coexist in a voxel we use:

$$p(z) = C(\beta_1, \beta_2)^{-1} \exp \left\{ \sum_{i \sim j} f(z_i, z_j) \right\}$$

where

$$f(z_i, z_j) = \begin{cases} 
\beta_1 & \text{if } z_i = z_j \\
-\beta_2 & \text{if } \{z_i, z_j\} = \{\text{CSF, WM}\} \\
0 & \text{otherwise}
\end{cases}$$

We call this model the Repulsion Potts Model

- Use a Bayesian formulation to solve it
Computational Issues—Table Lookup

Table lookup methods are used in various places due to:

- the nature of the data—intensities are integers between 0 and 255.
- the nature of the distribution from the Potts family—given neighbors, the tissue type of voxels having the same discrete distribution.
If the voxels are organized in a checkerboard pattern,

then black voxels are conditionally independent given white ones.

Black and white voxels can each be updated as a group.

This can be used for vectorized computation.

This can also be used for parallel computation.
Specifying parallel execution by compiler pragmas (directives)

```c
#pragma omp parallel for firstprivate(k, ldD, ...)
for (i = 0; i < n; i++) {
}
```

Specifying variable type

Implicit barrier for synchronization

```c
for (i = 0; i < n; i++) {
}
```
Overview of Functions of the Package

- The "Analyze", "NIIfTI", and raw byte file formats are supported for input and output
- Different functions for different methods are provided
- Initial values of the means, variances, and proportions of normal mixture models can be generated by the function `initOtsu`
- Various spatial input parameters for different methods can be obtained using the function `makeMRIspatial`
- There is a wrapper for functions with easier usage `mritc(intarr, mask, method)`
- Generic `summary` and `plot` methods are provided for the object of class "mritc"
- Different metrics for accuracy of predictions based on truth are available
An Example

R> T1 <- readMRI("t1.rawb.gz", c(181,217,181),
       format="rawb.gz")
R> slices3d(T1)
R> mask <- readMRI("mask.rawb.gz", c(181,217,181),
       format="rawb.gz")
R> tc <- mritc(T1, mask, method="MCMCsub")
R> plot(tc)

Figure: Tissue Classification