mritc: A Package for MRI Tissue Classification

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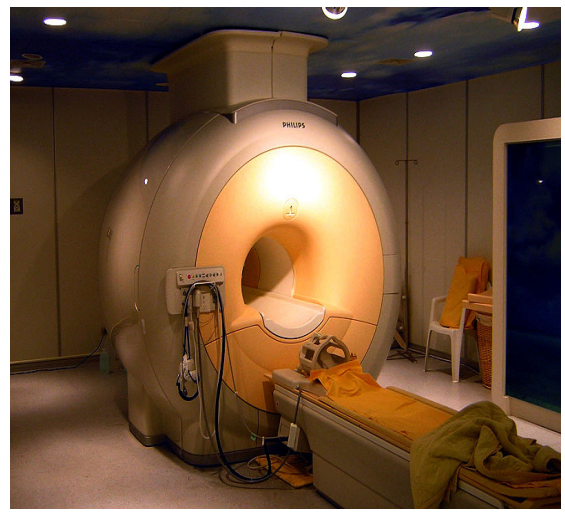
July 2010

Outline

- Basics of MRI Tissue Classification
- Available Methods
- Computational Issues
- Overview of the Package

Magnetic Resonance Imaging (MRI)

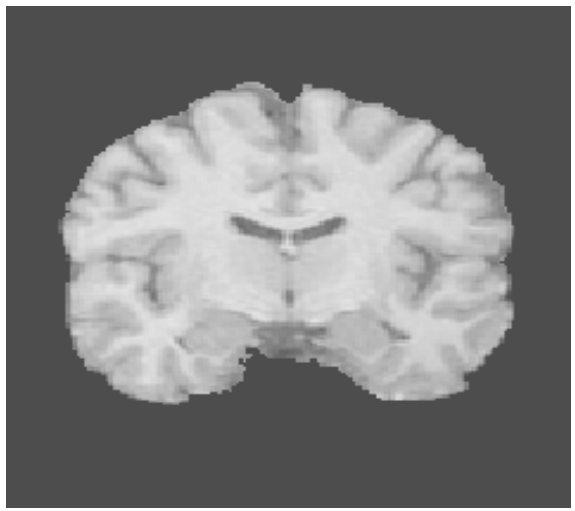
- MRI is a non-invasive method for imaging the inside of objects.
- MRI has many medical applications.
- Different contrast: T1, T2, PD
- Sometimes more than one image type is available.
- Each image is a 3D array of image intensities, one for each voxel (volume picture element).



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.



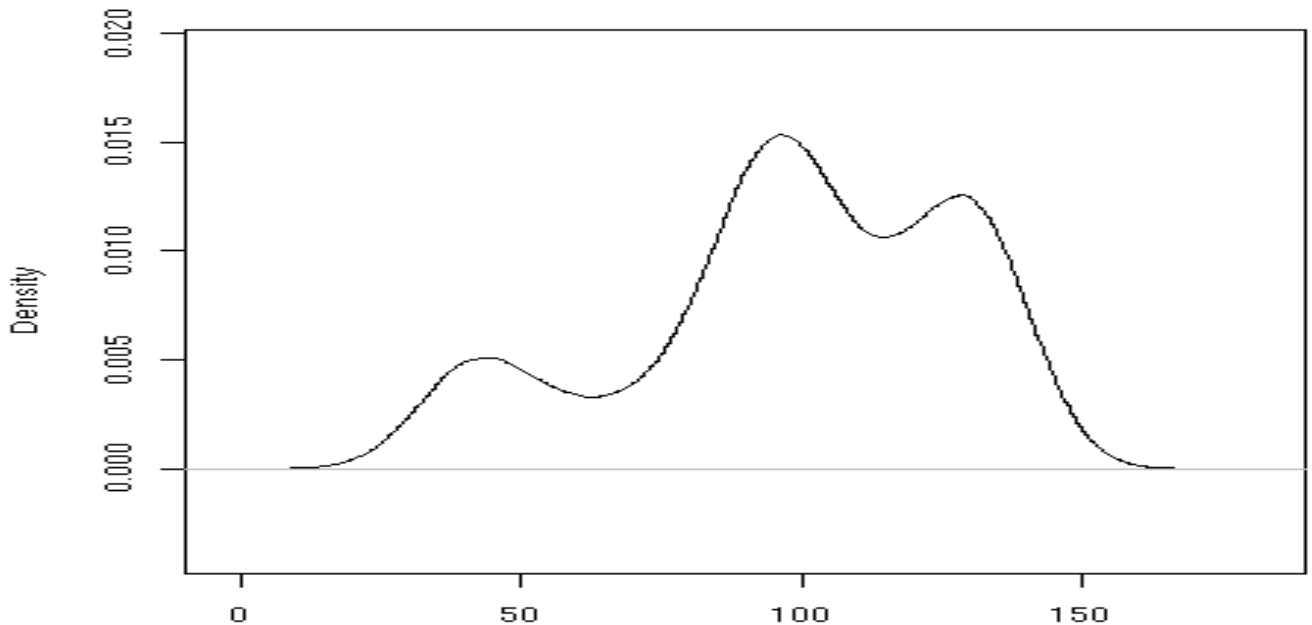
WM = light gray

GM = medium gray

CSF = dark gray

Basic Properties of the Data

- Data consist of image intensities $y_1, ..., y_N$ 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 $\mathbf{z}$, intensities are
  - independent
  - normally distributed,

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

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

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

- 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:

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

- This is an example of a Markov random field model.

The hidden Markov normal mixture model

$$p(\mathbf{y}|\mathbf{z}, \boldsymbol{\mu}, \boldsymbol{\sigma}^2)p(\mathbf{z})$$

can be fitted by

- Iterated Conditional Modes (ICM) algorithm—
  alternately maximizing each parameter conditional on all others being fixed.
- Hidden Markov Random Field EM (HMRFEM) algorithm—
  a variation of EM algorithm in the E step.

Incorporating Spatial Information

A Bayesian Formulation

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

$$p(\boldsymbol{\mu}, \boldsymbol{\sigma}^2, \mathbf{z}|\mathbf{y})$$

- Assume $\boldsymbol{\mu}, \boldsymbol{\sigma}^2, \mathbf{z}$ are independent and
  - $\boldsymbol{\mu}$ i.i.d. normal distribution
  - $\boldsymbol{\sigma}^2$ i.i.d inverse Gamma distribution
- Then the full conditionals satisfy
  - $\boldsymbol{\mu}$ independent normal
  - $\boldsymbol{\sigma}^2$ independent inverse Gamma
  - $\mathbf{z}$ Potts model with external field

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

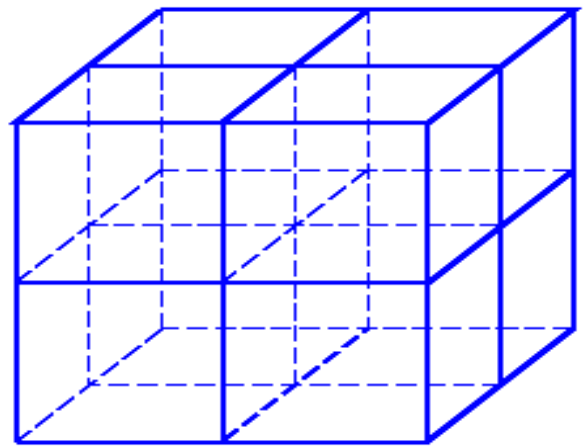
Partial Volume Effect

- 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:

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

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

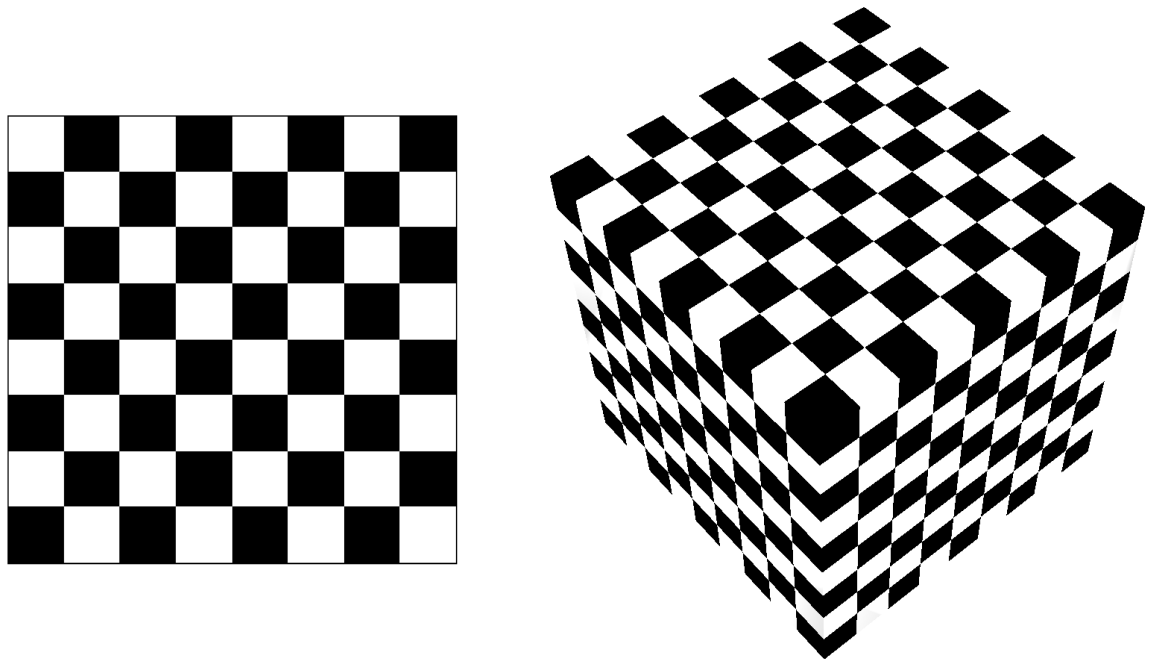
Computational Issues—Table Lookup

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.

Computational Issues—Conditional Independence

- 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.

Computational Issues——OpenMP

Specifying parallel execution by compiler pragmas (directives)

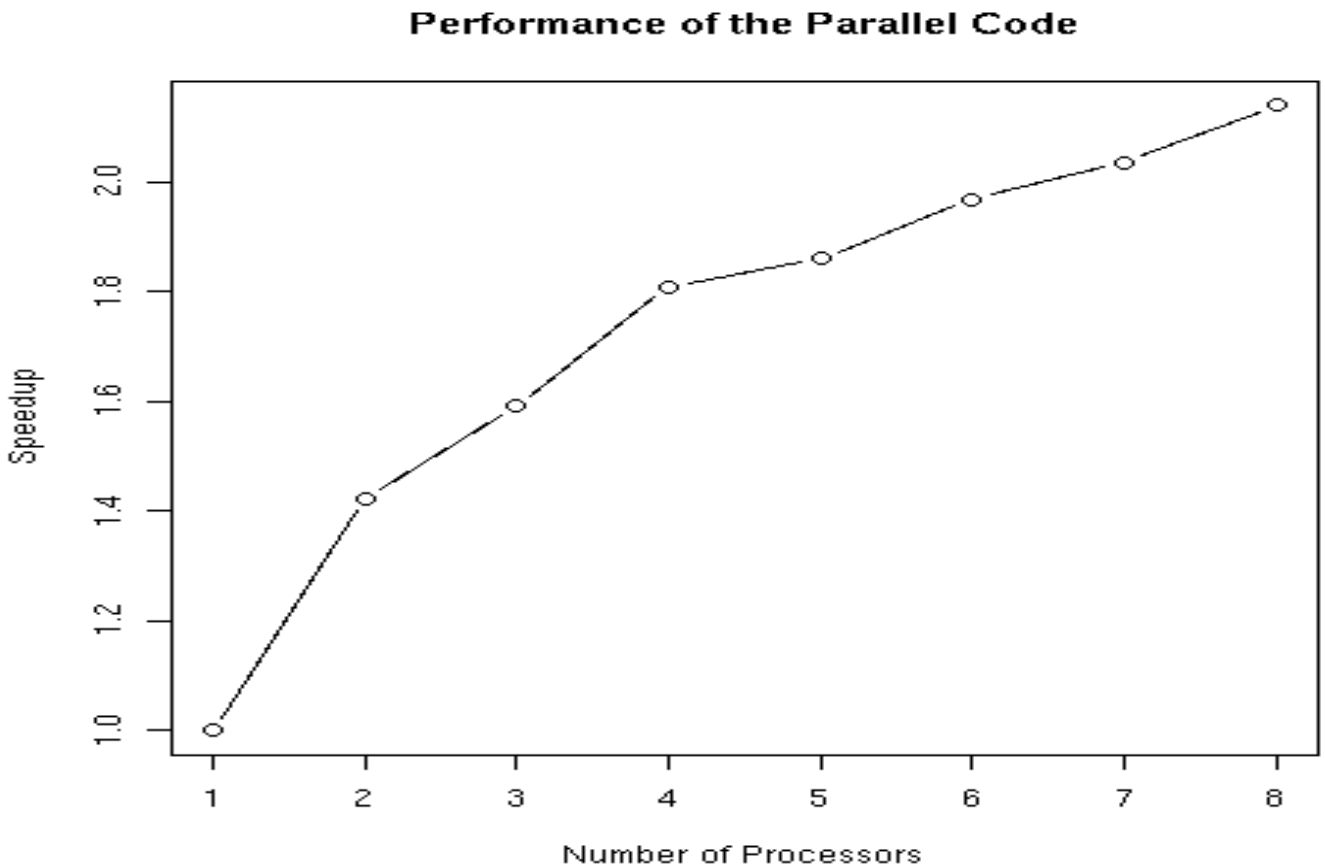
```
#pragma omp parallel for firstprivate(↩
    k, ldD, ...)
for (i = 0; i < n; i++) {
}
```

Specifying variable type

Implicit barrier for synchronization

```
for (i = 0; i < n; i++) {
}
```

Computational Issues——OpenMP



Overview of Functions of the Package

- The "Analyze", "NIfTI", 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