

A nonparametric, entropy-minimizing MRI tissue classification algorithm implementation using ITK

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Abstract. This paper focuses on the role of open-source software in the development of a novel magnetic resonance image (MRI) tissue classification algorithm. Specifically, we describe the use of existing classes in the Insight Segmentation and Registration Toolkit (ITK) and several new classes that were implemented to perform non-parametric density estimation and entropy minimization. These new classes also provide a general framework for nonparametric density estimation and related applications.

1 Introduction

Classification of brain tissue types from magnetic resonance images (MRI) is an important problem in biomedicine with applications in fields such as diagnosis and surgical planning. Manual segmentation of high-resolution 3D images is an extremely time consuming and subjective task; hence, automatic and semi-automatic brain tissue classification methods have been studied extensively in the field of biomedical image processing.

Automatic MRI tissue classification systems have to tackle several problems including additive noise, multiplicative bias fields and the partial voluming effect. Furthermore, these systems are typically iterative and require an initial rough classification to start iterating from. These problems have led to a class of systems that incorporate the following strategies:

1. Parametric statistical models of single-pixel image intensity for each tissue class,
2. Markov random field (MRF) models for removing the effects of measurement noise [1–5],
3. Bias field correction [3, 6], and
4. Digital brain atlas information [7, 8].

In [9], we introduce a new approach for removing the effects of imaging noise in tissue classification using a statistical framework. Our approach uses the intensity and spatial smoothness models (items 1-2) using an unsupervised learning approach that incorporates nonparametric statistics of local neighborhoods. It is compatible with state-of-the-art segmentation methods that use probabilistic brain atlases [7, 8] and bias field correction [3]. In [9], we compare the proposed algorithm against a state-of-the-art tissue classification method using synthetic data with ground truth. The results obtained with the proposed algorithm have higher overlap with the ground truth. Furthermore, the performance of our approach scales better with noise compared to other algorithms. For mathematical and experimental details we refer the reader to [9]. The rest of this paper focuses on the implementation of the algorithm in the Insight Segmentation and Registration Toolkit (ITK) [10, 11] framework.

2 MRI Tissue Classification Algorithm

Our goal is to design and implement the classes that are necessary for the algorithm outlined described in [9]. Figure 1 illustrates the flowchart for the algorithm; existing ITK classes are shown with a white background, new classes implemented for this algorithm are shown with a green (dark) background and data is shown with a blue (light) background.

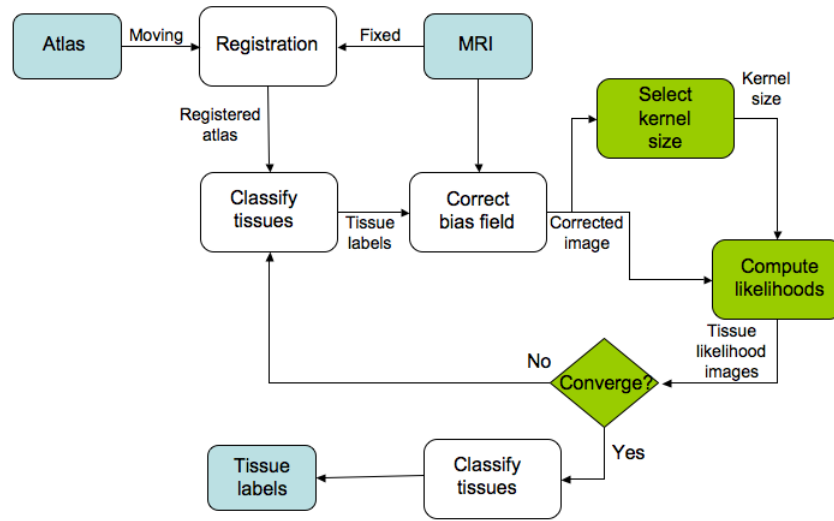


Fig. 1. MRI tissue classification algorithm flowchart. Blue (light) background: data, Green (dark) background: new classes, White background: previous ITK classes.

2.1 Atlas registration

In [9], we use the ICBM probabilistic atlas [12], which provides probabilities of gray matter, white matter and CSF classes for each pixel. The number of atlases passed on to the algorithm determines the number of tissue classes to be classified, one class for each atlas. Therefore, the method is not limited to MRI tissue classification or a specific number of classes; any problem in which the user has access to a set of pre-computed probabilistic atlases can make use of the algorithm. However, these atlases need to be registered with the data prior to classification.

Registration of various medical image modalities is one of the original and main goals of ITK; hence, a range of classes and algorithms dedicated to registration are present in the current toolkit. The classification algorithm expects a series of probabilistic tissue atlas images that have been registered with the MR image to be classified. Therefore, the registration stage is treated as a separate and independent entity in the overall pipeline. Users can plug in and try different registration algorithms. In our preliminary work, the results published in [9] were obtained using the stand alone *LandmarkInitializedMutualInformationRegistration* application, which is part of the *Insight Applications* package [10], with the affine transformation setup.

2.2 Classification

The actual classification stage simply iterates through all the pixels of the image, calls the tissue likelihood functions (membership functions) and sets the corresponding pixel in the output image to be the class index for which the product of the likelihood function and the prior function from the probabilistic atlas is largest. This functionality can be implemented using the *ImageClassifierBase* class tree in ITK. This class requires that a series of membership functions (class likelihoods in our case) and a decision rule function to be plugged in before requesting the output. However, *ImageClassifierBase* is currently not implemented to work with multiple threads. We will work on a multi-threaded implementation for this class.

The likelihood functions used in [9] are discussed briefly in Section 2.5. These functions are defined over image neighborhoods. In other words, the pixels in the neighborhood of every pixel is turned into a vector and placed in another image which then becomes the feature vector image. This is discussed next.

2.3 Generation of feature vectors.

We have a generic class that generates the samples in the feature space specific to the application at hand. This class is not shown in the flowchart for simplicity; however, it acts on the image data to generate the feature vectors at the outset of the algorithm and also after every bias field correction stage. We intend this class to be able to handle augmented feature spaces built from different kinds of features. For this particular application we define the feature space to consist of neighborhoods from the image. Thus, we need to create an image of vectors where the vectors are derived from a neighborhood around each pixel. We store these vectors in an *Image* class instantiated with a *PixelType* of *Vector*. We create this feature space by using neighborhood iterators to iterate over the entire image while creating one vector at each pixel location out of that pixel's neighborhood intensities.

2.4 Bias Field Correction

ITK's *MRIBiasFieldCorrectionFilter* class is currently used for the bias field correction stage. The bias field correction is updated at each iteration of the algorithm with a new mask that depends on the classification result at that iteration. In this framework, users are free to plug-in any bias field corrector.

2.5 Likelihood functions

New classes for non-parametric density estimation have been implemented. These are shown with a dark green background in the flowchart, Figure 1. These classes have two important functions: (i) to estimate the probability density of a feature vector given a sample and (ii) to automatically compute the necessary kernel parameters from the sample. **Density estimation:** We use the Parzen-window nonparametric density estimation technique [13] with an isotropic Gaussian interpolation kernel. The density estimate for tissue class k at pixel t is

$$p_k(z(t)) \approx \frac{1}{|A_k(t)|} \sum_{t_j \in A_k(t)} G(z(t) - z(t_j), \sigma), \quad (1)$$

where $z(t)$ is the feature vector at t and $A_k(t)$ is a subset of pixels that are locally clustered around pixel t and classified as belonging to class k at the present iteration.

Parameter selection: The likelihood function defined above depends on the parameter σ which determines the size of the Gaussian kernels used in the estimation. In [9], we describe an automatic technique for the selection of this parameter which entails the computation of the first and second derivatives of p_k with respect to σ . All density estimation classes are independent from the source that creates the feature vectors. Hence, they apply to any list of feature vectors whether it was created from an image or not.

2.6 Generation of density estimation sample

In order to process, in this case classify, every pixel in the image we need a set of vectors (sample $A_k(t)$) in the spatial locality of the pixel. The FeatureListGenerator class performs this task. The MRI classification algorithm randomly chooses the set of vectors from a Gaussian distribution centered at the pixel being processed. To perform this task we create another class that generates random Gaussian-distributed indices in the image. Since we intend the framework to be threaded eventually, we have created a class for a thread-safe random number generator. This class essentially relies on explicitly assigning a buffer/memory for the system-level random number generation function so that each instantiated object operates independently, using its private buffer, to generate random numbers.

3 Discussion

We have implemented the proposed MRI tissue classification in a flexible manner where the user will be able to experiment with different registration and bias field correction methods as well as plug in different kinds of kernels, i.e. non-Gaussian kernels, for nonparametric density estimation which operate on different kinds of feature vectors. Furthermore, the nonparametric density estimation classes can be reused in other image filtering and classification applications as well as non-image based algorithms. As mentioned previously, the density estimation classes operate on a list of feature vectors and can operate on non-image data. We plan to implement the image filtering approach discussed in [14].

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