Improvement of Pseudo Multispectral Classification of Brain MR Images

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Abstract— **Classification of brain tissues is becoming an increasingly useful tool for investigating the aging brain or disease-induced brain alterations. Numerous strategies have been proposed to classify brain tissues into white matter (WM), gray matter (GM) and cerebrospinal fluid (CSF). However, many of them fail when classifying specific regions with low contrast between tissues (e.g. cerebellum gray and white matter). Erroneous classification may lead to volume over- or under-estimation, thus leading to equivocal interpretations. In this work, instead of using gray scale images (T1-MPRAGE) to classify brain tissues, we use an improved pseudo multispectral classification (PMC) technique using CIE XYZ spaces and iterative K-mean clustering in order to enhance classification of the brain GM, WM and CSF. The accuracy of the proposed approach is assessed using atlas brain templates and compared with FSL classification (FMRIB, Oxford, UK).**

Keywords— **Classification, K-mean, Clustering, CIE XYZ.**

I. Introduction

The role of multimodality neuroimaging imaging has expanded during the last two decades in clinical and research setting, particularly when used in connection with advanced image analysis and visualization tools. The accurate interpretation of information pertaining to investigation of the aging brain or disease induced brain alterations relies on accurate and reproducible brain tissue classification, which is the preliminary step prior to segmentation. Numerous algorithms with different degrees of success have been proposed to classify brain tissues. This includes atlas-free techniques or methods relying on the use of an atlas. The existing principal approaches are based on histogram threshold determination [1], cluster analysis [2], the use of a priori information about anatomy [3], and Bayesian classification (e.g. Markov Random field model) [4]. An overview of MRI segmentation methods can be found in [5]. Some of these techniques produce good results but many of them fail in some regions where the contrast is low. Most of the proposed methods usually take as input a single channel gray scale image (T1-MPRAGE). In this work; we introduce an enhanced method which combines pseudo-multispectral color transformation and iterative and unsupervised K-mean clustering to improve brain tissue classification even in the presence of low SNR and partial volume effect. The performance of our method is evaluated using atlas templates as ground truth and compared with FAST-FSL classification (FMRIB, Oxford, UK).

II. Theory

In this section, we describe in detail the enhanced PMC classification algorithm. Color models or color spaces indicate the colors in a benchmark way by using a coordinate system and a subspace in which each color is represented by a single voxel of the coordinate system. Gray and binary color spaces are commonly used by image processing methods [6, 7]. However, the contrast between brain tissues in some regions is very low, e.g. the cerebellum (WM and GM interfaces). Consequently, classification methods fail and wrong classifications might occur. To overcome this problem, we transform, in the first step, the T1-MPRAGE image to multispectral data containing 3 different images (channels), rather than classifying using a single image information (e.g. gray scale image). In other words, each voxel in the initial image is represented in 3 different coordinate spaces CIE XYZ by applying different transformation matrices. In addition to pseudo multi-channel information, CIE XYZ space tries to take into account the logarithmic response of the eye, which enhances the classification in low contrast regions (e.g. cerebellum white matter and temporal lobe). To better separate neighboring values, normalized 3 channel data values are weighted by a root square function (RSF), which reduces regional low contrast between brain tissues. As a second step, an iterative and non-deterministic K-mean clustering is applied for image classification. Initially the number of brain tissue classes is randomly chosen and set to be maximal (>5 classes). The K-mean clusters the data around centroids computed as the mean value of clustered points so as to minimize the within-cluster sum of squares as follows:

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$$\arg\min \sum_{N}\sum_{i=1}^{k}\sum_{X\in S_j}\|X_i-\mu_0\|^2 \qquad (1)$$

where μ_0 the initial mean of data points X_i within S_j partitions, k is the number of clusters and N is the 3D channel images. After assigning each pattern to the nearest cluster using Euclidian distance measure, the algorithm computes for each pattern X its membership function $\psi(C_j \mid X_i)$ in each cluster S_j. This function defines the proportion of pattern X_i that belongs to the j[th] cluster C_j. For a minimal distance between the centroids and the data points, $\psi(C_j|X_i) = \{1\}$, otherwise the function is null. K-mean computes the cluster centroids again and updates the cluster center μ_j:

$$\mu_j = \frac{\sum_i^n \psi(Cj \mid Xi)Xi}{\sum_i^n \psi(Cj \mid Xi)} \; for\; j = 1, \dots, k \quad (2)$$

The algorithm repeats the classification with decreasing k until the cluster labels of the image does not change anymore. In order to evaluate our clustering; an error measurement is plotted versus different proposed number of clusters k and the plot elbow is then located. Elbow occurs at the most dramatic decrease in error measurement. The gap criterion formalizes this approach by estimating the elbow location as the number of clusters with the largest gap value. Therefore, under the gap criterion, the optimal number of clusters occurs at the solution with the largest local or global gap value within a tolerance range [9]. The gap criterion is defined as:

$$Gap_n(k) = E^*{}_n\{\log(W_k)\} - \log(W_k) \; and \; W_k = \sum_i^k \frac{1}{2n_k} D_k \quad (3)$$

where n is the sample size, k is the cluster number and W_k is the pooled within-cluster dispersion measurement. n_k is the number of data points in cluster k and D_k is the sum of the pairwise distances for all points in cluster k. The expected value $E^*{}_n\{\log(W_k)\}$ is determined by Monte Carlo sampling from a reference distribution, and $\log(W_k)$ is computed from the sample data. The optimal number of clusters is evaluated and reached based on the gap criterion and the corresponding centroid distribution. The centroid distribution is modeled beforehand using a set of 70 human brain data and a couple of simulated brain images. Each brain tissue (GM, WM and CSF) belongs to a specific distribution template. Once the optimal k is defined, the previously estimated brain tissue classes that are set randomly before are reassigned and adjusted to the new optimal classes. The enhanced PMC pipeline is illustrated in Fig. 1. The algorithm takes as input a T1 MPRAGE image and provides as output a label map of GM, WM and CSF.

III. Materials and Methods

To test our approach, we used 4 numerical brain atlas templates where the ground truth volumes of GM, WM and CSF are known beforehand. The numerical atlas templates were obtained from the Pediatric MRI Data Repository created by the NIH MRI Study of Normal Brain Development [8]. In addition, 10 clinical MRI studies scanned on a 3T Skyra (Siemens Healthcare, Germany) using T1-MPRAGE sequence with the following parameters: flip/TE/TR/TI/ = 100/4/9.7/20ms and voxel size of 1mm^3 was used to assess the accuracy of our classification approach. Atlas templates and *in vivo* data sets were classified into GM, WM and CSF using the proposed iterative algorithm and compared with FSL-FAST classification (FMRIB, Oxford, UK).

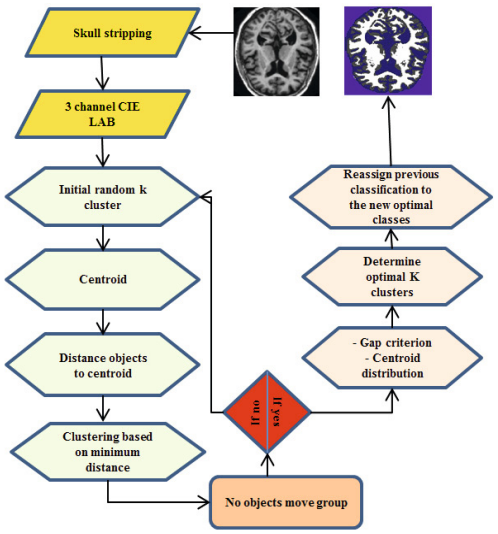

Fig 1 Enhanced PMC algorithm pipeline.

IV. Results and Discussion

Fig. 2 illustrates the results of PMC versus FAST-FSL classification and compared to the atlas templates (ground truth). The classification accuracy of each method was calculated and presented in Table 1. In general, both methods achieve a good brain tissue classification into 3 classes (GM, WM and CSF). However, FAST-FSL algorithm tends to underestimate the WM and CSF by 15% and overestimate the GM volume by 20%. PMC classifies brain tissues with a high accuracy (<8%).

Table 1 Accuracy of PMC and FAST-FSL classification [%].

	PMC			FAST-FSL		
	CSF	WM	GM	CSF	WM	GM
Temp 1	103	113	100	85	88	118
Temp 2	117	99	103	82	76	122
Temp 3	104	104	104	86	83	120
Temp 4	108	112	99	89	95	116
Mean	108	107	101	86	85	119
	Accuracy % ($\sigma = \pm 0.5$)					

The gray matter over estimation occurs in regions with low CNR and high partial volume effect (cerebellum WM and near the temporal lobe). Fig. 3 shows from left to right PMC, FAST-FSL silhouette plot and corresponding gap criterion used to define the optimal cluster numbers *k*. From FSL silhouette plot (Fig. 3 - middle), it can be noticed that most voxels in the 3 clusters have a large silhouette value, greater than 0.6, indicating that the cluster is somewhat separated from neighboring clusters. However, all clusters contain voxels with negative values, indicating that those voxels are not well separated and consequently the corresponding volumes overestimated (GM) or underestimated (WM and CSF), especially in regions with low contrast (temporal lobe region and cerebellum arbor vitae). PMC silhouette plot (Fig. 3 - left) indicates that these 3 clusters are better separated compared to FAST-FSL classification without any voxel with negative values, indicating an accurate classification of the 3 brain tissue classes. Based on the gap criterion, the optimal *k* value indicates that the optimal number of clusters is 3. Even if the maximum value of the gap criterion occurs at 5 clusters, the value at 3 clusters is within one standard error of the maximum, so the suggested optimal number of clusters is 3 (Fig. 3 - right). The PMC algorithm reassigns the previously estimated brain tissue classes to new optimal classes.

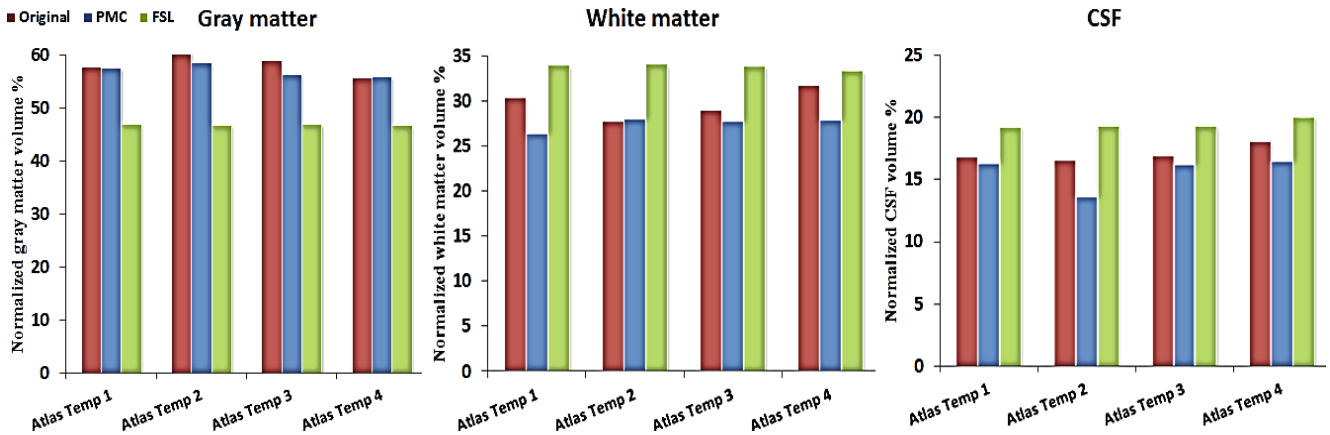

Fig 2 Atlas brain data classified using enhanced PMC and FAST-FSL compared with ground truth normalized GM, WM and CSF volumes by the total intra-cranial volumes.

For the *in vivo* data sets, Fig. 4 shows axial, sagittal and coronal slice of T1-MPRAGE and corresponding PMC and FAST-FSL classified brain maps. It should be noticed that in the cerebellum region, the arbor vitae (cerebellum WM) is better delineated and classified using the PMC approach than the FAST-FSL algorithm (see the arrows). PMC increases data dimensionality by converting each voxel into three different spectral spaces. The CIE XYZ representation provides additional information to the classifier (K-mean algorithm) and the low contrast between brain tissues is overcome even in regions suffering from low contrast (e.g. cerebellum). The algorithm takes 3-channel CIE XYZ images as input. It computes the intensity distribution and then initializes the centroids with *k* random intensities. The procedure is repeated until the cluster labels of the image do not change anymore [10]. Then data points are clustered based on the distance of their intensities from the centroid. Once the classification converges, the optimal cluster number is computed based on silhouette plot and gap criterion. The algorithm then reclusters the data points by grouping all points with the nearest centroids. The iterative version of the algorithm provides a fast and accurate classification combined with the CIE XYZ data information (less than 1 minute compared to an average of 5 minutes with FSL).

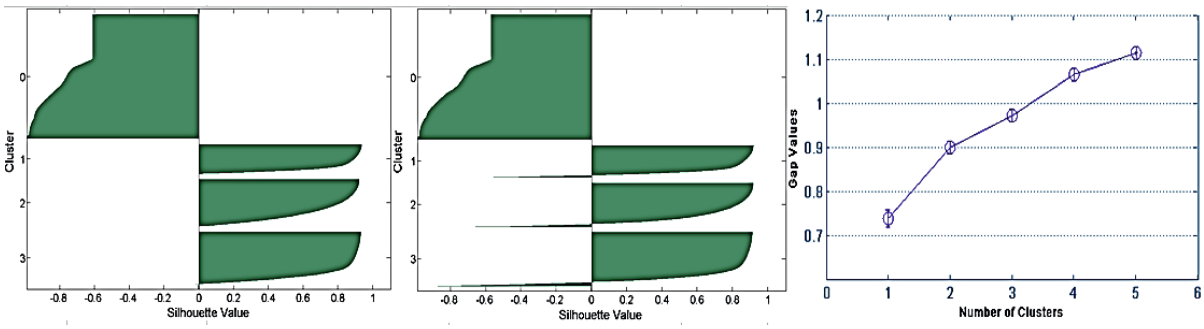

Fig 3 left and middle: Enhanced PMC and FAST-FSL silhouette plot. Right: gap value as function of the number of clusters.

V. Conclusion

A number of approaches have been proposed to better classify brain tissues; but the complexity of the problem leaves it an open area requiring further research and development efforts. In this work, we proposed an improved approach that looks promising. Enhanced PMC classification shows a high potential to improve automatic brain tissues classification results by extracting a maximum of image information from a single acquisition using pseudo-multispectral transformations and an enhanced fast, iterative and unsupervised K-mean clustering. This approach overcomes the low CNR and partial volume effect present in some brain regions, e.g. cerebellum arbor vitae and near the temporal lobe region. Further validation using a larger clinical database and potential integration in quantitative multi-modality imaging platforms need to be further investigated.

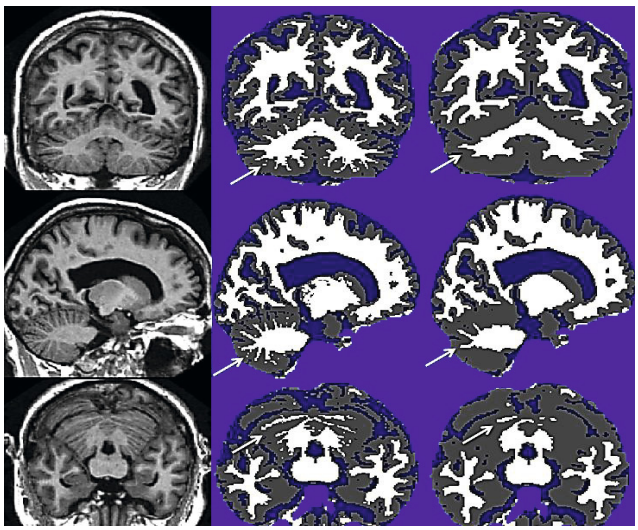

Fig 4 From top to bottom: axial, sagittal and coronal slice of T1-MPRAGE. From left to right: original MRI, PMC and FAST-FSL brain maps.

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