Segmentation based on Information Fusion Applied to Brain Tissue on MRI

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ABSTRACT

An information fusion based fuzzy segmentation method applied to Magnetic Resonance Images (MRI) is proposed in this paper. It can automatically extract the normal and abnormal tissues of human brain from multispectral images such as T1-weighted, T2-weighted and Proton Density (PD) feature images. Fuzzy models of normal tissues corresponding to three MRI sequences images are derived from histogram according to a priori knowledge. Three different functions are chosen to calculate the fuzzy models of abnormal tissues. Then, the fuzzy features extracted by these fuzzy models are joined by a fuzzy relation operator which represents their fuzzy feature fusion. The final segmentation result is obtained by a fuzzy region growing based fuzzy decision rule. The experimental results of the proposed method are compared with the manually labeled segmentation by a neuroradiologist for abnormal tissues and with anatomic model of BrainWeb for normal tissues. The MRI images used in our experiment are imaged with a 1.5T GE for abnormal brain, with 3D MRI simulated brain database for normal brain by using an axial 3D IR T1-weighted (TI/TR/TE: 600/10/2), an axial FSE T2-weighted(TR/TE: 3500/102) and an axial FSE PD weighted (TR/TE: 3500/11). Based on 4 patients studied, the average probability of false detection of abnormal tissues is 5%. For the normal tissues, a false detection rate of 4% - 15% is obtained in images with 3% - 7% noise level. All of them show a good performance for our method.

Keywords: MRI, brain tissue, segmentation, information fusion

1. INTRODUCTION

Image segmentation is a classical topic on image processing. The segmentation of tumor from medical images is still a difficult problem, because a large number of tumor types which vary greatly in size, shape, location, tissue composition and homogeneity have to be accounted for [1]. Numerous uncertainty characteristics should be considered by an automatic segmentation method. We can imagine a process of tumor diagnosis in clinic. Radiology experts check always different sequences of one patient, according to their a priori knowledge to combine the information provided by each image and contrast type in order to improve diagnosis. This information fusion process of human intelligence induces an idea of segmentation method designing. A segmentation system based on information fusion of features from multiple sources is preferable to capture redundancy and complement information. Our goal is to develop an automatic tumor segmentation based on fuzzy information fusion and this method can be also used for normal tissues.

Precise description of abnormal human brain tissues is very important for tumor’s diagnosis, for advice treatments, to assist operations, etc… Magnetic Resonance Imaging (MRI) can provide a lot of information about brain tissues from a variety of excitation sequences. To diagnose tissue abnormalities, like tumor, it’s necessary to use multispectral MR images in order to find some of its properties such as size, position, sort, and relationship with other tissues, etc... The precision, automatization, robustness and speed of abnormal tissue information extraction are very important for medical applications.

The information fusion includes the theory, techniques, and tools designed and applied for exploiting the synergy in the information acquired from multiple sources such that the resulting decision would be in some sense better than that
obtained if these sources were used individually [2]. Since the multisensor data fusion developed initially for military applications to combine data from multiple sensors and perform inferences that may not be possible from a single sensor, data fusion functional model has then been used for wide application domains. We introduce a fuzzy information fusion method based on this principle to try to solve the medical problem of the tissue segmentation of human brain from multiple MR image sequences.

Considering the ambiguous, complementary and redundant characters of different MR images, the fuzzy logic and information fusion techniques are one of the first choice to analyze brain tissue [3][4]. Many analysis techniques of MR images were published in the literature, such as a knowledge-based brain tumor extraction technique [5], the fusion technique of multimodality image, for example, Positron Emission Tomography (PET) and MRI/CT images used to evaluate the accuracy of tumor description [6]. The Fuzzy-Connectedness is efficient to quantify multiple sclerosis lesions [4]. Saha and Udupa proposed a theory and algorithms for scale-based connected image segmentation [7]. When many objects are to be identified in a single image, the method of a fuzzy connected object with multiple seeds is used effectively in specific medical applications [8].

In the domain of normal tissues segmentation, a lot of studies have been done and are described in the literature. Some methods, by deforming standard images, templates, or atlases using elastic matching techniques, or deformable models [9][10] have proven to be reliable and efficient for small and local shape changes. Some approaches start from a parametric statistical model, such as Gaussian intensity models [11][12], Explicit models [13], Markov random field models [14]. We can also use the fuzzy information fusion system to segment the normal tissues. The key problem is to create a fuzzy model for extracting feature information.

In this paper, we propose a fuzzy information fusion method to segment automatically tumor area and normal tissues of human brain from multispectral MR images. At first, a segmentation system (see figure 1) based on fuzzy information fusion is introduced as four steps: (1) data registration (2) feature extraction (3) features fusion, and (4) decision. Several fuzzy sets are given to define the specific observation universal. The linear registration method presented in [15] is employed for data registration to establish a common coordinate system among different data sources. A modelisation approach of normal tissues created from histogram and some membership functions built from a priori knowledge of tumorous tissues are proposed for fuzzy information modeling to create fuzzy feature spaces for different sources. We utilize a fuzzy relation for features fusion to combine these fuzzy feature spaces into a joined feature space. To obtain the segmentation result, a decision by fuzzy region growing is presented. One study using three MR image sequences, T1-weighted, T2-weighted and Proton Density (PD) feature images for one patient are taken as an example to illustrate the method efficiency for segmentation of tumorous area. The simulated MRI volumes with different noise levels, available on the Web site Brain Web [16], were used to evaluate our method. The obtained results are appreciated by experts in radiology.

Figure 1. Illustration of segmentation System based on feature fusion on MR images. Three MRI sequences T1, T2 and PD are original images. F_T1, F_T2 and F_PD are three feature spaces which correspond to the three registered images.
2. FEATURES EXTRACTION OF BRAIN TISSUES

2.1. Knowledge Based Fuzzy Information Modeling

Normal brain MR image is shown in figure 2, (a) is simulated volume of normal brain on T1 (b) is simulated volume of normal brain on T2, and (c) is simulated volume of normal brain on PD. Cerebral tumorous MR image of one patient is shown in figure 3, (a) is a brain tumor image on T1 (b) is a brain tumor image on T2, and (c) is a brain tumor image on PD. According to the description of radiology experts, the characteristics of brain tissues on the three types of MR images can be presented in table 1.

<table>
<thead>
<tr>
<th>Signal Intensity</th>
<th>Tissues</th>
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<tbody>
<tr>
<td></td>
<td>CSF</td>
</tr>
<tr>
<td>T1</td>
<td>--</td>
</tr>
<tr>
<td>T2</td>
<td>++</td>
</tr>
<tr>
<td>PD</td>
<td>++</td>
</tr>
</tbody>
</table>

The symbol “+” presents a hyper-signal; it means that the image intensity is very bright. The symbol “-” presents a hypo-signal, the intensity is very dark. The symbol “+-” means that the signal intensity is brighter than hypo-signal, and “-+” means that it is darker than hyper-signal. “--” means that the signal intensity is darker than the hypo-signal, and “++” means that it is brighter than the hyper-signal.

2.2. Modelisation of Cerebral Tumorous Tissues

2.2.1. Mathematic model of cerebral tumorous tissues

From table 1, we can conclude that the signal intensity of tumor is neither very bright nor very dark in T1, but it is the brightest in T2 and PD. Different functions can be used to describe this characteristic. By some experiments, we propose several mathematic functions to model the fuzzy information of tumor area presented in table 1. We define the feature spaces of T1, T2 and PD as $TS^1$, $TS^2$ and $TS^3$ respectively, and the corresponding membership functions of these spaces are defined as $\mu_{TS^1}$, $\mu_{TS^2}$, and $\mu_{TS^3}$.
\[\mu_{TS1}(v, s_1) = \begin{cases} 
0, & s_1 \leq a_1 \\
0.5 + 0.5 \sin\left(\frac{\pi}{a_1 - a_2}(s_1 + h_1 + b_2)\right), & a_1 < s_1 \leq b_1 \\
1, & b_1 < s_1 \leq c_1 \\
0.5 - 0.5 \sin\left(\frac{\pi}{c_1 - c_2}(s_1 - d_1 - b_2)\right), & c_1 < s_1 \leq d_1 \\
0, & d_1 < s_1 
\end{cases} \] (1)

\[\mu_{TS2}(v, s_2) = 0.5 + 0.5 \sin\left(\frac{\pi}{a_2 - b_2}(s_2 - a_2)\right), \quad a_2 < s_2 \leq b_2 \] (2)

\[\mu_{TS3}(v, s_3) = \begin{cases} 
0, & s_3 \leq a_3 \\
\frac{1}{2} \left(\frac{s_3 - a_3}{a_3 - b_3}\right)^2, & a_3 < s_3 \leq b_3 \\
1 - \frac{1}{2} \left(\frac{s_3 - c_3}{c_3 - b_3}\right)^2, & b_3 < s_3 \leq c_3 \\
1, & s_3 > c_3 
\end{cases} \] (3)

where \((a_1, b_1, c_1, d_1), (a_2, b_2)\) and \((a_3, b_3, c_3)\) are parameters for \(\mu_{TS1}, \mu_{TS2}\) and \(\mu_{TS3}\) respectively. The variables \(s_1, s_2\) and \(s_3\) are signal intensities and correspond to T1, T2 and PD images respectively. Variable \(v\) presents the voxel in human brain space \(B\). The parameters will be estimated through statistical values taken from T1, T2 and PD weighted images, respectively.

2.2.2. Statistic analysis of tumor features

For selecting the parameters of these models, a pre-segmentation of T1 image is used to quantify the fuzzy features of tumorous tissue. Because the T1 image shows a good contrast, a fuzzy Markovian segmentation method presented by Ruan et al in [14] shows numerous advantages. It is used to segment brain in different classes according to the three main brain tissues WM (white matter), GM (grey matter), and CSF (cerebrospinal fluid). Figure 4 is an example of segmentation obtained using Ruan’s method.

![Figure 4. Segmentation result of Ruan’s method. (a) is original T1-weighted image, and (b) to (l) show the result of the 11 resulting classes.](image)

Some characteristics of the tumor area are evident from the result of tissue segmentation:
tumor area isn’t present in classes 1 (CSF), 10 (WM) and 11 (WM)

- essential regions are presented in class 3 and class 4 (d, e)
- edema region is present in class 4, 5 and 6 (e, f, g). Its centre is found in class 5.

The segmentation result of T1-weighted image can be mapped to the T2 and PD weighted images which have been registered with T1-weighted image in data registration step. The statistical means of signal intensity, or grey level for each class are shown in figure 5. The values for T2 and PD presented in figure 5 are divided by 10 in order to compare clearly.

![Image of figure 5](image)

**Figure 5.** Signal intensity mean of each class for T1 (o), T2 (.) and PD (*), taken over the full volume, versus the class number

We can establish a relationship between the grey level mean of each class in full volume, called “class mean”, and possibility belonging to a tumor region:

- In T2, the pixel having intensity close to the maximal class mean are considered to be the probable tumor region.
- In PD, the maximal class mean corresponds to the environment of the probable tumor region, called probable edema region. The pixel having intensity close to maximal class mean are considered to be the probable tumor region. Then we can find the maximal classes mean that is correspondence to the edge of probable tumor region.
- In T1, the linear distribution of class means shows that the minimal and maximal class means do not correspond to the interesting region. The value close to minimum has the higher correlation with this region.

These characteristics are summarized in table 2 and one parameter selection result of membership functions is shown in figure 6.

**Table 2.** Correlation between probability of tumor region and class mean in volume

<table>
<thead>
<tr>
<th>Tissues</th>
<th>Class mean</th>
<th>T1</th>
<th>T2</th>
<th>PD</th>
</tr>
</thead>
<tbody>
<tr>
<td>tumor</td>
<td>near minimum</td>
<td>near maximal</td>
<td>near maximal</td>
<td></td>
</tr>
<tr>
<td>edema</td>
<td>near medium</td>
<td>maximum</td>
<td>maximum</td>
<td></td>
</tr>
<tr>
<td>CSF</td>
<td>minimum</td>
<td>maximum</td>
<td>minimum</td>
<td></td>
</tr>
</tbody>
</table>

![Table 2](image)

**Figure 6.** One parameter selection result for membership functions in section 3.2. (a) $\mu_{TS1}$, (b) $\mu_{TS2}$, (c) $\mu_{TS3}$
2.3. Fuzzy models of Cerebral Normal Tissues

There are three main normal tissues on cerebral image, CSF, GM and WM. There are different models for extracting these tissues features, like the Gaussian model used in [14]. It’s a good feature model for T1 image, but it requires complex and longer computing. Here we suggest a new modeling approach, we called it “histogram modification modeling”, shorten as HisMM. It is consisted of

Step 1. Search all the peaks and valleys of histogram

Step 2. Assume two (for PD) or three (for T1 and T2) maximum peaks correspond to pure tissues [14]. They are labeled as a center of feature model, i.e. they will get membership degree with 1.

Step 3. Each peak and valley will be a point of overturn. According to table 1, we can choose corresponding peak and valley to build model.

Step 4. Normalize the models taken from step 3 between [0, 1] to form a fuzzy model presented with membership function.

Figure 7. Example of HisMM on T1 image. (a) histogram in volume (b) fuzzy model of CSF (c) fuzzy model of GM, and (d) fuzzy model of WM.

Figure 8. Example of HisMM on T2 image. (a) histogram in volume (b) fuzzy model of CSF (c) fuzzy model of GM, and (d) fuzzy model of WM.

Figure 9. Example of HisMM on PD image. (a) histogram in volume (b) fuzzy model of CSF (c) fuzzy model of GM, and (d) fuzzy model of WM.
Figure 7 is an example of HisMM result on T1, and figure 8 is the fuzzy model on T2, figure 9 is that on PD. In each figure, (a) is the histogram labeled peak and valley (b) is the fuzzy model of CSF (c) is the fuzzy model of GM, and (d) is the fuzzy model of WM.

2.4. Creation of Fuzzy Features space

The fuzzy features of brain tumor can be extracted by using mathematic models as equations (1), (2) and (3). These membership functions can project signal intensity of original images onto fuzzy feature spaces which are represented in form of membership degree versus grey level. Two rules must be kept to make these models. One is the minimal redundancy and the other is maximal inclusion. The fuzzy feature space is carried out by using tumorous tissue models shown in figure 10. It projects the features of brain tumor on MR images into fuzzy features spaces $TS^1$, $TS^2$, and $TS^3$.

Figure 10. An example of fuzzy feature spaces. (a) $TS^1$, (b) $TS^2$, (c) $TS^3$.

Figure 11. Fuzzy feature spaces of normal tissues. First line presents the CSF feature space on T1, T2 and PD from left to right respectively. Second line shows the GM feature space on T1, T2 and PD from left to right respectively. Last line illustrates the WM feature space on T1, T2 and PD from left to right respectively.
The fuzzy models of normal tissues presented in section 2.3 are a membership function with membership degree versus gray level of image. They project also the signal intensity of original image onto different fuzzy features spaces presented by membership degree and shown in figure 11. The first line is the CSF space on T1, T2 and PD which corresponding to (b) of figure 7, 8 and 9 respectively; the second line is the GM space on T1, T2 and PD which corresponding to (c) of figure 7, 8 and 9 respectively; last line is the WM space which corresponding to (d) of figure 7, 8 and 9 respectively.

In the fuzzy feature space, the brighter signal corresponds to greater membership degree which belongs to applicable tissue.

3. FUZZY FEATURES FUSION

The feature extracted from an individual source is not sufficient to delineate the interesting object, because the information needed to distinguish different objects are not sufficiently precise from individual source. A common space existing in these three individual feature spaces induces a joined fuzzy feature space which corresponds to tumor area. A complement space among these three feature spaces also exist to present some probable normal tissues. A combination of these three feature spaces should give us a better feature description of tumor area. This operation is called feature fusion.

3.1. Fuzzy Relation Operation

We can infer that $T$ should be formed from the fuzzy relation of fuzzy feature spaces defined by

$$T : TS^1 \times TS^2 \times TS^3 \to [0,1]$$

(4)

In our application, there is a characteristic fuzzy relation such that: $\exists v$ of $B$, $v \in T$ with higher membership degree $\mu_T(v)$ if and only if $v \in TS^i$ with higher membership degree $\mu_{TS^i}(v, s_i)$, where $i=1, 2, 3$. Here, we propose the following formula to represent this relation:

$$\mu_T(v) = (\mu_{TS^1}(v, s_1) \cdot \mu_{TS^2}(v, s_2) \cdot \mu_{TS^3}(v, s_3))^{1/3}$$

(5)

In fact, equation (5) is a fuzzy relation of geometric mean. This fuzzy operator of fusion combines three fuzzy features space $TS^1, TS^2,$ and $TS^3$ to create a joined feature space $T$. It carries out an efficiency of more distinct features shown in figure 12.

![Figure 12](image)

Figure 12. Feature fusion result after operation of geometric mean. (a) joined space of figure 10; (b) joined space of figure 11’s first line; (c) joined space of figure 11’s second line; and (d) joined space of figure 11’s last line.

3.2. Fuzzy Intersection Operation

The analysis of these feature spaces mentioned above infer also the use of a fuzzy intersection operation. This is a fusion operation using fuzzy subset representation. Any fuzzy intersection operator can be used for fusing these features. For example:

- Zadeh Intersection ($\land$)
\[
\mu_{T\text{-Zadeh}}(v) = \left( (\mu_{T_2}(v, s_1) \wedge \mu_{T_3}(v, s_2)) \wedge \mu_{T_3}(v, s) \right) = \min \left\{ \mu_{T_2}(v, s_1), \mu_{T_3}(v, s_2), \mu_{T_3}(v, s) \right\}
\]

- Yager Intersection (\( \bar{Y} \))

\[
\mu_{\text{Yager}}(v) = \left\{ (\mu_{T_2}(v, s_1) \bar{Y} \mu_{T_3}(v, s_2)) \bar{Y} \mu_{T_3}(v, s) \right\}
\]

where \( a\bar{Y}b = 1 - \min\left\{ \min(1, (1-a)^\lambda + (1-b)^\lambda)^{1/\lambda} \right\} \lambda \in (0, \infty) \)

- Hamacher Intersection (\( \bar{Y} \))

\[
\mu_{\text{Hamacher}}(v) = \left\{ (\mu_{T_2}(v, s_1) \bar{Y} \mu_{T_3}(v, s_2)) \bar{Y} \mu_{T_3}(v, s) \right\}
\]

where \( a\bar{Y}b = \frac{ab}{\gamma + (1-\gamma)(a+b-ab)} \gamma \in (0, \infty) \)

The results of these fusion operations are shown in figure 13. The joined space increases with parameter \( \lambda \) increasing by using Yager operator. On the contrary, it increases with parameter \( \gamma \) decreasing by using Hamacher operator. The three operators produce similar spaces, and also similar to the result of geometric mean operation.

![Figure 13](image)

**Figure 13.** Join feature spaces established by fuzzy feature fusion operation of Zadeh intersection operator (a), Yager intersection operator with \( \lambda = 5 \) (b), \( \lambda = 3 \) (c) and \( \lambda = 1.5 \) (d), Hamacher intersection operator with \( \gamma = 5 \) (e) and \( \gamma = 3 \) (f).

### 4. VALIDATION AND RESULTS

#### 4.1. Segmentation of tumorous tissues

The MR images of 4 patients with glial cerebral tumor are given in this paper to present the effect of our method. Each of the 4 patients was imaged with a 1.5T GE using an axial 3D IR T1-weighted (TUTR/TE: 600/102), an axial FSE T2-weighted (TR/TE: 3500/102) and an axial FSE PD weighted (TR/TE: 3500/11). The image specifications for T1 image are that the total number of slices is 124, the thickness of each slice is 1.5mm, and the pixel size is 0.94×0.94 mm²; for T2 and PD images are that the total number of slices is 20, the thickness of each slice is 5mm, and the pixel size is 0.47×0.47 mm². They are registered by a software tool FLIRT provided by the Oxford Center for Functional Magnetic Resonance Imaging of the Brain.

A fuzzy region growing method presented in [17] is used to make sure of the final segmentation.

To evaluate the efficiency of the proposed method, two probability measures, correct detection and false detection, defined by

\[
P_c = \frac{N_R}{N_R} \quad \text{and} \quad P_f = \frac{N_D - N_R}{N_{norm}}
\]

were used to evaluate the efficiency of the proposed method, where \( N_R \) is the number of reference voxels marked by the expert, \( N_b \) is the number of voxels detected which are correct relative to the reference, \( P_c \) is the probability of correct detection relative to the reference by using the proposed automatic segmentation. \( N_D \) is the total number of voxels detected; \( N_{norm} \) is the number of voxel of normal tissue which is marked by an expert on the concerned abnormal MR slices. \( P_f \) is the probability of false detection; it presents the rate of incorrect detection: that is, our method gives a true result while the reference marks it false. The reference used here is the hand-labeled segmentation by a neuroradiology...
expert shown in figure 14 (a), (c), (e) and (g) for 4 patients while the result of our method is given in figure 14 (b) (d) (f) and (h). The average probability of correct detection is equal to 95% and the average probability of false detection is equal to 5% from a study on 4 patients.

Figure 14. Hand-labeled segmentation by an expert in neuroradiology for patient 1 (a), patient 2 (c), patient 3 (e), and patient 4 (g). (b), (d), (f) and (h) are the result obtained by proposed fuzzy segmentation.

4.2. Segmentation of Normal tissues

The simulated MRI volumes with different noise levels, available on the Web site Brain Web [16], were used to evaluate our method. Each volume set consists of 181×217×181 voxels with a cubic resolution 1×1×1 mm$^3$. They are simulated with the same pulse sequence parameters than tumorous images mentioned in section 4.1. The first line of figure 15 is the simulated MRI on T1, second line is that on T2 and last line is that on PD. They are images with 3%, 5% and 7% noise level from left to right.

The results of normal tissues segmentation by using the method proposed in this paper are compared with an anatomic model proven by [16] and shown in table 3. The first column of figure 16 is the anatomic model and from 2 to 4 columns is the segmentation result of normal tissue with 3, 5 and 7% noise level. CSF is shown in the first line of figure 16. GM is shown in second line and WM is shown in last line.

The ground truth is anatomic model. False positive is defined as where the segmentation result indicated tissue voxels where ground truth did not. False negative is defined as where the ground truth indicated tissue voxels where the segmentation result did not. So the false detection of normal tissue is defined as the summation of false positive and false negative.

Table 3. False detection rate of the normal tissues segmentation

<table>
<thead>
<tr>
<th>Tissues</th>
<th>False detection rate (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Noise level 3%</td>
</tr>
<tr>
<td>White matter</td>
<td>5.14</td>
</tr>
<tr>
<td>Gray matter</td>
<td>4.19</td>
</tr>
<tr>
<td>CSF</td>
<td>6.33</td>
</tr>
</tbody>
</table>
Figure 15. Simulated MRI volume on T1 (first line), T2 (second line) and PD (last line) with different noise level, 3% (left column), 5% (middle column) and 7% (right column).

Figure 16. Anatomic model (first column) and segmentation result with 3, 5 and 7% noise level (2 to 4 column) of normal tissues, CSF (first line), GM (second line) and WM (last line).
5. CONCLUSION

We have proposed in this paper an automatic segmentation system of brain tissue. It is based on fuzzy information fusion to segment automatically tumor area and normal tissue of human brain from multispectral MR images. The important technique of this system is the approach of feature extraction of brain tissue. Some mathematical models and “histogram modification modeling” are introduced to extract fuzzy features of brain tissue from different MR image sequences for creating fuzzy feature spaces corresponding to these sequences. The fuzzy relation among these feature spaces is a fusion operator of fuzzy features. The segmentation results present a good efficiency for synergy in the information acquired from different image sources and is appreciated by experts in radiology. In a further work, we will continue to study the optimal modeling and fuzzy information fusion operators in order to improve the robustness of our method.

REFERENCES