A Novel Hierarchical Approach in Segmentation of CT Head Images

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Abstract-This paper proposes a new hierarchical approach for segmentation of CT head images. At first (Firstly) intracranial area (ICA) and skull are automatically determined. Then (In the second step,) using fuzzy C-means method, ICA is segmented into 3 main groups of spatially localized regions having uniform brightness: lighter prototype (LP), darker prototype (DP) and normal brain white-gray mass. In the third step, special features are extracted for LP and DP regions individually. Finally two parallel rule-based expert systems label normal regions. The remaining regions considered as abnormal regions. Experiments conducted on real CT images show the efficiency and accuracy of the proposed method.

keywords: Otsu threshold; histogram equalization; fuzzy C-means; expert rule-based system

I. INTRODUCTION

There have been some useful algorithms to segment CT head images into several regions such as fuzzy C-means clustering method [1,2], watershed algorithm [3], thresholding method [4,5], k-means clustering algorithm [6], wavelet decomposition [7] and region growing method [8]. A number of authors have used intelligent systems for labeling different regions [9,10].

In this paper, a new hierarchical technique for segmentation of CT brain images is proposed. Almost all previous works on CT head image segmentation are focused on searching for abnormal regions [1,6,7,8,11]. So they are case sensitive because of wide variations of abnormal regions even in a special kind of pathology.

In this work, however, we focused on extraction of normal regions according to their invariable brightness, position and anatomical shape. The proposed method removes normal regions and the remaining regions would be suspicious of having pathological changes.

We extracts 6 different clusters in CT head image step by step: background, skull, normal brain white-gray matter, darker normal regions, lighter normal regions and regions suspicious of having any kind of pathological changes.

After removing background and skull, normal brain white-gray mass is eliminated. Remaining regions of brain are processed individually as lighter prototype (LP) and darker prototype (DP). LP includes either normal regions such as midline falx or abnormal regions such as hemorrhage. Similarly in DP there are both normal regions such as lateral ventricles and abnormal regions such as stroke lesions.

In order to distinguish normal regions, special features are extracted. These features are delivered to a pair of parallel expert rule-based systems that remove normal regions. Rest of the paper is organized as follows. Section 2 explains the procedure for extraction of intracranial area (ICA) and symmetry axis of the brain. In section 3 segmentation of ICA into several regions is described. Extraction of features is explained in section 4. Section 5 describes parallel expert rule-based systems. Finally, section 6 discusses the experimental results and possible future work.

II. EXTRACTION OF INTRACRANIAL AREA

Data set includes head CT images in the standard DICOM format (digital imaging and communication in medicine) with 256 grayscale values. Segmentation and labeling are applied on individual slices.

At first, intensity adjustment is applied in order to enhance the image. The skull is removed according to the fact that the largest connected white area in head CT image is skull [6]. Using a constant threshold, the image is converted into a black and white image and the skull area is detected. If the skull region missed its connectivity because of trauma, region closing is applied to the skull to prevent segmentation error in the following steps.

Subsequently in order to remove background, skull pixels and the brain pixels inside it are set to zero and watershed algorithm is applied to the black and white image. In this step the skull outer boundary is detected and background is completely removed. This procedure is shown in Fig.1.
As we know, symmetry is an important clue in brain image processing. In order to remove the variation of patient head axis and normalize all images into the vertical alignment, center of mass and symmetry axis of the image are detected using moments of the brain mass [8]. The result is shown in Fig.2.

### III. SEGMENTATION

The first step in segmentation is to remove normal white-gray brain mass. Using Otsu’s threshold method two prototypes are coarsely determined in this step: extra light prototype and extra dark prototype (LP and DP respectively). The remains of image are removed as the brain matter.

At first the peak to the left of the peak position in image histogram is searched. I_{w} and I_{b} show the intensity of that point in LP and DP respectively. I(i) is considered as the contrast of each nonzero pixel. n_{w} or n_{b} stand for number of nonzero pixels in LP and DP respectively. Below is the procedure:

\[
LP:\n\text{for } i=1:n_{w} \\
\text{if } I(i)<I_{w} \text{ then } I(i)=0; \\
\text{end} \\
\text{end} \\
\]

\[
DP:\n\text{for } i=1:n_{b} \\
\text{if } I(i)>I_{b}/2 \text{ then } I(i)=0; \\
\text{end} \\
\text{end} \\
\]

In order to intensify regions of interest, histogram equalization is applied on LP and DP independently. A median filter is also utilized to reduce salt and pepper noise. Subsequently the 2D space of image is reduced to 1D contrast space and Fuzzy C-means method is applied to remove remains of normal brain white-gray matter. Fig.3 shows the results.

### IV. FEATURE EXTRACTION

Prior to classification the features for every region are extracted in LP and DP image. According to the anatomical shape and position of different brain regions, some features are extracted just for one of the two prototypes. Table I lists and describes all extracted features. As mentioned before
different features are used for LP and DP regions; this is shown in the first column of Table I.

<table>
<thead>
<tr>
<th>Feature</th>
<th>Explanation</th>
<th>Prototype</th>
</tr>
</thead>
<tbody>
<tr>
<td>Area</td>
<td>Number of pixels in the region</td>
<td>LP, DP</td>
</tr>
<tr>
<td>Mean</td>
<td>The average of pixels contrast in the region</td>
<td>LP</td>
</tr>
<tr>
<td>Eccentricity</td>
<td>The value between 0 and 1 (an ellipse whose eccentricity is 0 is actually a circle, while an ellipse whose eccentricity is 1 is a line.)</td>
<td>LP, DP</td>
</tr>
<tr>
<td>Symmetry</td>
<td>The mean difference between symmetric points' intensity</td>
<td>DP</td>
</tr>
<tr>
<td>Distance</td>
<td>The distance between center of mass of the region and symmetry axis</td>
<td>DP, LP</td>
</tr>
<tr>
<td>Orientation</td>
<td>The angle between the x-axis and the major axis of the ellipse that has the same second-moments as the region</td>
<td>LP</td>
</tr>
</tbody>
</table>

V. LABELING

The Final step is to label and remove remaining normal regions. There are different normal regions in brain, appearing lighter or darker than brain mass e.g. ventricles, sagittal sinuses or CSF. Two parallel expert rule-based systems in If-Then form work on the features and label abnormal regions.

For every normal region a group of rules should be completely satisfied. Rules and constant threshold values are achieved through experimental results according to anatomical facts about brain and manual labeling. Region that doesn’t satisfy rules for any of normal regions is labeled as pathologically abnormal. A part of rule-based system for midline falx and lateral ventricles is shown below.

**Midline falx:**
1. $x \in LP$
2. $Area < \alpha_0$
3. $Eccentricity > \sigma_0$
4. $Distance > \delta_0$
5. $Orientation > \theta_0$

**Lateral ventricle:**
1. $x \in DP$
2. $a_i < Area < \beta_i$
3. $Symmetry < \delta$
4. $Distance < \lambda_i$
5. $Eccentricity < \sigma_1$

Note that if the size of lateral ventricles was extraordinary (as in hydrocephalus) they would be labeled as abnormal regions. Feature “Mean” is used for LP in order to distinguish between normal white brain mass and calcification regions.

The same procedure is used for removing all other normal regions in brain. The remaining regions are labeled as pathologically abnormal. As it said before the proposed method is not sensitive to the type, shape and position of abnormal region. Fig. 4 shows the final labeling results in different slices. Note that normal regions shown in different colors. Red color is used for abnormal regions.

VI. DISCUSSION

The proposed method was applied on real CT images gathered from digital scanner in Alzahra Hospital in Isfahan. The dataset includes 267 slices in DICOM format collected using PaxPlus scanning software from 14 abnormal and 27 normal patients. Manual labeling is supposed as the approved reference for evaluating proposed method.

The results show that labeling error, number of misclassified regions divided by the total number of regions, is very low (about 3%). In addition overall error, the number of slices with misclassified regions divided by total number of slices, is about 9%. It means that 243 slices are labeled correctly. Experimental results confirmed that the system works efficiently and accurately. Improvement of the proposed method will be our future work in order to annotate different abnormal regions in image.
Figure 4. Labeling: left side column shows ICA image, right side column shows labeling result, abnormal regions are shown in red

REFERENCES


