

Quantitative intracerebral brain hemorrhage analysis

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ABSTRACT

In this paper a system for 3-D quantitative analysis of human spontaneous intracerebral brain hemorrhage (ICH) is described. The purpose of the developed system is to perform quantitative 3-D measurements of the parameters of ICH region and from computed tomography (CT) images. The measured parameter in this phase of the system development is volume of the hemorrhage region. The goal of the project is to measure parameters for a large number of patients having ICH and to correlate measured parameters to patient morbidity and mortality.

Keywords: image segmentation, expert system, CT, C-means clustering, ICH

1. INTRODUCTION

In this work we are addressing a problem of developing a system for automatic and semi-automatic quantitative measurements of CT images. The crucial step in quantitative measurement is segmentation of the CT image into homogeneous regions which correspond to different tissue classes. For us, of particular interest is the ICH region. Other tissue classes are brain, skull, and calcifications. A number of approaches to segmentation of head or brain images have been presented in past years: pattern recognition techniques,¹ rule based systems², and knowledge-based approach³ are some of them. One approach to hemorrhage quantitative analysis has been presented in.⁴

The technique proposed here has a hierarchical structure and combines the qualities of unsupervised fuzzy clustering and rule-based system labeling. The previous technique developed by the authors^{5,6} used unsupervised clustering and backtracking tree search algorithm.

The rest of this work is organized as follows: In the second section we describe our segmentation method, where the first subsection describes our implementation of the C-means clustering algorithm and the second subsection describes a simple rule-based system which uses results produced by the clustering algorithm as input and labels image regions with the tissue labels. In the third section we are describing the computer realization of the proposed algorithm and developed additional semi-automatic segmentation method which is not part of our automatic segmentation procedure, but rather a parallel method for obtaining results or for manual computer-assisted correction of segmentation results. In the fourth section results of our approach are presented, followed by the discussion in the last section.

2. A METHOD FOR THE IMAGE SEGMENTATION

The input CT head image is processed in two stages. The first stage uses an unsupervised clustering algorithm which partitions the input image into a number of regions having uniform brightness. The second stage is a rule-based system devoted to the interpretation of the clustering results. The rule-based system assigns a label to each of regions obtained by clustering algorithm. Both stages are described in more details in the following subsections.

2.1. Clustering algorithm

The clustering algorithm used for partitioning the input CT head image into multiple smaller regions is presented in this subsection. Two layer unsupervised clustering strategy that has been presented in⁷ is used as a basic algorithm strategy. The algorithm is described in Figure 1.

The reason for use of FMLE is in its good performance in the presence of variable cluster densities. On the other hand FMLE requires starting from good initial conditions which are assured by output of the FCM. The resulted cluster centers obtained by the FCM algorithm from the first step are input into the FMLE algorithm.

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- 1: **repeat**
- 2: Cluster the data with fuzzy C-means (FCM)
- 3: Cluster the data with fuzzy modification of the maximum likelihood estimation (FMLE)
- 4: Increase number of clusters C and choose additional cluster center
- 5: **until** Stopping criterium is met

Figure 1. The clustering algorithm

- 1: **repeat**
- 2: Determine initial cluster centers
- 3: Compute the degree of membership of all feature vectors in all the clusters u_{ij} .
- 4: Compute new cluster centers V_i' from feature vectors and their memberships to clusters and update the degree of membership from u_{ij} to u'_{ij} , according to step 2.
- 5: **until** $\max_{ij} |u_{ij} - u'_{ij}| < \epsilon$, $\epsilon \in (0,1)$.

Figure 2. Fuzzy C-means clustering

2.1.1. Fuzzy C-means algorithm

At the first step of the clustering strategy FCM algorithm performs clustering of the input data. FCM is based on minimization of the objective function (1) which represents the distance error of feature vectors from the cluster centers. The objective function is minimized with respect to U , a set of memberships of all feature vectors in all clusters and to V , a set of cluster centers.

$$J_q(U, V) = \sum_{j=1}^N \sum_{i=1}^K (u_{ij})^2 d^2(X_j, V_i) \quad (1)$$

where X_j is the j th m -dimensional feature vector, V_i is the center of the i th cluster, u_{ij} is the degree of membership of X_j in the i th cluster, $d^2(X_j, V_k)$ is distance between X_j and V_i , N is the number of data points and C is the number of clusters.

Clustering of the input data has been performed through optimization of 1 and steps described in Figure 2. The degree of membership u_{ij} , and new cluster centers V_i' are calculated from the following expressions:

$$u_{ij} = \frac{\frac{1}{d^2(X_j, V_i)}}{\sum_{k=1}^C \frac{1}{d^2(X_j, V_k)}} \quad (2)$$

$$V_i' = \frac{\sum_{j=1}^N (u_{ij})^2 X_j}{\sum_{j=1}^N (u_{ij})^2} \quad (3)$$

2.1.2. Fuzzy Maximum Likelihood Algorithm

At the second step of the clustering strategy fuzzy modification of the maximum likelihood estimation (FMLE) has been used.

The FMLE algorithm has almost the same flow of data processing as FCM. The main difference is the distance measure $d_e^2(X_j, V_i)$ which has exponential character and is based on maximum likelihood estimation. This distance is used in computing of $h(i|X_j)$, the probability of selecting the i – th cluster given the j – th feature vector. Substituting Equation 5 instead of Equation 2 in FCM algorithm results in the fuzzy modification of the maximum likelihood estimation.

$$d_e^2(X_j, V_i) = \frac{(\det(F_i))^{1/2}}{P_i} \exp\left(-\frac{(X_j - V_i)^T F_i^{-1} (X_j - V_i)}{2}\right) \quad (4)$$

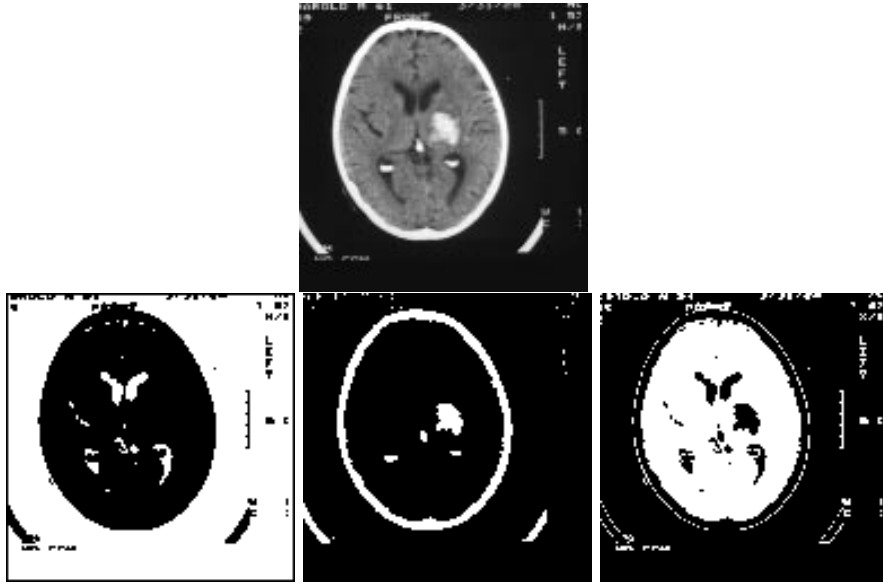


Figure 3. Results of the clustering algorithm. First row: original CT head image. Second row: dark, bright, and gray regions of the original CT head image (white areas).

$$h(i|X_j) = \frac{\frac{1}{d_e^2(X_j, V_i)}}{\sum_{k=1}^C \frac{1}{d_e^2(X_j, V_i)}} \quad (5)$$

where F_i is the fuzzy covariance matrix of the i -th cluster, and P_i the *a priori* probability of selecting the i -th cluster.

$$P_i = \frac{1}{N} \sum_{j=1}^N h(i|X_j) \quad (6)$$

$$F_i = \frac{\sum_{j=1}^N h(i|X_j)(X_j - V_i)(X_j - V_i)^T}{\sum_{j=1}^N h(i|X_j)} \quad (7)$$

The next important step in the clustering strategy is choosing of additional cluster center. A performance of an unsupervised clustering algorithm depends on the mechanism for selection of new cluster centers. The problem of selecting a new cluster center for this particular unsupervised fuzzy clustering algorithm has been discussed in.⁸ The main idea is to place the $(C + 1)$ -th center in a region where data points have low degree of membership in the existing C clusters. The Equation 8 for selection of the new cluster center has been proposed in⁸ and used in this work.

$$p = \arg \min_j \max_i u_{ij}, \quad V_{k+1} = X_p \quad (8)$$

The maximum number of clusters used in the algorithm is three. Although the number of clusters is known, the unsupervised algorithm is used because it avoids the initial guess problem present in supervised clustering algorithms. This unsupervised clustering algorithm creates a number of spatially localized image regions having uniform brightness.

Figure 3 presents the results of the clustering algorithm which has determined dark, bright, and gray regions of the original CT head image. Bright regions correspond mostly to the skull, hemorrhage and calcifications regions. The artifacts from the CT scanner are also determined as bright regions. Dark regions are background region and some parts of the brain like ventricle region. Gray regions belong mostly to brain region. There are also some artifacts from CT scanner (markers, letters) that are determined as gray regions.

2.2. Rule-Based System Labeling

The second stage of image processing in this work is an image labeling algorithm. The image labeling algorithm assigns a label to each of the image regions obtained by the unsupervised clustering algorithm. In this work we have used a rule-based system for region labeling. The rule-based system has been developed using the expert system shell "C Language Integrated Production System" (CLIPS) ^{.9,10} The motivation for the use of the rule-based system comes from the fact that a more extensive expert knowledge is required for successful ICH determination. Such a complex knowledge is difficult to represent using only conventional algorithms such as backtracking tree search labeling. The rule-based system developed using CLIPS shell consists of three basic components:

1. fact-list
2. knowledge-base or rule-base
3. inference engine

A rule-based system written in CLIPS is a data-driven program where the data are represented by facts from the fact-list. The forward chaining inference engine decides which rules should be fired and when.

The aim of the rule-based system is to assign one of the following labels to each region: background, skull, brain, calcifications, and ICH. The rules from the knowledge base have been derived from a priori knowledge about the relations between the brain regions and their properties. These rules are independent units that are not procedurally linked to other rules. Facts from the fact-list have been derived from input CT image and determined by several region features, region-neighborhood, and region-label relations. The features used to characterize regions are brightness (bright, dark, and gray regions) and area which is described by the number of pixels contained in the region.

For example, the following fact presented in CLIPS syntax describes a bright region with the area equal to 125 pixels from the image with dimensions (128×128)

(region (id 7) (neighbor 1 5 15) (area 125) (brightness bright))

In this example, the region identity number is equal to 7 and is adjacent to the regions with the identity numbers 1, 5, and 15.

Rules in the knowledge base can be modified or updated providing a great flexibility of this approach. The classification of the rules can be done by means of a label which they assign to the selected region. There are rules for the background, skull, brain, ICH and calcifications. The rules are fired in the following manner. The first two rules that should be fired are rules which looks for the largest bright and dark regions. These two initial regions are labeled as skull and background region. After that program looks for all regions which are adjacent to these two region. Accordingly to the rules presented in the following subsections these adjacent regions are labeled as background, skull or brain regions. Each labeled region is added to the fact-list as a new fact with the information of the label assigned to the region. It causes firing new rules which leads the program toward labeling of all regions. The rules are fired until there are no more regions to label. If it happens that some region remains unlabeled it is easy to add new rule which can describe its particular case.

The rules are presented in the following subsections in **if/then** form.

Background labeling rules

The following rules define the properties of the regions which belong to the background area.

1. **if** region has only one adjacent region **and** adjacent region is background
then region is background
2. **if** region is adjacent to skull **and** adjacent to background **and** not bright
then region is background
3. **if** region is adjacent to brain **and** adjacent to background **and** not bright
then region is background
4. **if** region has only one adjacent region **and** adjacent region is skull **and** is dark
then region is background

5. **if** region is adjacent to background **and** adjacent to non-labeled region **and** non-labeled region is bright **and** is gray
then region is background and adjacent non-labeled region is background
6. **if** region is dark **and** has the largest area among dark regions
then region is background

Brain labeling rules

These rules define the properties of the brain regions.

1. **if** region is adjacent to skull **and** area > 1000 **and** is gray
then region is brain
2. **if** region has only one adjacent region **and** adjacent region is brain **and** is not bright
then region is brain
3. **if** region is adjacent to brain **and** is adjacent to non-labeled region **and** non-labeled region is bright **and** non-labeled region area < 20 **and** is dark
then region is brain

Skull labeling rules

The skull area is determined according to the following rules.

1. **if** region is bright **and** has the largest area among bright regions
then region is skull
2. **if** region is adjacent to brain **and** is adjacent to background **and** is bright
then region is skull

Hemorrhage labeling rules

The hemorrhage area is labeled according to the following rules.

1. **if** region has only one adjacent region **and** adjacent region is brain **and** region area>19 **and** region is bright
then region is hemorrhage
2. **if** region is adjacent to brain region **and** region area>50 **and** region is bright
then region is hemorrhage

Calcifications labeling rules

Calcifications are determined by the following three rules.

1. **if** region has only one adjacent region **and** adjacent region is brain **and** region area<20 **and** is bright
then region is calcification
2. **if** region has two adjacent regions **and** adjacent regions are brain **and** region area<20 **and** is bright
then region is calcification
3. **if** region has three adjacent regions **and** adjacent regions are all brain regions **and** region area < 20 **and** is bright
then region is calcification

3. COMPUTER REALIZATION

In this section we describe implementation of the proposed algorithms. The C-means clustering algorithm presented in this work is implemented in C programming language using the Khoros image processing environment. The rule-based system was developed using the CLIPS programming language. For the development of the graphic user interface the Tcl/Tk programming language is used, and for some parts Motif API on top of the Xlib. The software was developed on the Sun Ultra 1 workstation.

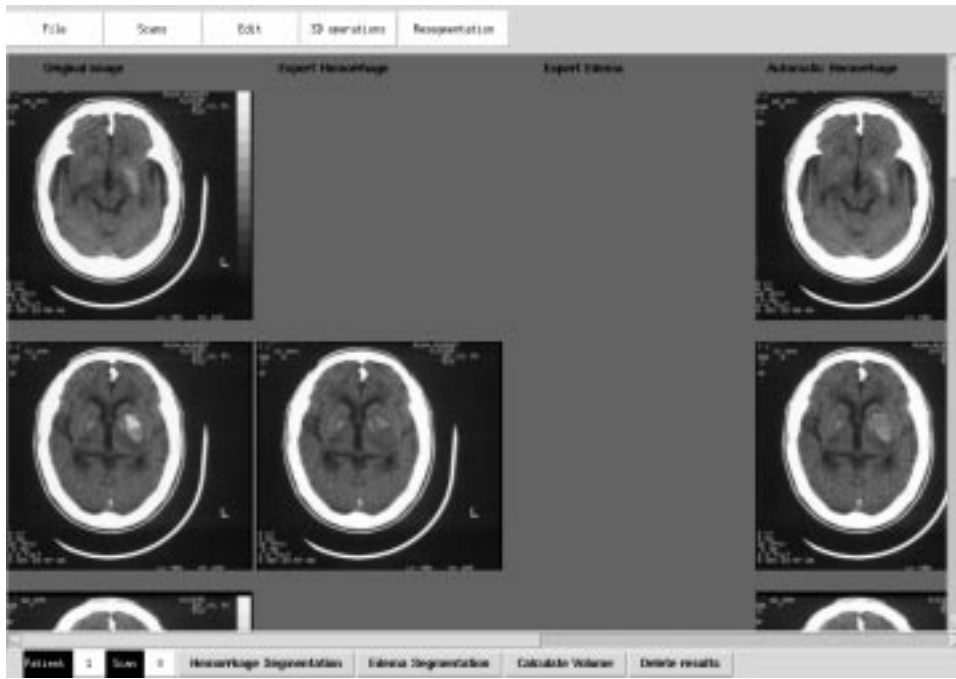


Figure 4. The graphical user interface.

3.1. Graphical user Interface

The graphical user interface was developed in order to visualize results of the algorithms and to make them easier to use. The interface is shown in Figure 4. From the GUI user can select patient from database, start segmentation procedure, view segmentation results, calculate region dimensions. The GUI allows display of all original and segmented CT images from one scan at the same time. Also it is possible to start semi-automatic procedure for segmentation which is described in the next subsection of this work. The semi-automatic procedure was needed in cases when our automatic method does not perform well enough.

3.2. Region based semi-automatic segmentation

This method is based on interactive region growing process. In this approach, the user performs segmentation through the process of repetitive addition of partial regions, until the desired region is segmented. The user starts by drawing a curve through the region that is considered to be the part of the desired region. The algorithm computes the image features along the user-defined path and the computed features are used in the region-growing process. The image features that are computed are the mean image brightness along the curve, and the standard deviation of the brightness along the curve. These parameters are used to control a region-growing process that results in a partial region that is added to the previously segmented regions. The process is repeated until the user is satisfied with the look of the segmented region.

Let L_i be a curve drawn by the user in i -th iteration inside the ROI and let $(X_0, Y_0), (X_1, Y_1), \dots, (X_{n-1}, Y_{n-1})$ be the points along that curve. Let $B(X, Y)$ be the brightness of the point (X, Y) . Also, let B_i be the mean brightness on the curve L_i and S_i its standard deviation. Let R_i be a region grown in i -th iteration and R union of all R_i let the C be the numerical constant interactively determined by the user by moving the slider in the graphic interface. This allows user to determine the size of the grown region. Other features besides brightness can also be used for growing criteria. In our case results obtained using the brightness only are satisfactory because the region of interest has relatively uniform brightness.

The region-based interactive segmentation algorithm is shown in Figure 5.

The graphical user interface for the interactive segmentation algorithm is shown in Figure 6. The method allows interactive adjustment of the growth parameter.

```

1:  $i = 0$ 
2: repeat
3:   Obtain Curve  $L_i$  consisting of  $n$  points from the user
4:   Calculate  $B_i$ 
5:   Calculate  $S_i$ 
6:    $j = 0$ 
7:   repeat
8:     Grow region  $R_i$  from point  $(X_j, Y_j)$  using following rule:
9:     if  $-C * S_i < B_i(X, Y) - B < C * S_i$  then
10:       Point  $(X, Y)$  belongs to the ROI
11:     end if
12:      $j = j + 1$ 
13:   until  $j = n$ 
14:    $R = R \cup R_i$ 
15:    $i = i + 1$ 
16: until algorithm is stopped by user

```

Figure 5. The algorithm for region-based segmentation.

	Planimetric method			Proposed algorithm		
Study	Baseline	1 hour	24 hours	Baseline	1 hour	24 hours
1	8.4	17.5	24.8	7.4	17.0	26.1
2	11.3	11.1	10.6	8.8	8.5	11.1
3	19.0	19.7	19.9	15.9	15.9	15.2
4	11.1	10.8	7.6	10.2	12.2	8.5
5	16.1	27.3	17.8	11.0	25.6	21.3

Table 1. ICH volumes obtained by the planimetric method (left) and by the our algorithm (right)

4. RESULTS

In this section are presented the measurements and statistical analysis of ICH volumes that are segmented from the CT images. In order to verify the system for the automatic measurement of ICH regions the scans of five patients were measured using a conventional planimetric method. The description of that method is as follows: Regions of interest are manually outlined and then segmented out on a slice-by-slice bases. The area of each hemorrhage is measured and multiplied by the slice thickness to get the total volume.

The results of comparison are shown in Table 1. On the left are shown results of the planimetric method and on the right are results obtained using the proposed method. There are five patients having hemorrhage in the table. Each patient had three CT scans: baseline, 1-h scan, and 24-h scan. Statistical significance t -tests were performed on these measurements to evaluate the significance of the difference of our algorithm with respect to planimetric method. The statistic tests had shown “No significant difference” with $P < 0.05$. The correlation coefficient among these two methods was 0.92.

5. CONCLUSION

In this paper we describe a method for quantitative analysis of CT head images, in particular for determining volume of the intracerebral brain hemorrhage (ICH). The method is based on fuzzy clustering and expert system labeling, and enables automatic determination of the volume of the ICH region. Since the method does not always perform correct segmentation, an additional semi-automatic segmentation method is developed which expert (neuroradiologists) can use if he is not satisfied with the results of the automatic segmentation. A graphical user interface is developed to enable efficient use of the software by neuroradiologists.

The validation of the method has been performed using manual planimetric measurements performed by the radiologists. A statistical study has been performed that has shown the validity of the method. The developed

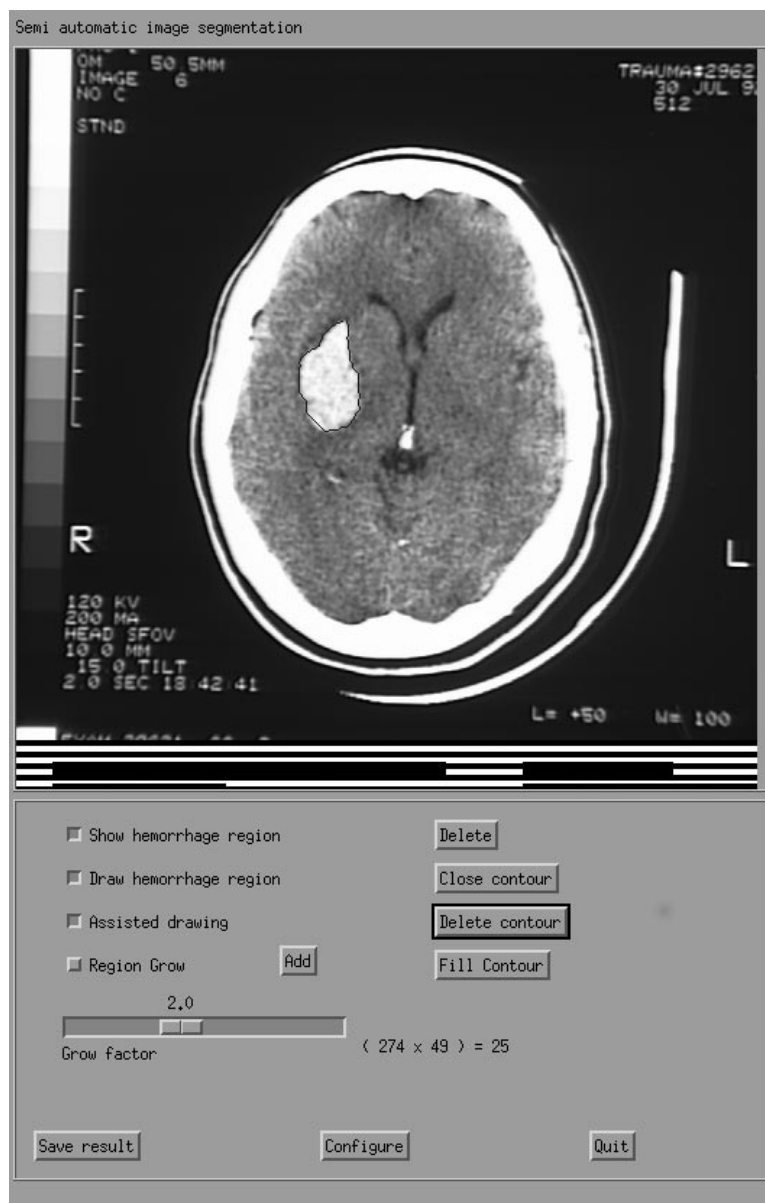


Figure 6. The graphical user interface for the semi-automatic segmentation.

system for brain image analysis is a new tool that may help understand this serious disease and improve the selection of the appropriate treatment.

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