Multiresolution Simulated Annealing for Brain Image Analysis

Sven Loncaric *a and Zoran Majcenic^a

^aFaculty of Electrical Engineering and Computer Science, Unska 3, Zagreb, Croatia

ABSTRACT

Analysis of biomedical images is an important step in quantification of various diseases such as human spontaneous intracerebral brain hemorrhage (ICH). In particular, the study of outcome in patients having ICH requires measurements of various ICH parameters such as hemorrhage volume and their change over time. A multiresolution probabilistic approach for segmentation of CT head images is presented in this work. This method views the segmentation problem as a pixel labeling problem. In this application the labels are: background, skull, brain tissue, and ICH. The proposed method is based on the Maximum A-Posteriori (MAP) estimation of the unknown pixel labels. The MAP method maximizes the a-posterior probability of segmented image given the observed (input) image. Markov random field (MRF) model has been used for the posterior distribution. The MAP estimation of the segmented image has been determined using the simulated annealing (SA) algorithm. The SA algorithm is used to minimize the energy function associated with MRF posterior distribution function. A multiresolution SA (MSA) has been developed to speed up the annealing process. MSA is presented in detail in this work. A knowledge-based classification based on the brightness, size, shape and relative position toward other regions is performed at the end of the procedure. The regions are identified as background, skull, brain, ICH and calcifications.

Keywords: simulated annealing, Markov Random Field, CT, multiresolution, ICH

1. INTRODUCTION

The field of medical image analysis is heavily tied to the problem of image segmentation. Image segmentation is a commonly required step, but because of the nature of medical images it is not simple. The problem of analysis of computed tomography (CT) head images, namely quantitative analysis of human spontaneous intracerebral brain hemorrhage (ICH), is a field of certain interest. A precise segmentation of ICH is necessary for image-based measurement of the ICH volume. The most difficult step in image-based measurement of ICH region is image segmentation. After the correct segmentation it is necessary to identify which region represents the ICH. Once the procedure is completed it is possible to extract ICH size.

A number of techniques have been applied to the problem of CT head image segmentation including clustering algorithms $(^{1,2,3})$, neural networks $(^{4,5,6})$, morphological methods $(^{7,8})$ and knowledge-based methods $(^{9})$. A number of stochastic approaches to the image analysis is presented in literature $(^{10,11})$.

The work presented in this paper is based on a simulated annealing (SA) algorithm. SA is a stochastic method for function optimization. In this work it is used for segmentation based on optimizing the energy function. Details of SA algorithm can be found in Section 2. A multiresolution SA (MSA) algorithm that is applied to the problem of CT head image segmentation is presented in Section 3. Finally, after the successful segmentation a region creation and identification process is taken. Section 4 explains the details of this process. Results and discussion are presented in Section 5. Conclusions are presented in Section 6.

2. SIMULATED ANNEALING ALGORITHM FOR IMAGE SEGMENTATION

The image segmentation problem is approached as the pixel labeling problem. The definition of a pixel labeling problem requires us to define a set of objects that need to be labeled, and a set of object labels. A set of objects in image segmentation problem is a set of pixels that form the image. The set of object labels consists of pattern classes in the image, in our case the three levels of brightness. It is defined as $L = \{l_1, l_2, \ldots, l_G\}(^{10})$. The pixel labeling problem is a problem of estimating the true pixel labeling $\mathbf{x} = \{x_1, x_2, \ldots, x_M\}$. The image is viewed as a realization of a random field. The random field is a two-dimensional sequence of random variables. The image is denoted $\mathbf{Y} = \{Y_1, Y_2, \ldots, Y_M\}$, where Y_t is the feature vector associated with the *t*-th pixel. Contextual

^{*} Send correspondence to Sven Loncaric: E-mail: sven.loncaric@fer.hr; www: http://helga.zesoi.fer.hr

1: Choose an initial temperature T.

- 2: Initialise $\hat{\mathbf{x}}$ by choosing x_t as the color \hat{x}_t that maximises $P(Y_t = y_t | X_t = x_t)$ for each pixel t.
- 3: repeat
- 4: Let i = 0
- 5: repeat
- 6: Perturb x into z by randomly choosing site t and setting its label to a random value in the interval $\{0, 1, \dots, G-1\}$

7: Let
$$\Delta = U(\hat{X}_t = \hat{x}_t | Y_t = y_t) - U(\hat{X}_t = z | Y_t = y_t)$$

- 8: if $\Delta > 0$ then
- 9: replace \hat{X}_t by z
- 10: **else**
- 11: replace \hat{X}_t by z with probability $e^{\Delta/T}$
- 12: **end if**
- 13: Let i = i + 1
- 14: **until** $i = N_{iter}$
- 15: Replace T by f(T) where f is the monotonically decreasing function.
- 16: until frozen.

Figure 1. Simulated annealing algorithm.

information (neighborhood influence) is also included in the process of labeling through statistical dependence among neighboring pixels given in the form of Markov Random Field (MRF). In the process of the pixel labeling the observed feature vectors $\mathbf{Y}=\mathbf{y}$, and the contextual information as an MRF $P(\mathbf{X}=\mathbf{x})$, are used to find the optimal estimate of the true labeling \mathbf{x} . The Maximum A-Posteriori (MAP) method estimates $\hat{\mathbf{x}}$ by maximizing the posterior probability of $\mathbf{X}=\hat{\mathbf{x}}$, given $\mathbf{Y}=\mathbf{y}$.

$$P(\mathbf{X} = \mathbf{x} | \mathbf{Y} = \mathbf{y}) = \frac{P(\mathbf{Y} = \mathbf{y} | \mathbf{X} = \mathbf{x}) P(\mathbf{X} = \mathbf{x})}{P(\mathbf{Y} = \mathbf{y})}$$

Acquiring a MAP estimate demands us to minimize a complicated function of M variables, where M is a number of pixels in the image. One possible solution to this problem is the use of a simulated annealing algorithm.

Simulated annealing is a method used for function optimization. It is a method that simulates the cooling process of a metal. In its mathematical form it is capable to find the global minimum of a function. It makes no assumptions about the discontinuities of a function, but it is highly computationally demanding. The SA procedure is given in Figure 1.

The described SA algorithm defines P(.|.) as a conditional probability density function of the gray levels in the image for a specified label. The probability density function is approximated with a Gaussian function of the form

$$P(.|.) = \exp{-\frac{(y_t - \mu_l)^2}{2\pi\sigma_l}}$$

In Figure 1, G is the number of labels in the image, and U(.|.) is the energy function that defines the energy of a single pixel. The energy U consists of two parts. The first part describes how well the pixel's label fits its gray value. The numerical value can be acquired by the expression 1 - P(.|.), where P(.|.) is the probability density function. The second part describes how compatible is the pixel with its neighborhood in terms of its label. The neighborhood influence is calculated by checking the 4-neighborhood (up, down, left, right), to see weather the pixel's label matches with the surroundings. If that is not the case, the energy U is increased by k-times a constant factor, k being the number of pixels in the neighborhood which do not match the viewed pixel label.

The choice of a cooling function f must be made carefully. The temperature must not be lowered too fast in order to avoid the risk of getting stuck in local minima. If the temperature is lowered slowly enough the SA ability to accept the higher energy states based on current temperature will allow us to escape the local minima. There are two basic ways to lower the temperature. Theory demands a infinitesimally slow logarithmic decrease to guarantee the discovery of the global minimum. However, in practical realizations the following linear function is found to work satisfactory:

$$f(T) = \alpha * T, 0 < \alpha < 1$$

- 1: Let S be the original image at resolution $N \times N$
- 2: Let $\{S_0, S_1, \ldots, S_{k-1}\}$ be the multiresolution pyramid of k levels, where $S_0 = S$, obtained by binary subsampling the original image S.
- 3: Perform the SA segmentation on the image of the lowest resolution S_{k-1} .
- 4: for z = k 2, ..., 0 do do
- 5: Obtain temporary image T by interpolating image S_{z-1} by a factor of 2
- 6: Clear pixel list L
- 7: for all pixels in T do
- 8: Let p(l) be an array of probabilities, $p(l) = P(Y_t = y_t | X_t = l), l = 0, ..., G 1$
- 9: **if** p(pixel's label currently in T) is not equal to max p(l) **then**
- 10: add four pixels, obtained by expansion of pixel at lower resolution to list L. {The four pixels in question are those expanded from the lower resolution and created from the same pixel as the one being checked.}
- 11: **end if**
- 12: **end for**

13: Perform SA segmentation of the image S_z using T as initial image and only test pixels from the list L. 14: end for

Figure 2. Multiresolution SA algorithm.

3. MULTIRESOLUTION SEGMENTATION USING SA

SA as the optimization method is very useful because it puts no restrictions on the function to be optimized. However, the price is high computational complexity. In case of an image sized 512×512 the number of variables (pixels that need to be labeled) is 262,144. Because of such a large number of variables the time used for optimization by the SA is long. In order to solve this problem and to make the SA more useful for image segmentation we have developed a multiresolution SA (MSA) algorithm. The general idea is to reduce the number of variables to be optimized and so reduce the computational burden. The proposed multiresolution SA algorithm is presented in Figure 2.

The image enlargement is performed by interpolation of the lower resolution image. It is done by replication of each pixel to four pixels. The label of a pixel at the lower resolution is used as the label for the four pixels at the higher resolution. Expansion is done by placing the pixel's label at site (x,y) to pixels, of the higher resolution image, at sites (2x,2y), (2x+1,2y), (2x,2y+1) and (2x+1,2y+1). Labels placed in such a manner do not necessarily represent the best labeling, so it becomes necessary to perform a check of the each label inherited from the previous level. The check is based on how the pixel's gray level fits the probability density function, of the gray levels, of the three types of regions present in the image. If the label inherited from the previous level is not the best, the entire cluster of four pixels is placed on the list for reassessment. The entire cluster is placed on the list so that the pixel's neighborhood is also reassessed. Each checked pixel is given its optimal label based on its gray level. The list L is a list that contains a number of pixel coordinates in the form (x,y). These are sites that need reassessment in the next iteration of the SA algorithm, and the only pixels we work with during the segmentation. This reduction of the number of variables is the reason for increased speed of the MSA compared to the SA. The segmented image and a list of pixels for reassessment created in this way is passed to the SA algorithm. The conventional SA algorithm is used for segmentation at this resolution level. The procedure is repeated for all resolution levels until the desired resolution is reached.

4. REGION LABELING

The output of the MSA is a segmented image. However, the region labels are still unknown. Such information is necessary if we want to perform some sort of measurement on a specific region in image. In our case that region of interest is ICH and its size.

Regions are created following a set of rules that describe their appearance and neighborhood. The basic features by which we identify a region are size and brightness. The background of the image is the largest black region on the image. However in a background we can include the simbols produced by the CT machine. In order to achieve this we need to rely on the neighborhood rules. Before that we must identify the skull region, it is the largest white region on the image. Now every region that is a neighboor of the background and it is not a skull is added to

1: Let (x, y) be the starting point in the image 2: Let l = GetPixelLabel(x, y) the label of that region 3: Let retreat = false, posx = x, posy = y; 4: if not *retreat* then insert pixel position (posx, posy) on a region pixel list $5 \cdot$ insert pixel position (posx, posy) on a stack 6: 7: end if if GetPixelLabel(posx + 1, posy) = l and pixel at (posx + 1, posy) is not in region then 8: posx = posx + 19: goto 4 10: 11: end if 12: if GetPixelLabel(posx, posy - 1) = l and pixel at (posx, posy - 1) is not in region then posy = posy - 113:goto 4 14:15: end if 16: if GetPixelLabel(posx - 1, posy) = l and pixel at (posx - 1, posy) is not in region then posx = posx - 117:goto 4 18:19: **end if** 20: if GetPixelLabel(posx, posy + 1) = l and pixel at (posx, posy + 1) is not in region then 21:posy = posy + 1goto 4 22:23: end if 24: Let retreat = true25: Get pixel position from stack and put it in posx and posy26: if stack is not empty then 27:goto 4 28: end if

Figure 3. Region creation process.

the background. The gray matter is the largest gray region of the image. Smaller black regions that border with gray matter or the skull are identified as ventricles. The ICH is a white region which borders with gray matter. Calcifications are small intensly white regions that have roughly the same size.

Regions are created using the region growing algorithm. This algorithm is very simple in our case since it is performed on the segmented image. Given a start point it will follow all pixels that are the same as the initial one. After a process of a region building, a regions border is also created. Using such information it is possible to check weather two regions border. We go through all the border pixels and check weather they are next to another region's border.

The above mentioned region creation algorithm is given in Figure 3.

5. RESULTS AND DISCUSSION

The coding and testing was done on a PC with Pentium 200MMX processor running Linux. Analysis of the CT head images was done on images of resolution 512×512 . The images were segmented using both conventional SA algorithm described in Section 2, and MSA algorithm described in Section 3. The initial level of the multiresolution pyramid had resolution of 64×64 and four levels were used up to resolution of 512×512 . Since both algorithms use SA for segmentation, but with different number of variables, they share the same cooling function with a constant factor of $\alpha = 0.975$ and initial temperature of 10. The number of iterations was set to one quarter of the total number of pixels to be labeled (meaning the number of pixels on the whole image or in the list L).

When the quality of the segmentation is concerned it can be observed in Figures 4 and 5 that it is virtually the same for both SA and MSA. The main difference between the two algorithms is the time of execution. The average time needed for segmentation using SA is 12 min, and MSA 2 min. The comparison of time spent on segmentation



Figure 4. Original image



Figure 5. Comparison of the segmentation quality using SA (middle) and MSA (right) methods

shows that the MSA is up to six times faster that the conventional SA. Such result is primarily because of the low detail in the original image. Low detail allows us to shrink the image and not loose information. Shrinked image is quickly segmented and expanded. Because of the lack of detail most pixels after the expansion will be correctly classified and will not end up on the list for reassesment. Figures 6, 7, and8 show the process of MSA segmentation. The region labeling procedure divides the image into regions of interest as it can be seen in the example images shown in Figures 9 and 10. The process is relatively fast and accurate. The detected ICH region is then analyzed and its area calculated.

6. CONCLUSION

The MSA has shown to be a successful upgrade of the SA algorithm when dealing with the low detailed images such as CT head images. When applied to the images rich in detail the resulting execution time is longer than for conventional SA. Region labeling is a relatively easy task in case of the CT head images because of the small number of regions and simple neighborhood rules. The proposed procedure has successfully determined and extracted ICH region.



Figure 6. Original image



Figure 7. Segmentation results at resolutions of 64x64 and 128x128

REFERENCES

- J. C. Bezdek, L. O. Hall, and L. P. Clarke, "Review of MR image segmentation techniques using pattern recognition," *Medical Physics* 20, pp. 1033–1048, 1993.
- 2. S. Loncaric, D. Cosic, and A. P. Dhawan, "Segmentation of CT head images," in *Proceedings of the 10th International Symposium Computer Assisted Radiology*, p. 1012, Elsevier, Amsterdam, 1996.
- 3. S. Loncaric, D. Cosic, and A. P. Dhawan, "Hierarchical segmentation of CT images," in *Proceedings of the 18th Annual Int'l Conference of the IEEE EMBS*, IEEE, 1996. Amsterdam.
- 4. G. I. Chiou and J.-N. Hwang, "A neural network-based stochastic active model (NNS-SNAKE) for contour finding of distinct features," *IEEE Transactions on Image Processing* 4, pp. 1407–1416, 1995.
- M. Ozkan, B. Dawant, and R. J. Maciunas, "Neural-network-based segmentation of multi-modal medical images: A comparative and prospective study," *IEEE Transactions on Medical Imaging* 12, pp. 534–544, 1993.
- S. C. Amartur, D. Piraino, and Y. Takefuji, "Optimization neural networks for the segmentation of magnetic resonance images," *IEEE Transactions on Medical Imaging* 11, pp. 215-220, 1992.



Figure 8. Segmentation results at resolutions 256x256 and 512x512 pixels.



Figure 9. Skull and brain regions extracted.

- S. Loncaric, A. P. Dhawan, T. Brott, and J. Broderick, "3-D image analysis of intracerebral brain hemorrhage," *Computer Methods and Programs in Biomedicine* 46, pp. 207–216, 1995.
- J. G. Thomas, R. A. Petters, and P. Jeanty, "Automatic segmentation of ultrasound images using morphological operators," *IEEE Transactions on Medical Imaging* 10, pp. 180–185, 1991.
- C. Li, D. B. Goldgof, and L. O. Hall, "Knowledge-based classification and tissue labeling of MR images of human brain," *IEEE Transactions on Medical Imaging* 12, pp. 740–750, 1993.
- R. Dubes and A. Jain, "Random field models in image analysis," *Journal of Applied Statistics* 16, pp. 131–164, 1989.
- 11. D.-W. Kim, G.-H. Lee, and S.-Y. Kim, "Stochastic segmentation of severely degraded images using gibbs random fields," *Optical Review* **3**, pp. 184–191, 1996.



Figure 10. ICH and calcifications regions extracted.