

A multi-phase, probabilistic approach to image segmentation in MRI and CT studies

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Abstract

This paper presents an approach for segmentation of digital medical images using a multi-phase probabilistic approach. The first phase of the approach is enhancement of the image data using an unsharp mask sharpening algorithm. This vastly improved the clarity of the images prior to segmentation. The segmentation of an object within the image is then achieved through two more phases. The first phase is a thresholding process, where each pixel is scored based on a similarity criterion for a chosen seed point. Pixels with a score satisfying a required minimum are selected into the segmented region. A second phase is then instituted for pixels not initially selected. This phase involves a probability selection, based on a Monte Carlo simulation. A probability for each pixel is formulated based on the pixel's intensity and location. This probability is then compared against a random probability to determine if the pixel is included in the segmented region. To facilitate the processing of multiple image slices, an automated relocation algorithm was developed to move determined seed points from image to image as the shape, size, or location of the object (i.e. organ) changes. The concepts and techniques developed were tested on three separate medical studies with one being shown in this paper. The results showed that the image enhancement process outlined features and details within the data that were not previously apparent. The segmentation process extracted the desired object more completely when compared to other segmentation techniques.

Keywords: image segmentation, probabilistic, region growing, thresholding, Monte Carlo, medical imaging, DICOM.



1 Introduction

It is commonplace in current medical practice for digital medical studies such as Computed Tomography (CT) and Magnetic Resonance Imaging (MRI) to be used for diagnosis and treatment. These technologies are increasing the amount and quality of digital medical data available to physicians. With this increase, new mathematical methods to find and represent pertinent information in this data must be created. Physicians must be presented with highly accurate and informative representations with which to base their decisions. Image segmentation is one such area that can benefit greatly from newly developed methods so that improved representations of organs can be extracted from medical studies to aid in a variety of diagnosis and treatment scenarios.

The selection of pixels for a segmented object can be thought of as a mathematical assignment problem. Essentially, there is a set of pixels (desired object) that needs to be located from a larger set of pixels (the entire medical study). This is analogous to the problems encountered in design optimization, where design variable values must be found from a large and sometimes infinite amount of choices. Currently, in design optimization, probabilistic approaches such as Simulated Annealing and Genetic Algorithms are the best methods available in terms of solution quality and performance. Thus, it was hypothesized that applying similar probabilistic techniques to image segmentation would yield improved results in terms of the selected pixels.

The created method uses two steps for the actual segmentation: 1) a pixel scoring system similar to a traditional thresholding segmentation process, and 2) a probabilistic multi-seed region growing process. This method also incorporates a significant amount of automation. A user need only select desired seed points on the first image of a study. From that point the method locates the object in every slice automatically and presents the user with a 3D interactive representation of the object.

2 Background

2.1 Digital medical imaging

The discovery of the x-ray [1] revolutionized how physicians diagnose and examine patients by allowing the “inside” of a patient to be viewed for treatment decisions. Imaging technologies progressed to the current state where MRI and CT scans are now commonplace. CT scans are cross-sectional images obtained from different angles of the patient’s body, using x-ray equipment [2]. MRI imaging is based on the emission and absorption of energy in the radio frequency (RF) range of the electrostatic spectrum. The scanned object will absorb and emit different variations in the phase and frequency of the RF range. These spatial variations are basis of producing MRI images [3]. MRI and CT produce accurate and high quality digital images of multiple cross sections of a patient’s body. If multiple cross sections are sequentially scanned (i.e. a medical study), they can be joined to produce a 3D object through surface or volume rendering.



Commonly, the data obtained from medical scans is stored in the Digital Imaging and Communications in Medicine (DICOM) [4] format, which was introduced by the National Electrical Manufacturers Association (NEMA). The DICOM format stores image data as well as other pertinent information such as the patient's name, type of scan, and dimensions and scale of the image.

2.2 Digital image segmentation

Image segmentation involves separating a selected object from the rest of the image data. There are several different techniques available, but most can be categorized into two types [8, 9]:

1. Region based segmentation
2. Edge based segmentation

The created method uses a primarily region based approach through the techniques of thresholding and region growing. Thresholding [10] separates the image data into two parts: the object, and the background. This assumes that the modality of the image's pixel intensity is discriminate. Pixels with intensity levels within the threshold range are categorized as the object, and pixels with intensity levels outside this range are categorized as backgrounds. The algorithm can be defined as:

$$F(x, y) = \begin{cases} 1, & T_{\min} \leq I(x, y) \leq T_{\max} \\ 0, & I(x, y) > T_{\min}, I(x, y) < T_{\max} \end{cases} \quad (1)$$

Region growing [11,12] is a process that group pixels or previously subdivided regions within the image, into a larger main region based on a predefined selection criterion usually having to do with similarity of intensity values. To initialize region growing, seeds are placed within the object desired to be segmented. From these seeds, the region will grow by inspecting each pixel in the adjacent area and comparing it in some manner with the seed's intensity value.

The current segmentation methods available are limited to the settings of the single selection criteria used. Pixels are given one opportunity to be selected. This approach does not look at the properties of the object as a whole, as a probability based method will. Thus, a significant number of pixels that belong to the object of interest are frequently omitted.

3 Method development

3.1 Method description

A flowchart of the segmentation method is shown in Figure 1. If chosen, image data is first sharpened. Then, seed points are selected by a user. If needed, the seeds are automatically repositioned so they lie in the object to be segmented. Following this, the two phase segmentation approach occurs. This is repeated for all image slices in a study.



Of note is that the segmentation is done in two-dimensional space, an image slice at a time. This was performed to aid in the computational efficiency of the method. Since typical medical studies can have upwards of 10-12 million data points, a 3D method may require a large part or all of the data to be loaded into a computer's memory. This significantly increases processing time and computational resources needed to process the data.

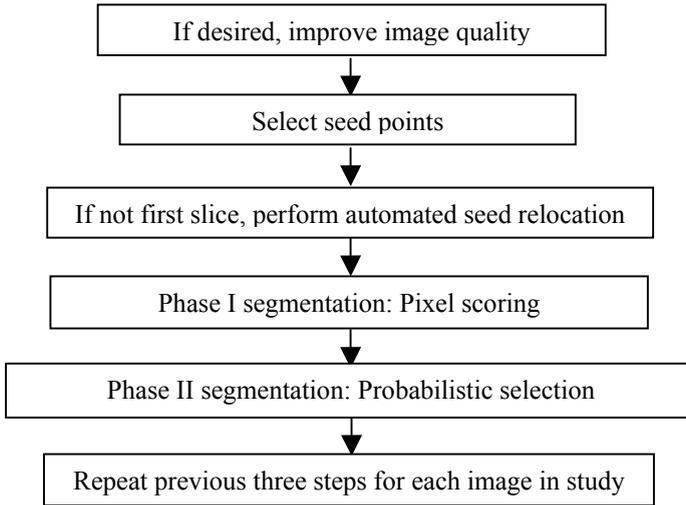


Figure 1: Flowchart of segmentation process.

3.2 Digital image enhancement – Unsharp mask filtering

Naturally, image quality has an extensive effect on the segmentation process. The quality of an acquired image is dependent on: 1) the type and complexity of the equipment used, 2) noise during data acquisition, and 3) the resolution of the image. When the quality of an image is poor, enhancement can be performed to increase the contrast between pixels of different organs to improve the results of segmentation. Thus, an unsharp mask algorithm (USM) was added to the segmentation method. The concept of unsharp mask filtering [5-7] is different from regular image sharpening algorithms in that it involves initially blurring the image to produce a low pass filtered version. The blurred version is then subtracted from the original version, leaving only the high pass filtered portion of the image or a sharper image. This can be mathematically expressed as:

$$f_s(x, y) = Af(x, y) - Bf_b(x, y) \quad (2)$$

where $f_s(x, y)$ denotes the final sharpened image, and $f_b(x, y)$ represents the blurred (low pass filtered) version of $f(x, y)$, the original image. A and B represent positive constants with $A \geq B$ and $A - B = 1$. The constants A and B denote how much information from the original image is used in the new image. As A gets

relatively larger than B, more information from the original image is retained. The condition of $A-B=1$ guarantees that the resulting intensity level is of the same magnitude as the original. Typical values for A and B would be 2 and 1, respectively. In this research many value combinations were used to explore their effect on the segmentation process.

A user has the option whether to apply unsharp masking to the dataset based on initial image quality. Using the unsharp algorithm sometimes introduces noise into the resultant image. To account for this, an additional noise filtering algorithm is available. This algorithm eliminates most of the noise in the image while still maintaining the heightened contrast between image objects.

3.3 Seed selection and relocation

The segmentation process is initialized by the selection of seed pixels. The user selects a defined number of pixels as seeds within the target object. The suggested minimum number is five, but can be changed by the user. This selection only occurs on the first image slice. For the remaining slices the seed points are repositioned automatically. During this stage, each seed's location from the previous slice is mapped onto the current slice. These newly mapped pixel intensities are compared to the corresponding intensity of the original seed pixels known to be in the object of interest. If they are not equal, the algorithm evaluates the pixels surrounding the new pixels for equal or similar intensities using a greedy optimization search. If a pixel with the desired intensity value or within a small user specified percentage (usually 2-5%) is found, it becomes the new seed. Otherwise, the algorithm reverts to the seed mapped from the previous slice.

Once new seeds are set, a similarity criterion for each seed is created. This criterion is defined as a set of ranges of pixel intensity values. The intensity value of each seed is used as the median with a user prescribed deviation to define the range.

3.4 Phase I segmentation – Pixel scoring

This is the first of two steps of actual segmentation. In this phase every pixel within a local neighborhood for a given seed is evaluated and compared to the similarity criterion for that seed. When a pixel satisfies the similarity criterion for a specific seed i , it is allocated a score of one.

$$S(x, y) = \begin{cases} 1 & b_{low}(i) \leq I(x, y) \leq b_{upper}(i) \\ 0 & b_{low}(i) > I(x, y), b_{upper}(i) < I(x, y) \end{cases} \quad (3)$$

where $S(x, y)$ is the score of a particular pixel, and $b_{low}(i)$ and $b_{upper}(i)$ are the upper and lower values of the intensity range for that seeds' similarity selection criterion. This phase is a thresholding process.

By applying a scoring system, the algorithm can eliminate the selection of regions by seeds that are not within the object of interest. A seed can lie outside



the object when the automated relocation process does not locate a new seed in the object.

Once scoring of all pixels is completed for each seed, the number of points attained by each pixel is tallied and analyzed. Only pixels that have obtained scores equal to or more than the minimum score requirement, S_{\min} , are selected and grown. The minimum score is set to be at least half of the number of seeds used for region growing. For example, if five seed points are used, the minimum score is set to be three. Based on the scoring system, pixels are then segmented into regions, $R(x,y)$. Pixels are allocated a value of one if they meet S_{\min} and are defined to be in the object.

$$R(x, y) = \begin{cases} 1 & S(x, y) \geq S_{\min} \\ 0 & S(x, y) < S_{\min} \end{cases} \quad (4)$$

The scoring system ensures that pixels are only grown in a region when the similarity selection criteria of multiple seed points are satisfied. This greatly improves the confidence that a selected pixel is truly part of the object.

3.5 Phase II segmentation – Probabilistic selection

The second phase of segmentation provides a second chance to pixels that were not selected in pixel scoring. Unlike the first phase that uses information from all seeds, this phase is an independent process for each seed.

This is the most unique aspect of this method. It is a probabilistic approach to pixel evaluation. To do this, the Monte Carlo algorithm [13] was implemented. Monte Carlo is very popular in heuristic optimization and uncertainty methods such as Simulated Annealing (SA). Monte Carlo provides a way to generate an acceptance probability for a current design point (e.g., a pixel). A second probability is generated randomly and the two are compared. Depending on the outcome the design point is accepted or rejected.

In this phase each seed is used to individually grow a region. For each pixel that was not selected previously a probability is generated and is compared to a randomized probability. If the pixel's probability exceeds the randomized probability it is accepted into the region. The probability selection criterion developed is based on the Monte Carlo probability selection criterion used in the Simulated Annealing (SA) heuristic optimization algorithm.

The probability of a pixel being accepted into the object region during this phase depends on two key factors:

1. the distance of the pixel from the seed
2. the difference between the intensity of the pixel to the intensity of the current seed

The further away a pixel is from the seed location, the lesser the probability of it being accepted into the active region. The probability will also decrease as the difference between the intensity values of the pixel and the seed point increases.

The distance of the current pixel from a seed can be defined as $r_{region}(x,y)$:

$$r_{region}(x, y) = \sqrt{(x_{seed} - x)^2 + (y_{seed} - y)^2} \quad (5)$$



where x_{seed} and y_{seed} are the coordinates of the seed, and x and y are the coordinates of the current pixel. The variable r_{max} is defined as the maximum allowable value for $r_{region}(x,y)$, and controls the radius of the search within the image. By default this value is assumed to be the distance between two corners of an image separated diagonally. Thus, the segmentation computations will still occur if a seed is placed in a corner and the pixel examined is in the corner diagonally opposite. The largest value r_{max} can be is:

$$r_{max,default} = \sqrt{R^2 + C^2} \quad (6)$$

where R and C are the number of row pixels and column pixels in the image, respectively. However, r_{max} can be adjusted relative to the default value, such as, $0.25(r_{max,default})$ if a smaller search radius for each seed is desired.

The ratio of the radius of the search region, $r_{region}(x,y)$ to the maximum allowable r_{max} is denoted as r_2 and defined as:

$$r_2(x, y) = 1 - \frac{r_{region}(x, y)}{r_{max}} \quad (7)$$

The difference between the intensity of the seed, I_{seed} , and the intensity of the current pixel, $I(x,y)$ is defined as, $\delta(x,y)$:

$$\delta(x, y) = |I_{seed} - I(x, y)| \quad (8)$$

Following this computation, a pixel's selection probability taken from the SA algorithm is computed as:

$$Pr_1(x, y) = e^{-a} \quad (9)$$

$$a = \frac{\delta(x, y)}{r_2(x, y)} \quad (10)$$

From equations (10) and (11), Pr_1 approaches a value of 1 as δ gets smaller, or as r_2 gets larger. Once Pr_1 is computed, the second probability, Pr_2 , a random floating point number between zero and one is generated. The two probabilities are compared simply by:

$$R(x, y) = \begin{cases} 1 & Pr_1 \geq Pr_2 \\ 0 & Pr_1 < Pr_2 \end{cases} \quad (11)$$

A score of one assigns the pixel to the object, whereas zero does not. Unlike the first phase, any pixel satisfying this criterion for any seed is accepted as an object pixel.

4 Discussion of results

The method was applied to three medical data studies. Due to space limitations, only results for one of the three test cases are presented in this paper. There are significant improvements when using the probabilistic segmentation algorithm as opposed to a conventional segmentation technique such as thresholding. The regions extracted were visually more complete. Also, the method was also able to capture when a single object turned into multiple ones in a study. The dataset



presented is an MRI study of the abdomen and kidney section of the body. Each slice is 512 pixels by 512 pixels resolution in 16-bit greyscale with 50 slices in the study. The object selected for segmentation is the aorta, which in this study moves down the abdomen and splits into two vessels around the kidneys.

Figure 2 shows two versions of slice #111, the original and the image obtained after processing by USM sharpening. Comparing the images in Figure 2, the USM process has been able to define and highlight details that are not as readily apparent in the original image. The mixture of organs is more clearly delineated and thus sizes and deformities (if present) are more readily viewable. It is this qualitative comparison that is commonly used to compare image enhancement and segmentation techniques. These datasets do not have known solutions, thus no quantitative comparison can be made as to the number of pixels selected versus a known quantity.

Figure 3 illustrates the process of seed relocation as the object's characteristics change from slice to slice. The arrows indicate the location of the seeds. Since the changes in seed locations between individual slices are small, the results are shown in intervals of 10 slices to demonstrate trends. It is observed that the seed relocation algorithm accurately placed seed pixels in both parts of the object when it split into two regions.

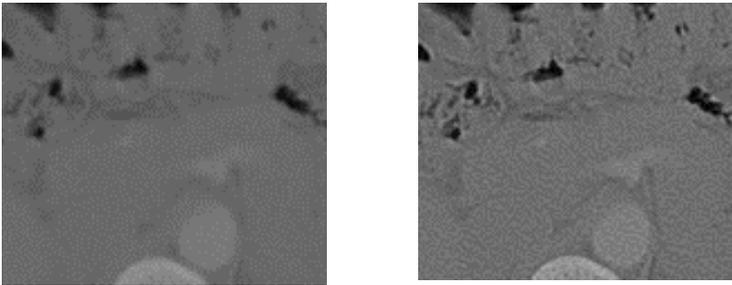


Figure 2: Comparison of the original image (left) and image after unsharp masking sharpening (right) for slice #111 of dataset.

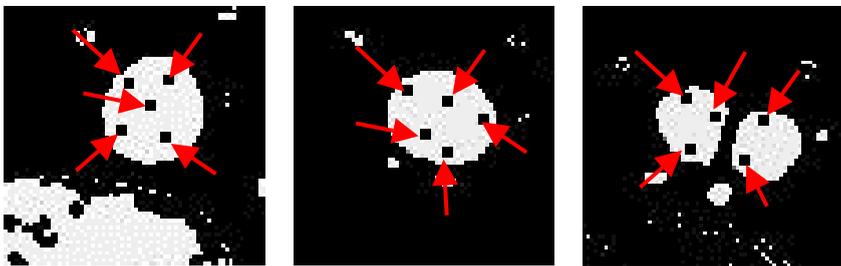


Figure 3: Illustration of the automated seeds relocation algorithm for 3 slices in a dataset (slices #101, #111, and #121 from left to right).

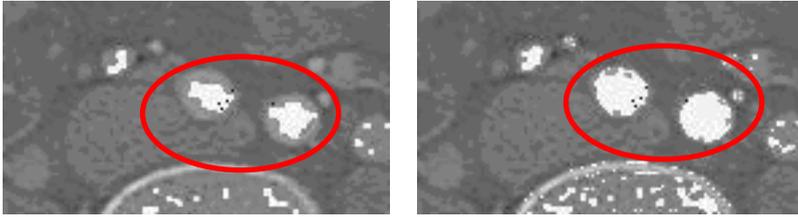


Figure 4: Comparison of the object from conventional thresholding (left), and the object from the 2-phase segmentation (right) on slice #133.

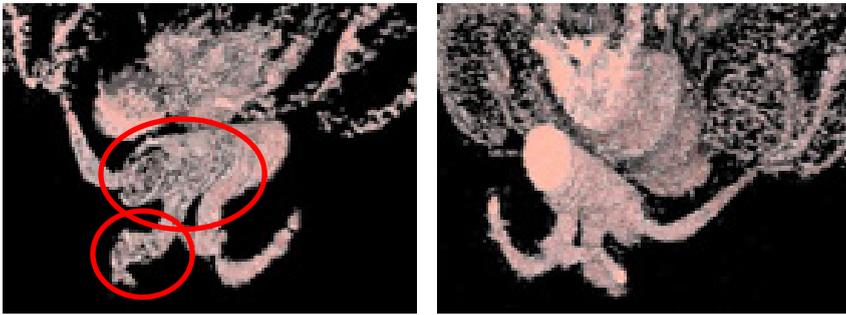


Figure 5: Volume renders of segmented object with thresholding segmentation (left), and probabilistic segmentation (right).

The effects of the probability selection of the segmentation method are shown in Figure 4. The object of interest is highlighted in circles. The image on the left was processed using regular thresholding segmentation, while the image on the right was processed with the probabilistic segmentation method. The improvement achieved can be clearly seen in the figure. The probabilistic segmentation method identified the object completely during segmentation, whereas conventional thresholding only selected the object partially.

Figure 5 compares segmentation methods through 3D volume rendering for the entire study. The extracted object has been identified as smaller arteries splitting from the aorta. Again, it is clearly shown that the probabilistic segmentation method selects the aorta and associated vessels coming out of it much more completely than conventional thresholding. Particular areas of weakness for thresholding segmentation have been circled in the figure.

5 Conclusions and summary

This paper presented a new segmentation method incorporating probabilistic mathematics to aid in pixel selection. The method is a multi-phase approach with image sharpening and a two phase segmentation process for object creation from a digital medical study. The test cases performed have shown significant

improvement in visual clarity and object selection compared to conventional segmentation techniques. The multi-phase segmentation method not only manages to capture multiple regions belonging to a single object, it also manages to select “stray” pixels that otherwise wouldn’t have been selected with ordinary selection criteria. In addition, much of the processing has been completely automated. A user need only select a small number of seed pixels in a single image at the beginning to have a full 3D object segmented.

Although the results are encouraging, there is still significant work to be performed. First, an improved criterion for the scoring phase of segmentation needs to be developed. Second, a method to map the original greyscale image into an interpolated colour space may help to improve pixel selection. Lastly, more advanced probability methods need to be explored to further refine the segmentation process.

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