Liver tumor volume estimation

Lu, Rui

2006

Lu, R. (2006). Liver tumor volume estimation. Master's thesis, Nanyang Technological University, Singapore.

<https://hdl.handle.net/10356/4837>

<https://doi.org/10.32657/10356/4837>

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Liver Tumor Volume Estimation

Lu Rui

School of Electrical & Electronic Engineering

A thesis submitted to the Nanyang Technological University
in fulfillment of the requirement for the degree of
Master of Engineering

2006

Acknowledgments

First of all, I would like to thank all the people who have contributed directly or indirectly in helping me go through the whole period of my candidature. I would like to extend my deepest appreciation to the following people:

- My sincere thanks to my supervisor, Assistant Professor Pina Marziliano, for her valuable comments on my work and her timely assistance and support, and for always being so patient with me when I felt deeply depressed and could not go on with anything.
- I would also like to thank Dr Thng Choon Hua, Doctor of the Department of Oncologic Imaging, National Cancer Centre of Singapore, for giving me valuable suggestions from the medical side and providing all the data used in this study.
- Big thanks to my parents who have always supported me and encouraged me whenever I am confronted with any difficulties. I thank them for all the things they have done for me.
- Thanks to my boy friend Feng Chen who helps me through all this and brings fun to my life.
- Last but not least, I would like to thank Yanyan, also student of Prof

Marziliano, who has always shared her research experience with me and made the lab an interesting place for work.

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Summary

Liver cancer is one of the most popular diseases around the world and it causes a large amount of death every year. For an accurate diagnosis of this disease, there is a great need to estimate the volume of liver tumors from CT abdominal images for both the assessment of response to chemotherapy and the diagnostic decision on tumor resection. The goal of this research is to estimate the liver tumor volume by segmenting the liver tumor and reconstructing the 3D volume by interpolation.

In this study, two new methods to extract the liver tumor regions are developed. The first method involves a combination of thresholding, morphological operations and Fuzzy c-Means clustering techniques. Results show that tumor lesions, except the ones close to the liver brink, can be effectively extracted from the CT images. The second method uses an active contour model to detect the boundaries of the tumors. In this method, the tumor region is extracted based on the minimization of an energy function and it yields a good description of the tumor boundary, while the initial contour has to be indicated by an operator manually.

Interpolation methods for the reconstruction of 3D volume are also studied in this thesis. We implemented five methods on four sets of data obtained from the National Cancer Centre of Singapore: linear, cubic spline, modified cubic spline,

Dirichlet apodization and Hanning apodization. Results show that, contrary to the 1D and 2D cases in the literature, the linear method performs as well as the other methods due to the relative large inter-slice distance with only about half the computational load. We also used shape-based interpolation on our segmented contours to achieve higher resolution, while saving a lot of time by performing interpolation after, rather than before segmentation.

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Chapter 1

Introduction

1.1 Motivation

Primary liver cancer (cancer that starts in the liver) is one of the most common malignancies in the world and it causes a large amount of death every year. The American Cancer Society estimates that 17,550 new cases of primary liver cancer and bile duct cancer will be diagnosed in the United States during 2005. About 15,420 people will die of liver cancer in the United States during 2005 [1]. In contrast to many other types of cancer, the number of people who get liver cancer and die from it is increasing. What is more, this cancer is about 10 times more common in developing countries in East Asia, Africa, and Asia than in the US. In many of these countries, liver cancer is the most common type [1]. In order to make diagnostic decisions such as liver resections, doctors will need to know the tumor volume, and further, the functional liver volume, which is equal to the liver volume minus the tumor volume. Thus, an important task in radiology is the determination of tumor volume. The estimation of liver tumor volume also finds its application in the evaluation of chemotherapies applied to

1.1. Motivation

cure liver metastases. Metastases are secondary lesions induced by an original cancer. The liver is a common site of metastatic disease.

The examination of liver tissue pathology is performed with various medical imaging modalities such as ultrasonography(US), computed tomography(CT) and magnetic resonance imaging(MRI). CT is one of the most common and robust imaging techniques for the detection of liver lesions and is known for its sensitivity at detecting differences in density of the various tissues in a cross-section. Based on CT images, computer-aided diagnostic (CAD) systems have been developed to help doctors diagnose precisely and objectively. However, until now there has been little research focused on the liver compared with other organs such as the lungs, brain, breasts, etc. This is due to the many difficulties in understanding the various aspects of liver disease [2].

Estimation of the liver tumor volume involves several operations and the accurate segmentation of liver tumor from an abdominal image is one of the most important steps in 3D representation for liver volume measurement, liver transplant, and treatment planning [3]. In order to estimate the tumor volume, it is necessary to well and consistently segment the lesion from the whole image. Since manual segmentation is inconvenient, time consuming and depends on the individual operator to a large extent, automatic segmentation is much more preferred.

In order to enhance the raw segmentation result, interpolation or other reconstruction methods are required to retrieve the intermediate contour images. Interpolation is widely used to decrease the inter-slice distance, which makes it a fundamental operation in medical image processing. In volume estimation, interpolation is also needed to achieve higher accuracy.

1.2. Objectives

1.2 Objectives

The objectives of this study are to develop a scheme of CT abdominal image processing for the purpose of liver tumor volume estimation. The proposed scheme should have the following functions:

1. Automatic or semi-automatic liver tumor boundary extraction.
2. 3D interpolation of the segmented tumor, which is supposed to enhance the segmentation result.
3. Volume calculation based on the segmented and interpolated pieces.

1.3 Major Contributions of the Thesis

In this thesis, we describe a novel scheme for the estimation of the liver tumor volume based on CT abdominal images. We solve this medical problem of volume estimation by breaking it down into two image processing problems: segmentation and interpolation. This scheme assists radiologists in their routine work and promises to provide more precise evaluation than the manual practice. In addition, this scheme can be easily extended to the processing of images of other organs, such as brain, lung and stomach.

Another major contribution is that we manage to incorporate *a priori* information into our segmentation methods rather than using only the gray-scale intensity values. For example, anatomical knowledge is used in the first segmentation method to help segmenting the liver. By exploring the area and position of the liver, we successfully segment the liver tissue using an adaptive thresholding method.

1.4. Organization of the Thesis

We also manage to reduce human input from the operator, such as seed point placing, or initialization of parameters. In this study, parameters are determined in advance on the basis of the analysis of various images. In both segmentation methods, we determine the parameters of the models by analyzing the image features.

We compare five different interpolation methods and make conclusions for our case. In addition, we use a shape-based interpolation method to interpolate between the segmented tumor contours, which saves the processing time for segmentation to a large extent.

Finally, we develop criteria for the evaluation of segmentation and interpolation methods. The common evaluation criteria in image processing are usually not valid for medical images and the policy to judge a processing method is to evaluate its performance from the clinical side. In this study, we develop some objective measures that are to some extent in accordance with the clinical measures.

1.4 Organization of the Thesis

The rest of this thesis is organized as follows:

Chapter 2 gives a brief review of the medical background of our problem. We introduce the reporting and evaluation of tumor in the medical world and discuss the difficulties associated with the segmentation of the liver tumor. Our approach to the volume estimation problem is also stated in this chapter.

In Chapter 3, we review the existing segmentation methods and interpolation methods. Some of the most commonly used segmentation and interpolation methods are introduced here with their features and characteristics analyzed.

1.4. Organization of the Thesis

Chapter 4 describes our new hybrid segmentation method. The details of each step of this method are introduced first. We then describe the implementation and give discussions.

In Chapter 5, we present a segmentation method based on the active contours to segment liver tumors. We first introduce the concept of active contour models and energy functions. Then we describe our approach to use this for tumor segmentation. Implementation results and discussions are given.

In Chapter 6, we investigate several interpolation methods and evaluate their performances with respect to the signal-to-noise ratio. We then introduce the shape-based interpolation method and use it on our segmented tumor set. We also visualize the tumor based on the original set and the interpolated set.

Conclusions and recommendations for future research are presented in Chapter 7.

Chapter 2

Medical Background and the Proposed Scheme for Volume Estimation

2.1 Medical Background

2.1.1 Liver Cancer

A tumor is an abnormal lump or mass of tissue. Tumors can be benign (not cancerous) or malignant (cancerous). Liver cancer is one of the most common malignancies in the world and is much more prevalent in many of the developing countries than in the industrialized world. Its incidence is highest in sub Saharan Africa, China, Southern Asia, and Japan. Japan is the exception of the industrialized countries. China accounts for about 45% of the world's cases [4]. Because liver cancer is rarely discovered early, the prognosis is often poor. Yet even in advanced cases, treatment can help relieve symptoms and improve quality of life.

2.1. Medical Background

Two choices are available to treat liver metastases or liver cancer: hepatic surgery, with partial resection of the liver (hepatectomy) or chemotherapy. In both cases, it is of great use to evaluate the relative size of the lesions and an important issue associated with the measurement is a standard criteria for reporting the tumor size, which we will discuss in detail in Section 2.1.3.

2.1.2 Imaging Modality

Computed Tomography (CT) is a powerful nondestructive evaluation (NDE) technique for producing 2D and 3D cross-sectional images of an object from flat X-ray images. A typical CT imaging system is shown in Figure 2.1. A very important area of the application of CT, which is rapidly growing in importance, is the radioactive treatment of tumors. In this study, we use CT abdominal images to aid liver disease diagnosis for it offers high quality images that enable doctors to look into patients' bodies at a relatively low cost. A typical CT abdominal image is shown in Figure 2.2.

2.1.3 Evaluation of Response to Treatment

Advances in cancer therapy are made by continual investigation and evaluation of treatment results and their incorporation in the practice of oncology. This requires comparisons between results and necessitates the availability of appropriate data in a suitable form. Thus, standardization of assessment and of reporting of results is an important step that aims at increasing the amount of usable therapeutic information at the disposal of the physician [5].

For this purpose, two existing standards are commonly used:

2.1. Medical Background

Figure 2.1: A Computed Tomography system (Siemens Somatom Sensation 64).

2.1. Medical Background

Figure 2.2: A typical CT abdominal image.

2.1. Medical Background

1. WHO Criteria

In 1981, the International Union Against Cancer and the World Health Organization(WHO) developed uniform guidelines [5] so that the results of different trials could be compared. This criteria measures the tumor by multiplying the longest perpendicular diameters in the axial plane and has become the most commonly used by investigators around the world [5].

2. RECIST

RECIST stands for Response Evaluation Criteria in Solid Tumors [6]. It was developed by a joint effort of the European Organization for Research and Treatment in Oncology, the National Cancer Institute of the United States, and the National Cancer Institute of Canada Clinical Trials Groups. It measures the tumor in an unidimensional way, i.e., the longest lesion diameter in the axial plane [6].

The comparison of these two standards are given in Table 2.1. Although these two standards are widely used in practice, recent researches show that, however, they are not as precise as the volumetric assessment. In [7], Prasad *et al* compared unidimensional methods (RECIST), bidimensional (WHO) and volumetric assessment and found that volumetric assessment gave different results in 12 out of 37 patients. In [8], Ercolani *et al* showed that the total volume of metastases was the strongest predictor of survival in patients with colorectal liver metastases and not the number nor the location of metastases. In [9], Van Hoe *et al* showed that 3D measurements are reproducible and may potentially replace 1D or 2D measurements, which indicates the feasibility and possibility of 3D tumor volume measurements.

2.2. Proposed Scheme for Volume Estimation

Table 2.1: Treatment-response classification and tumor measurement techniques [10]

Category	WHO Criteria (area)	RECIST (diameter)
Complete response	Tumor disappearance	Tumor disappearance
Partial response	50% reduction in cross-product	30% reduction in diameter
Stable disease	Size between that for partial response and that for progressive disease	Size between that for partial response and that for progressive disease
Progressive disease	25% increase in cross-product	20% increase in diameter

2.2 Proposed Scheme for Volume Estimation

2.2.1 The Proposed Scheme

In this study, we have a set of images of the same patient, which all consist of several objects, and our aim is to reconstruct the volume of a specific object. We show this in Figure 2.3.

In this study, we solve this by the following steps:

1. Automatic or semi-automatic tumor segmentation.
2. Interpolation between the segmented contours.
3. Volume estimation using the interpolated contours.

2.2. Proposed Scheme for Volume Estimation

Figure 2.3: Illustration of the volume estimation problem.

2.2.2 Difficulties in Liver Tumor Segmentation

Segmentation is the most important and also most difficult part of this problem. Although segmentation of organs and lesions has been a hot research topic, little has been focused on the liver area. There are several factors associated with this:

1. First, other internal organs such as the kidney, heart, and stomach are located adjacent to the liver.
2. Second, the difficulty also lies in the fact that the intensity of the liver and liver tumor are different for different patients. The intensity also depends on the imaging circumstances, such as the parameter of the CT machine.
3. Noise is always existent in these images, which further adds to the difficulty of perfect segmentation.

Chapter 3

Segmentation and Interpolation Methods

3.1 Segmentation Methods

3.1.1 Medical Image Segmentation

Diagnostic imaging is an invaluable tool in medicine. Magnetic resonance imaging (MRI), computed tomography (CT), digital mammography, and other imaging modalities provide an effective means for noninvasively mapping the anatomy of a subject. These technologies have greatly increased knowledge of normal and diseased anatomy for medical research and are a critical component in diagnosis and treatment planning [11].

The growing size and number of these medical images have necessitated the use of computers to facilitate processing and analysis. In particular computer algorithms for the delineation of anatomical structures and other regions of interest are becoming increasingly important in assisting and automating specific radio-

3.1. Segmentation Methods

logical tasks. These image segmentation algorithms play a vital role in numerous biomedical-imaging applications, such as the quantification of tissue volumes, diagnosis, localization of pathology, study of anatomical structure, treatment planning, and computer-integrated survey.

The purpose of segmentation is to extract object information from given scenes and to output this as a structure system. Segmentation is needed for most of the 3D imaging operations. It is also the most difficult out of all the operations. Segmentation may be thought of as consisting of two related tasks—recognition and delineation [12]. Recognition is the high-level task of determining roughly the whereabouts of the object in the scene. Delineation is the low-level task of determining the precise spatial extent of the object and its graded composition.

Approaches to recognition may be broadly classified into two groups: automatic and human assisted. In automatic methods, one of two approaches is taken. In the knowledge-based approach, artificial intelligence techniques are used to represent knowledge of objects in the body region of interest. Usually, a preliminary delineation of objects is done first and then object hypotheses are formed and tested. This loop may be executed several times before an acceptable solution is found. For the atlas-based approach, an atlas representing the geometry and topological relationships of the objects in the body region is constructed first. Subsequently, certain geometric entities, such as points, ridges, contours, and anatomic planes, identified in the given scene (delineation step) for the same body region are mapped to match with homologous entities in the atlas. This mapping is then applied to the whole scene to recognize object regions/boundaries in the scene from such information stored in the atlas [12]. In most recognition tasks, trained human operators outperform any computer algorithms. On the contrary, computer algorithms exist that are more precise,

3.1. Segmentation Methods

accurate, and efficient than human delineation of object regions. The most general approach to segmentation, manual contour tracing, is time-consuming and inaccurate. Therefore, manual segmentation is unacceptable for large 3D data sets.

In medical applications, it is important to distinguish between two types of recognition tasks, the first for identifying pathological growths such as lesions in the breast and lungs via X-ray projection images, and the second for identifying the anatomic organs in scenes [12]. The pathologies are detected commonly via the classical two-stage pattern recognition approach: scene-intensity-based feature extraction and pattern classification. Unfortunately, this paradigm is ineffective for the second task of recognizing anatomic organs. As such, approaches that consider shape of and relationship among objects are preferred.

Approaches to delineation, on the other hand, are studied far more extensively than those for recognition. In fact, usually delineation itself is considered to be the total segmentation problem. That is, whatever is output by the delineation method is considered to represent the object of interest. Two classes of methods exist for delineation: boundary based, in which the output structure represents the boundary of the object, and region based, in which the output structure represents the region occupied by the object. In both groups, the output structure may be hard (crisp) or fuzzy. In the hard case, the structure is a hard set of certain elements, each with a membership value in the structure of either 0 or 1. This representation does not allow capturing graded composition of objects. In the fuzzy case, the structure is a fuzzy set with a degree of membership (between 0 and 1) associated with each element [12].

If we combine the two strategies of recognition—automatic and human assisted—with the four groups of delineation approaches, there are eight classes of segmen-

3.1. Segmentation Methods

tation strategies possible, as shown in Figure 3.1.

Figure 3.1: Classification of segmentation methods.

3.1.2 Boundary-Based Methods

1. *Hard, Boundary-Based, Automatic Methods*

There are mainly two classes of approaches for creating hard boundary representations of objects from scenes of their body region. In the first group, it is assumed that an object surface is specifiable via a fixed scene intensity threshold value. That is, the surface in the scene domain on which the scene intensity is the specified value is taken to be the structure representing the object. This group of approaches is commonly referred to as iso-surfacing. In the second group, the rate of change of scene intensity (scene intensity gradient) is used to locate and form the boundaries [12]. These are known as gradient based methods.

3.1. Segmentation Methods

There are two popular groups of iso-surfacing methods. The first is the digital surface method, which outputs a digital representation of the object surface. The second group of methods output the object surface as a set of triangular or other polygonal elements and are usually referred to as polygonal surface methods.

The gradient-based method lies on the fact that in the vicinity of the object boundary, the magnitude of the intensity gradient is much greater than at points far away from the boundary. The result of edge detection depend on the gradient mask and some examples of masks are Sobel, Roberts, Prewitt and Robinson. The advantage of these kinds of methods is that they are computationally fast and do not require *a priori* information about the image content. The disadvantage is that often the edges do not enclose the object completely.

2. *Fuzzy, Boundary-Based, Automatic Methods*

The mathematical concepts of closure, orientedness and connectedness have not been developed in a fuzzy setting for defining boundaries, unlike in the hard setting discussed in the Hard, Boundary-Based, Automatic Methods. Computational methods, however, have been proposed that are used in volume visualization. The basic idea is to somehow assign a degree of boundary-ness to every voxel in the scene without worrying about connectedness, orientedness, or closure properties [12].

3. *Hard, Boundary-Based, Assisted Methods*

The simplest method in this category is the slice-by-slice manual outlining of object boundaries. When the object regions have multiple contours and/or holes in the slices, even this simple idea poses challenges to imple-

3.1. Segmentation Methods

ment, especially if we need to obtain a binary scene representation of the segmented structure.

We will describe two commonly used methods in this category.

- *Active Contours*

A class of more sophisticated assisted methods has evolved during the past 10 years whose aim is to minimize the degree of assistance needed. These are usually referred to as active contour, active boundary, and snakes. Active contours, proposed by M. Kass *et al* in [13], are one kind of deformable model. In this model, first, an initial contour is specified which lies in the vicinity of the edge of interest. Then this contour is deformed algorithmically to make it drawn toward the edges in the image. A deformation energy function defined in terms of the geometric degrees of freedom is associated with the deformable model. The energy grows monotonically as the model deforms toward the target edges. A central problem in the use of snakes is the choice of appropriate forms for the energies. Since it is difficult to guarantee that the optimization process finds the global minimum of the energy, usually the contour shape corresponding to a local minimum is found and accepted. The more important considerations are: (1) accuracy—the degree to which the contour found agrees with the true boundary; (2) precision—the extent of repeatability of the method; and (3) efficiency—the extent of operator help taken by the method, especially compared to manual boundary tracing. Although these methods are used in a variety of applications, their precision and efficiency do not seem to have been evaluated carefully [12].

3.1. Segmentation Methods

- *Live Wire*

Live wire [14], also known as intelligent scissors, is another approach to interactive boundary detection. With live wire the segmentation process is directly steered by the user who has immediate control over the automatically suggested object contours. The contours are found as minimal paths with respect to a cost function similar to the external energy function of active contours.

3.1.3 Region-Based Methods

1. *Hard, Region-Based, Automatic Methods*

These methods can be considered to output a binary scene in which the voxel with intensity 1 represents the region occupied by the structure. The input is a set of scenes representing the same body region. Two classes of methods may be identified: thresholding and clustering.

- *Thresholding*

In these methods, a threshold is selected and an image is divided into groups of pixels having values less than the thresholds and groups of pixels with values greater or equal to the threshold. Several methods exist in the literature: global methods based on gray-level histograms, global methods based on local properties, local threshold selection, and dynamic thresholding. Thresholding, however, seldom produces perfect results and is always used together with other methods. In [2], [15] and [16], thresholding was used to retrieve the preliminary liver boundary. Because of its simplicity and efficiency, thresholding is perhaps the most commonly used method.

3.1. Segmentation Methods

- *Clustering*

The basic premise in clustering techniques is that structures manifest themselves as separate clusters of points in a “feature space” of property values. Clustering algorithms achieve region segmentation by partitioning the image into sets or clusters of pixels that have strong similarity in the feature space. In this approach, the segmentation problem is translated into the problem of identifying and delineating clusters in the feature space. One of the most commonly used hard clustering methods is the k -Nearest Neighbor (k NN) method. All clustering methods have parameters whose values need to be somehow determined. If the parameters are fixed in an application, the effectiveness of the method in routine processing cannot be guaranteed. Usually some user assistance becomes necessary eventually for each study [12].

2. *Fuzzy, Region-Based, Automatic Methods*

These methods can be thought of as outputting a gray scene in which the voxel intensity represents the degree of objectness of the specific voxel of the original image. The simplest among these methods is fuzzy thresholding, which is a generalization of hard thresholding. It is commonly used with a single input scene. Many of the hard clustering methods can be generalized to output fuzzy object information. Note that fuzzy thresholding is a form of fuzzy clustering.

An approach to more generalized fuzzy clustering is the fuzzy c-means method [17]. As with hard clustering methods, the effectiveness of fuzzy clustering methods in routine applications cannot be guaranteed; as such,

3.1. Segmentation Methods

some user assistance on a per-scene basis is usually needed. In [2], J. -S. Hong *et al* applied the Fuzzy c-Means method on the extracted liver to segment the tumor region and found that it can determine the threshold regardless of a changing intensity.

3. *Hard, Region-Based, Assisted Methods*

The simplest method in this category is manual painting of regions using a mouse-driven paint brush. This is the region dual of manual boundary tracing. For most medical applications, boundary tracing is perhaps less time consuming than painting of regions.

In contrast to this completely manual recognition and delineation scheme, there are methods in which recognition is manual but delineation is automatic. Region growing is a popular method in this group [18]. Whereas thresholding focuses on the difference of pixel intensities, the region growing method looks for groups of pixels with similar intensities. This algorithm starts with at least one seed per region. Neighbors of the seed are visited and the neighbors that satisfy the condition are added to the region. Pixels that satisfy the condition of more than one region are allocated to one of these arbitrarily [19]. The advantage of region growing is that it is capable of correctly segmenting regions that have the same properties and are spatially separated.

4. *Fuzzy, Region-Based, Assisted Methods*

Since some of the fuzzy, region-based, automatic methods eventually need human assistance for correct segmentation in large, routine applications, these techniques fall in this category; for example, a k NN method, which requires training for each study. One example of this class of methods is

3.1. Segmentation Methods

the fuzzy connectedness technique [12].

3.1.4 Other Approaches

Artificial neural networks (ANNs) are also commonly used segmentation methods. They are parallel networks of processing elements or nodes that simulate biological learning. Each node in an ANN is capable of performing elementary computations. Learning is achieved through the adaptation of weights assigned to the connections between nodes [11]. A variety of neural network architectures have been used for medical image processing, such as: Feed-forward ANN, Kohonen ANN and Hopfield ANN. ANNs represent a paradigm for machine learning and can be used in a variety of ways for image segmentation. The most widely applied use in medical imaging is as a classifier, in which the weights are determined by using training data and the ANN is then used to segment new data. ANNs can also be used in an unsupervised fashion as a clustering method, as well as for deformable models [11].

In addition, mathematical morphology is also widely used for medical image segmentation. The watershed algorithm is a method based on mathematical morphology which partitions images into homogeneous regions [11]. The method can suffer from oversegmentation, which occurs when the image is segmented into an unnecessarily large number of regions. Thus, in medical applications, it is usually followed by a post-processing step to merge separate regions that belong to the same structure.

3.1. Segmentation Methods

3.1.5 Key Challenges of Segmentation

In spite of about four decades of research in segmentation, several key challenges remain [12]:

- To develop general methods that can be easily adapted to a given application;
- To keep human assistance required in practical segmentation on a per-scene basis to a minimum;
- To develop fuzzy methods that can realistically handle uncertainties in data;
- To assess the efficacy of segmentation methods.

Future research in the segmentation of medical images will strive toward improving the accuracy, precision, and computational speed of segmentation methods, as well as reducing the amount of manual interaction. Possibly the most important question surrounding the use of image segmentation is its application in clinical settings. For segmentation methods to gain acceptance in routine clinical applications, extensive validation is required on the particular methods in question [11]. Furthermore, one must be able to demonstrate some significant performance advantage over traditional methods to warrant the training and equipment costs associated with using computerized methods. It is unlikely that automated segmentation methods will ever replace physicians, but they will likely become crucial elements of medical-image analysis. Segmentation methods will be particularly valuable in areas such as image-guided surgery, in which visualization of the anatomy is a critical component [11].

3.2. Interpolation Methods

3.2 Interpolation Methods

Interpolation is a commonly used operation in image processing, computer graphics, and medical imaging. Interpolation methods may be broadly classified into two groups: scene-based and object-based. In scene-based techniques, the intensity values of the resulting interpolated images (scenes) are derived directly from the intensity values of the given scene [20–27]. In object-based methods [28–30], interpolation is not guided systematically by the grid system as in scene-based approaches, but is directed by some object information derived from the scene. There has been repeated evidence in the literature of the superior performance of object-based over scene-based approaches. Shape-based interpolation [28–30] is an example of object-based methods. Its motivation came from applications which required slice-by-slice help from a user for the difficult segmentation task. By doing interpolation after, rather than before, the time to be spent by a user in the segmentation task is significantly reduced in such applications. Although saving user time was the original motivation, it was shown that, in applications where this is not a consideration, segmentation followed by shape-based interpolation gives more accurate results than the conventionally used linear grey-level interpolation followed by segmentation [31].

3.2.1 Mathematical Formulation

Interpolation is the process of estimating the intermediate values of a continuous event from discrete samples [32].

The mathematical formula of classical interpolation is given by [33]:

$$f(\mathbf{x}) = \sum_{\mathbf{k} \in \mathbb{Z}^q} f_{\mathbf{k}} \phi_{int}(\mathbf{x} - \mathbf{k}) \quad \forall \mathbf{x} = (x_1, x_2, \dots, x_q) \in \mathbb{R}^q \quad (3.2.1)$$

3.2. Interpolation Methods

where $f(\mathbf{x})$ is the interpolated function evaluated at some coordinate $\mathbf{x}$ in a space of dimension q , while $f_{\mathbf{k}}$ and $\phi_{int}(\mathbf{x})$ are the sample values and interpolation kernels, respectively.

As an alternative algorithm, the generalized interpolation in a space of dimension q is given by [33]:

$$f(\mathbf{x}) = \sum_{\mathbf{k} \in \mathbb{Z}^q} c_{\mathbf{k}} \phi(\mathbf{x} - \mathbf{k}) \quad \forall \mathbf{x} \in \mathbb{R}^q \quad (3.2.2)$$

where $f(\mathbf{x})$ is the interpolated function, while $c_{\mathbf{k}}$ and $\phi(\mathbf{x})$ are coefficients and interpolation kernels, respectively.

3.2.2 Specific Examples of Basis Functions

In this section, we introduce some of the most commonly used basis functions.

1. *Nearest-Neighbor*

The basis function associated with nearest-neighbor interpolation is the simplest of all. Its expression is given by [33]

$$\phi^0(x) = \begin{cases} 0 & x < \frac{-1}{2} \\ 1 & \frac{-1}{2} \leq x < \frac{1}{2} \\ 0 & \frac{1}{2} \leq x \end{cases} \quad (3.2.3)$$

2. *Linear*

The basis function associated with linear interpolation is widely used because its implementation is quite simple while it performs satisfactorily in

3.2. Interpolation Methods

many cases. Its expression is given by [34]

$$\beta^1(x) = \begin{cases} 1 - |x| & |x| < 1 \\ 0 & 1 \leq |x| \end{cases}. \quad (3.2.4)$$

3. *B-splines*

There is a whole family of basis functions made of B-splines β^n . Their expressions are given by [34]

$$\beta^0(x) = \begin{cases} 1 & |x| < \frac{1}{2} \\ \frac{1}{2} & |x| = \frac{1}{2} \\ 0 & |x| > \frac{1}{2} \end{cases}, \quad (3.2.5)$$

and

$$\beta^n(x) = \sum_{k=0}^{n+1} \frac{(-1)^k (n+1)}{(n+1-k)!k!} \left(\frac{n+1}{2} + x - k\right)_+^n \quad \forall x \in \mathbb{R}, \forall n \in \mathbf{N}, \quad (3.2.6)$$

where by definition

$$(x)_+^n = (\max(0, x))^n \quad n > 0. \quad (3.2.7)$$

4. *Sinc*

The sinc interpolation corresponds to ideal filtering which can hardly be approximated. In application, we often use a certain approximation of the sinc function, which will cause aliasing and blurring. The sinc function is

3.2. Interpolation Methods

given by:

$$\text{sinc}(x) = \frac{\sin x}{x}. \quad (3.2.8)$$

Since no function can be at the same time band-limited and finite support, we cannot find a finite-support synthesis function ϕ for use. Thus, the classical solution is simply to truncate the sinc itself by multiplying it with a finite-support window. This process is named apodization [33].

5. *Dirichlet Apodization*

The Dirichlet apodization is a lazy approach, which is the sinc function multiplied by a rectangular window of size W , defined as [33]:

$$\text{sinc}_W^D(x) = \frac{\sin(\pi x)}{\pi x} \beta^0\left(\frac{x}{W}\right). \quad (3.2.9)$$

6. *Hanning Apodization*

The Hanning apodization is the sinc function multiplied by a Hanning window of size W , which is defined as [33]:

$$\text{sinc}_W^H(x) = \text{sinc}_W^D(x) \left(\frac{1}{2} + \frac{1}{2} \cos\left(\frac{2\pi x}{W}\right) \right), \quad (3.2.10)$$

where W is an even integer.

Of course, there are other kinds of interpolating functions like Key's functions and Schaum's functions, which we will not discuss here since they are not often used in 3-D interpolations for efficiency or other concern.

3.2. Interpolation Methods

3.2.3 Improvements in Interpolation Methods

Various improvements have been made to improve the results of interpolation. In [35], surface information, which is obtained at each voxel using local gradient, is used to guide the interpolation. If the voxel to be interpolated is found on a surface or its vicinity, interpolation is performed along the direction parallel to the surface, otherwise interpolation is done along the vertical z -direction. In [36], correspondence is established between points in consecutive slices, and then this correspondence is used to estimate data between the slices by linear interpolation. In [37], W. -C. Lin *et al* proposed a method to identify a force field acting on one contour and try to distort it to be like the other contour and its advantage lies in its superior capabilities in handling the branching problem and making use of the graphics rendering method for solid objects composed of slices of voxels.

Chapter 4

A New Hybrid Method for Liver Tumor Segmentation

In this chapter, we describe a new hybrid method used to extract tumor boundaries from CT abdominal images. We begin with an introduction of two region-based methods: thresholding and clustering, followed by mathematical morphology. Our method is then described in detail and the implementation results are shown. We compare our results with manually traced contours by experts.

4.1 Thresholding and Clustering

Thresholding and clustering are two commonly used region-based methods which are employed in our experiments and we will describe them respectively in the following sections.

4.1. Thresholding and Clustering

4.1.1 Thresholding

Gray-level thresholding is the simplest, yet often effective, segmentation method. In this approach objects or structures in the images are assigned a label by comparing their gray-level value to one or more intensity thresholds. A single threshold serves to segment the image into only two regions, a background and a foreground; more commonly however, the objective is to segment the image into multiple regions using multiple thresholds.

Thresholds are either global or local, i.e., they can be constant throughout the image, or spatially varying.

- *Global Thresholding*

Global thresholding is based on the assumption that the image has a bi-modal histogram and, therefore, the object can be extracted from the background by a simple operation that compares image values with a threshold value [38]. Once the threshold is set, segmentation is then accomplished by scanning the image pixel by pixel and labelling each pixel as object or background, depending on whether the gray level of that pixel is greater or less than the threshold value. The threshold is usually selected as the minimum between two modes on a histogram. Global thresholding is computationally simple and fast, while it fails if there is a low contrast between the object and the background, and if the image is noisy, which is always the case in medical images.

In Figure 4.1, we show a computer generated image with even illuminance. The histogram and the segmentation result by global thresholding is shown in Figure 4.2. We can see that global thresholding can achieve perfect segmentation in this case. However, if the original image is unevenly illu-

4.1. Thresholding and Clustering

minated, as shown in Figure 4.3, the results will not be satisfactory. We show the histogram and segmentation result of the unevenly illuminated image in Figure 4.4.

Figure 4.1: Original Image for Segmentation. Image taken from Digital Image Processing, Second Edition, Rafael C. Gonzalez and Richard E. Woods.

- *Local (Adaptive) Thresholding*

In many applications, a global threshold cannot be found from a histogram or a single threshold cannot give good segmentation results over an entire image. In these cases, we will have to turn to local (adaptive) thresholding. Local thresholding techniques compute different thresholds for subsections of the image.

Basically, there are two local thresholding methods. In the first one, an image is first divided into rectangular overlapping subimages and the histograms are calculated for each subimage. If a subimage has a bimodal

4.1. Thresholding and Clustering

Figure 4.2: Histogram of the original image and the segmentation result by global thresholding. (a) Histogram of the original image. (b) Segmentation result by global thresholding.

Figure 4.3: Original Image (uneven illumination) for Segmentation. Image taken from Digital Image Processing, Second Edition, Rafael C. Gonzalez and Richard E. Woods.

4.1. Thresholding and Clustering

Figure 4.4: Histogram of the original image and the segmentation result by global thresholding (the uneven illumination case). (a) Histogram of the original image. (b) Segmentation result by global thresholding.

histogram, then the minimum between the histogram peaks should determine a local threshold. If a histogram is unimodal, the threshold can be assigned by interpolation from the local thresholds found for nearby subimages. In the second method, a threshold can be selected using the mean value of the local intensity distribution.

For example, for the image in Figure 4.3, we divide it into 4 subimages, as shown in Figure 4.5. The segmentation results are shown in Figure 4.6. We can see that the result is better than the global thresholding. If we further divide it into more subimages, the result will be further improved.

4.1.2 Clustering

The basic premise in clustering techniques is that structures manifest themselves as separate clusters of points in a “feature space” of property values. The proper-

4.1. Thresholding and Clustering

Figure 4.5: Image subdivided into four individual subimages.

Figure 4.6: Segmentation result by adaptive thresholding.

4.1. Thresholding and Clustering

ties considered may be the original scene intensities or those computed from scene intensities (such as gradients). To identify and define structures, the appropriate clusters in the feature space are identified. Thus, the segmentation problem is translated into the problem of identifying and delineating clusters in the feature space. One of the most commonly used clustering method is the Fuzzy c-Means method.

Common clustering methods are formulated around a criterion function or objective function that is used to express the quality of the clusters. A variety of criterion functions can be designed to fit a particular problem, but the most popular objective function is the within-group sum-of-squared-error function. Let c be an integer, $1 < c < n$, where c is the number of clusters, and let $X = \{\mathbf{x}_1, \dots, \mathbf{x}_n\}$ denote a set of n feature vectors in feature space $\mathfrak{R}^p$; X is the numerical object data; the j th object has $\mathbf{x}_j$ as its numerical representation; x_{jk} is the k th characteristic associated with object j . The within-group sum-of-squared-error function can then be defined as [39]

$$J_1(U, \mathbf{v} : X) = \sum_{k=1}^n \sum_{i=1}^c u_{ik} \|\mathbf{x}_k - \mathbf{v}_i\|^2 \quad (4.1.1)$$

where $\mathbf{v} = (\mathbf{v}_1, \mathbf{v}_2, \dots, \mathbf{v}_c)$ is a vector of (unknown) cluster centers, $\mathbf{v}_i \in \mathfrak{R}^p$ for $1 \leq i \leq c$, $u_{ik} = u_i(\mathbf{x}_k)$ is the membership of $\mathbf{x}_k$ to the i th cluster, and U is a hard or conventional c partition of X . Optimal partitions U^* of X are taken from pairs $(U^*, \mathbf{v}^*)$ that are “local minimizers” of J_1 . Generalization of Equation (4.1.1) to the infinite family called the Fuzzy c-Means functionals is given as follows:

$$J_m(U, P : X) = \sum_{k=1}^n \sum_{i=1}^c (u_{ik})^m D_{ik,A}, \quad (4.1.2)$$

4.1. Thresholding and Clustering

where

$$m \in [1, \infty) \text{ is a weighting exponent on each fuzzy membership,} \quad (4.1.3)$$

$$U \in M_{fcn}, \text{ where } M_{fcn} \text{ is a constrained fuzzy } c\text{-partition of } X, \quad (4.1.4)$$

$$\mathbf{v} = (\mathbf{v}_1, \mathbf{v}_2, \dots, \mathbf{v}_c) \text{ are } c \text{ vector prototypes in } \mathbb{R}^p, \quad (4.1.5)$$

$$A \text{ is any positive definite } p \times p \text{ matrix,} \quad (4.1.6)$$

$$D_{ik,A} = \|\mathbf{x}_k - \mathbf{v}_i\|_A = \sqrt{(\mathbf{x}_k - \mathbf{v}_i)^T A (\mathbf{x}_k - \mathbf{v}_i)}. \quad (4.1.7)$$

Thus, the Fuzzy c-Means theorem is as follows:

Theorem 1 (Fuzzy c-Means (FCM) [39] [40]). Assume $D_{ik,A} > 0, \forall i, k$. Then (U, v) may minimize J_m subject to the constraints given by (4.1.3) to (4.1.7) only if

$$u_{ik} = \left[\sum_{j=1}^c \frac{\|\mathbf{x}_k - \mathbf{v}_i\|_A^{2/(m-1)}}{\|\mathbf{x}_k - \mathbf{v}_j\|_A^{2/(m-1)}} \right]^{-1}, \text{ for all } i, k, \quad (4.1.8)$$

$$\mathbf{v}_i = \frac{\sum_{k=1}^n (u_{ik})^m \mathbf{x}_k}{\sum_{k=1}^n (u_{ik})^m}, \text{ for all } i. \quad (4.1.9)$$

The FCM procedures approximately minimize J_m by Picard iteration through Equation (4.1.8) and Equation (4.1.9). A brief specification of these procedures is given below.

Algorithm 1 (Fuzzy c-Means (FCM) Algorithm [40]).

Step 1. Given unlabelled data set $X = \{\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n\}$. Fix $c, T, \|\cdot\|_A$, and $\epsilon > 0$.

Step 2. Initialize $U_0 \in M_{fcn}$. Choose $m > 1$. Compute all c weight vectors $\{\mathbf{v}_{i,0}\}$.

4.1. Thresholding and Clustering

Step 3. For $t = 1, 2, \dots, T$

(i) (a) Compute all $c \times n$ memberships $\{u_{ik,t}\}$; (b) Update all c weight vectors $\{\mathbf{v}_{i,t}\}$.

(ii) Compute

$$E_t = \|\mathbf{v}_t - \mathbf{v}_{t-1}\| = \sum_{i=1}^c \|\mathbf{v}_{i,t} - \mathbf{v}_{i,t-1}\|. \quad (4.1.10)$$

(iii) If $E_t \leq \epsilon$, stop, $u_{ik}^ = u_{ik,t}$, $\mathbf{v}_i^* = \mathbf{v}_{i,t}$; else, next t .*

End.

Usually, the fuzzy partition U_{FCM} obtained by FCM is subsequently defuzzified using the maximum membership conversion, which is defined as follows.

Maximum membership (MM) conversion of U in M_{fcnu} to U_{MM} in M_{cn} [40]:

$$u_{MM_{ij,k}} = \begin{cases} 1, & u_{ij,k} \geq u_{ij,s}, 1 \leq s \leq c, s \neq k, \\ 0, & \text{otherwise,} \end{cases} \quad (4.1.11)$$

for $1 \leq k \leq c$, $1 \leq i \leq m$, $1 \leq j \leq n$.

Here M_{fcnu} and M_{cn} stands for the sets of unconstrained fuzzy and crisp c -partitions of X , respectively.

Tissue class assignments for these segmentations are subsequently done by human operators.

In Figure 4.7 and Figure 4.8, we show a computer generated image and the segmentation result by FCM.

4.1. Thresholding and Clustering

Figure 4.7: Original image generated by Matlab.

Figure 4.8: Segmentation result of FCM.

4.2. Mathematical Morphology

4.2 Mathematical Morphology

Morphology offers a unified and powerful approach to numerous image processing problems. The power of mathematical morphology stems from the fact that any translation invariant operator between complete lattices can be represented by means of elementary morphological operators. An image operator can be built by composing elementary morphological operators. In this section, we will discuss four basic morphological operators: dilation, erosion, opening and closing [38], which we will use for our image processing. Examples of these operators can be found in Figure 4.9.

Dilation Dilation generally expands an image. With A and B as sets in $\mathbb{Z}^2$, the dilation of A by B , denoted $A \oplus B$ and defined by [38]

$$A \oplus B = \{z | (\hat{B})_z \cap A \neq \emptyset\}, \quad (4.2.12)$$

where $\hat{B}$ is the reflection of set B and given by

$$\hat{B} = \{w | w = -b, \quad \text{for } b \in B\}, \quad (4.2.13)$$

and $(A)_z$ is the translation of set A by point $z = (z_1, z_2)$ defined as

$$(A)_z = \{c | c = a + z, \quad \text{for } a \in A\}. \quad (4.2.14)$$

Equation (4.2.12) is based on obtaining the reflection of B about its original and shifting this reflection by z . The dilation of A by B then is the set of all displacements, z , such that $\hat{B}$ and A overlap by at least one element

4.2. Mathematical Morphology

(see Figure 4.9 (a)). It can also be written as

$$A \oplus B = \{z | [(\hat{B})_z \cap A] \subseteq A\}. \quad (4.2.15)$$

Set B is commonly referred to as the structuring element in dilation, as well as in other morphological operations.

Erosion Erosion generally shrinks an image. For sets A and B in $\mathbb{Z}^2$ the erosion of A by B , denoted by $A \ominus B$, is defined as [38]

$$A \ominus B = \{z | (B)_z \subseteq A\}. \quad (4.2.16)$$

This equation indicates that the erosion of A by B is the set of all points z such that B , translated by z , is contained in A (see Figure 4.9 (b)).

Dilation and erosion are duals of each other with respect to set complementation and reflection [38]. That is,

$$(A \ominus B)^c = A^c \oplus \hat{B}. \quad (4.2.17)$$

where A^c is the complement of set A defined as

$$A^c = \{w | w \notin A\}. \quad (4.2.18)$$

Opening Opening generally smoothes the contour of an object, breaks narrow isthmuses, and eliminates thin protrusions. The opening of set A by structuring element B , denoted $A \circ B$, is defined as [38]

$$A \circ B = (A \ominus B) \oplus B. \quad (4.2.19)$$

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Therefore, the opening A by B is the erosion of A by B , followed by a dilation of the result by B (see Figure 4.9 (c)).

Closing Closing generally smoothes sections of contours but, as opposed to opening, it generally fuses narrow breaks and long thin gulfs, eliminating small holes, and fills gaps in the contour. The closing of set A by structuring element B , denoted $A \bullet B$, is defined as [38]

$$A \bullet B = (A \oplus B) \ominus B. \quad (4.2.20)$$

Therefore, the closing of A by B is simply the dilation of A by B , followed by the erosion of the result by B (see Figure 4.9 (d)).

Morphological operations can be used to construct filters similar to the spatial filters and are used in this study to improve the segmentation results.

4.3 A New Hybrid Method Using Region-Based Methods and Anatomical Information

In this section, we describe our approach to segmentation of liver using a hybrid method, which involves adaptive thresholding, Fuzzy c-Means clustering and morphological operations.

4.3.1 Adaptive Thresholding

In CT imaging, the intensity of the liver varies with respect to different patients and imaging environment. Thus, although the liver region maintains a constant

4.3. A New Hybrid Method Using Region-Based Methods and Anatomical Information

Figure 4.9: Four basic morphological operators. (a) Dilation; (b) Erosion; (c) Opening; (d) Closing. In these figures, A stands for the original image, B is the structural element with x be the origin, and C is the result of various operations performed on A and B, with the original image (A) in dashes.

4.3. A New Hybrid Method Using Region-Based Methods and Anatomical Information

image intensity throughout, a fixed threshold for extraction is not profitable. In this study, we use an adaptive thresholding to extract the liver region. First, a histogram of a certain upper left area of the CT slice is analyzed. The second highest peak value (the highest peak value represents the background) is selected as the middle intensity of the liver region. A certain margin is then imposed to ensure the extraction of the whole liver area. Here, both the position and area of the certain region and the margin value are selected empirically. In this study, the upper left area is manually set as 350×220 , and the margin is set as 10%. After this, we get a binary image indicating the membership of liver region (see Figure 4.10(b)).

4.3.2 Morphological and Knowledge-Based Processing

After the pixels in the determined range of intensity are extracted, the result looks like scattered sand. We first delete all the pixels extracted in the lower right part, since the liver only exists in the left and upper area. We then use morphological closing, followed by opening to gather scattered pixels and make them appear as areas (see Figure 4.10(c)).

After this, we see that small segments from other organs still appear in our binary image. Since we know in advance that the area of the liver region is quite big, we can use this to eliminate all the small areas. In order to achieve this, we label all the connected regions, calculate their area, set a threshold and eliminate the regions with small areas. Again, the threshold is set empirically and it works well as long as it is large enough. In this study, we set the threshold to 10000 pixels (see Figure 4.10(d)).

Since the resulting liver region is still not satisfactory, we perform morpholog-

4.3. A New Hybrid Method Using Region-Based Methods and Anatomical Information

ical operations again. Erosion is first performed to eliminate sand noises and is followed by closing and opening, which are conducted to smooth the image (see Figure 4.10(e)). In order to eliminate the small holes in the liver region, we fill in all the gaps inside this region(see Figure 4.10(f)). A quite satisfactory result is obtained after the combination of the procedures. In Figure 4.10(h), we show the extracted liver area.

4.3.3 Fuzzy c-Means clustering

There are various kinds of liver diseases, and currently it is not easy to discriminate these diseases because each disease includes various aspects [2]. Our study focuses on distinguishing a lesion from blood vessel segmented from the liver region. We use the Fuzzy c-Means clustering (FCM) method to segment the lesion and blood vessel. Since the tumor lesion is darker than normal liver tissue and blood vessel is lighter than normal liver tissue, there are four clusters in all, together with the background. Hence we set cluster number $c = 4$. FCM minimizes the iterative optimization of the membership function defined in Equation (4.1.2) based on the similarity between the data and the center of a cluster. When using this model, the user can choose m arbitrarily with $m \in [1, \infty)$. If m is set to a high value, the system becomes robust to noise, yet it takes a longer time, here, we set m to 2 [2].

4.3.4 Identification of Tumor and Morphological Post-Processing

After running FCM, we get 4 clusters, together with the cluster center values. Since the clustering center of the tumor cluster is the second lowest, we set the cluster with the second lowest center value to be the cluster of tumor pixels (see

4.3. A New Hybrid Method Using Region-Based Methods and Anatomical Information

Figure 4.10: Segmentation of the liver region. (a) Original CT abdominal image; (b) Extraction of liver region through adaptive thresholding; (c) Liver region after the first set of morphological operations; (d) Elimination of small areas; (e) The second set of morphological operations; (f) Liver region extracted after filling-the-gaps; (g) Final output of the liver region segmented; (h) The individual liver region.

4.4. Experiments and Discussions

Figure 4.11(b)). We then smooth the output by morphological closing, followed by morphological opening. Finally, we label the different connected segmented regions, and eliminate the small ones, supposing these are only imaging noises (see Figure 4.11(c)). The extracted tumor region is illustrated in Figure 4.11 (d).

4.4 Experiments and Discussions

4.4.1 Experimental Data

In this study, we use CT abdominal images of two different patients from the Department of Oncologic Imaging, National Cancer Centre of Singapore for evaluation. Each set contains 10 images of size 512×512 .

4.4.2 Simulation Results

In Figure 4.12, Figure 4.13 and Figure 4.14, we show examples of the tumor boundaries obtained by our proposed method compared to the manually traced boundaries on the CT abdominal images which contain suspected tumor regions.

4.4.3 Discussions

Since both cases here have been infected with multi-lesions, which is much more complex than the single lesion case, there is no existing quantitative criteria to evaluate the results, and we can only judge it from the medical experts' view. Figure 4.12, Figure 4.13 and Figure 4.14 show that this hybrid method yields quite satisfactory results in segmenting tumor lesions from CT abdominal images

4.4. Experiments and Discussions

(a)

(b)

(c)

(d)

Figure 4.11: Segmentation of the tumor region. (a) Original CT abdominal image; (b) Tumor extracted after FCM; (c) Tumor extracted after morphological operations; (d) Final output of the tumor extraction.

4.4. Experiments and Discussions

(a)

(b)

(c)

(d)

Figure 4.12: Results of segmentation by a hybrid method. Left column: tumor boundary manually traced by experts; Right column: tumor boundary traced by hybrid method.

4.4. Experiments and Discussions

(a)

(b)

(c)

(d)

Figure 4.13: Results of segmentation by a hybrid method (continued). Left column: tumor boundary manually traced by experts; Right column: tumor boundary traced by hybrid method.

4.4. Experiments and Discussions

(a)

(b)

(c)

(d)

Figure 4.14: Results of segmentation by a hybrid method (continued). Left column: tumor boundary manually traced by experts; Right column: tumor boundary traced by hybrid method.

4.4. Experiments and Discussions

according to the experts. In the images used in this experiment, there are multi-lesions in all slices and the proposed method is tested to be able to handle the multi-lesion cases. This method is shown to be effective in detecting lesions with an average intensity that is not much different compared to the intensity value of the normal liver tissue. However, we can see from Figure 4.12(d) and Figure 4.13(d) that this method tends to ignore the lesions near the boundary of the liver. We can easily see that these lesions are eliminated from the liver regions in the thresholding procedure, and since the extraction of the tumor is conducted on the extracted liver region, these lesions will not be detected. To avoid this, we may perform corrections after the extraction of the liver by checking the curvature of concave areas of the liver. Often the missed area of the liver caused by a lesion has large curvature. Another issue associated with this method is the choice of the thresholding margin. A large margin may result in the incorporation of other organs while a small one may eliminate some parts of the liver. An optimal margin may be chosen through testing and analysis of histogram and is under investigation.

Chapter 5

Active Contour Method

This chapter begins with an introduction to deformable models. Then a semi-automatic algorithm is developed to segment tumors from CT abdominal images. We compare our results with manually traced contours.

5.1 Deformable Models

Methods to formulate and represent the shapes of objects are central to computer graphics modeling. Geometric methods have been particularly useful for modeling stationary, rigid objects whose shapes do not change over time. Unfortunately, purely geometric modeling primitives are inert. Deformable models were developed to modeling and animation founded on laws governing the dynamics of nonrigid bodies and they respond in a natural manner to applied forces, ambient media, constraints, and collisions with other objects in a simulated physical environment [41].

In the past few decades, deformable models have been extensively studied and widely used in medical image segmentation. Deformable models were first

5.1. Deformable Models

proposed by Terzopoulos and collaborators [13, 41]. The mathematical foundations of deformable models represent the combination of geometry, physics, and approximation theory [42]. Geometry serves to represent object shape, physics imposes constraints on how the shape may vary over space and time, and optimal approximation theory provides the basis of mechanisms for fitting the models to measured data. Deformable models are curves or surfaces defined within an image domain that can move under the influence of internal forces, which are defined within the curve or surface itself, and external forces, which are computed from the image data [43]. The internal forces are designed to keep the model smooth during deformation and the external forces are designed to move the model toward some desired features within an image. By constraining extracted boundaries to be smooth and incorporating *a priori* knowledge about the object shape, deformable models offer robustness to both image noise and boundary gaps and allow integrating boundary elements into a coherent and consistent mathematical description. Attempts have been made to use deformable models in medical image segmentation [44, 45].

Deformable models have proven to be effective in segmenting, matching and tracking anatomic structures by exploiting (bottom-up) constraints derived from the image data together with (top-down) *a priori* knowledge about the location, size and shape of these structures. They are capable of accommodating the significant variability of biological structures over time and across different individuals [46].

The deformable model that has attracted the most attention to date is the active contour models, also known as “snakes” [13], which is discussed in the following section.

5.2. Active Contours

5.2 Active Contours

Snakes are planar deformable contours that are useful in several image analysis tasks. They are often used to approximate the locations and shapes of object boundaries in images based on the reasonable assumption that boundaries are piecewise continuous or smooth.

The basic premise of the energy minimizing formulation of deformable contour is to find a parameterized curve that minimizes the weighted sum of internal energy and external energy. Geometrically, a snake is a parametric contour embedded in the image plane $(x, y) \in \mathbb{R}^2$. The contour is represented as $\mathbf{v}(s) = (x(s), y(s))^\top$, where x and y are the coordinate functions and $s \in [0, 1]$ is the parametric domain. The shape of the contour subject to an image $I(x, y)$ is indicated by the functional [42]

$$\mathcal{E}(\mathbf{v}) = \mathcal{I}(\mathbf{v}) + \mathcal{P}(\mathbf{v}). \quad (5.2.1)$$

The functional can be viewed as a representation of the energy of the contour, and the final shape of the contour corresponds to the minimum of this energy. The first term of the functional is the internal deformation energy and is given by [42]

$$\mathcal{I}(\mathbf{v}) = \int_0^1 w_1(s) \left| \frac{\partial \mathbf{v}}{\partial s} \right|^2 + w_2(s) \left| \frac{\partial^2 \mathbf{v}}{\partial s^2} \right|^2 ds. \quad (5.2.2)$$

It characterizes the deformation of a stretchy, flexible contour. The physical parameter functions dictate the simulated physical characteristics of the contour: $w_1(s)$ controls the “tension” of the contour while $w_2(s)$ controls its “rigidity”.

The second term in Equation (5.2.1) couples the snake to the image. It is

5.2. Active Contours

traditionally defined as [42]:

$$\mathcal{P}(\mathbf{v}) = \int_0^1 P(\mathbf{v}(s)) ds, \quad (5.2.3)$$

where $P(\mathbf{v}(s)) = P(x(s), y(s))$ denotes a scalar potential function whose local minima coincide with intensity extrema, edges, and other image features of interest. For extraction of intensity edges, a commonly used potential function is [45]

$$P(x, y) = -c|\nabla I(x, y)|^2 \quad (5.2.4)$$

where $I(x, y)$ is the image intensity, ∇ is the gradient operator, and c is a weight associated with the image energies. Another slightly different edge functional is also widely used which is given by [42]

$$P(x, y) = -c|\nabla[G_\sigma * I(x, y)]|^2 \quad (5.2.5)$$

where $G_\sigma * I$ denotes the image convolved with a Gaussian smoothing filter whose characteristic width σ controls the spatial extent of the local minima of P .

In medical images, however, the general shape, location, and orientation of anatomical structure is known, and this knowledge may be incorporated into the deformable model in the form of the initial conditions, data constraints, and constraints on the model shape parameters, or into the model fitting procedure.

5.3. Segmentation of Tumor Using Active Contours

5.3 Segmentation of Tumor Using Active Contours

In this section, we describe our approach to tumor segmentation based on active contour models. In Section 5.3.1 and Section 5.3.2, we define our internal and external energy functions respectively.

5.3.1 Internal Energy

The internal energy term, $\mathcal{J}$, controls the properties of the snake and it is expressed as

$$\mathcal{J}(\mathbf{v}) = \int_0^1 w_1(s) \left| \frac{\partial \mathbf{v}}{\partial s} \right|^2 + w_2(s) \left| \frac{\partial^2 \mathbf{v}}{\partial s^2} \right|^2 ds. \quad (5.3.6)$$

The values of the parameters $w_1(s)$ and $w_2(s)$ are chosen empirically. Here, we set $w_1 = w_2 = 0.15$. The internal energy provides an efficient interpolation mechanism for recovering missing data.

5.3.2 External Energy

As stated in Section 3.2, there are a large number of optional external energy functionals, and here we define

$$\mathcal{P}(\mathbf{v}) = \int_0^1 P(\mathbf{v}(s)) ds = - \int_0^1 c |\nabla G_\sigma * I(x, y)|^2 ds. \quad (5.3.7)$$

The values of parameter c and σ are also chosen empirically and we set $c = 1$, $\sigma = 1$.

5.4. Implementation Schemes

Initial contour is placed manually in the vicinity of the target edge and it deforms until the energy function reaches its minima.

5.4 Implementation Schemes

There are several existing implementation schemes for the active contour methods, such as dynamic programming [47] and the greedy algorithm proposed by D. J. Williams *et al* [48].

5.4.1 Dynamic Programming

The approach by dynamic programming was proposed by A. A. Amini *et al* in 1988 [47]. Vision researchers reported the need for dealing with nonuniqueness and local minima and this problem is extremely important and commonly arises when there is a need to minimize an energy function of some form, such as that in the active contour model. Dynamic programming ensures global optimality of the solution, it is numerically stable, and it allows for hard constraints to be enforced on the behavior of the solution within a natural and straightforward structure. The optimization problem is set up as a discrete multistage decision process and is solved by a “time-delayed” discrete dynamic programming algorithm [47].

5.4.2 Greedy Algorithm

In [48], D. J. Williams *et al* proposed a greedy algorithm which has the performance comparable to the dynamic programming and variational calculus approaches. It retains the improvements of stability, flexibility, and inclusion of

5.5. Experiments and Discussions

hard constraints introduced by dynamic programming but is more than an order of magnitude faster than that approach. A different formulation is used for the continuity term than that of the previous authors so that points in the contours are more evenly spaced. The even spacing also makes the estimation of curvature more accurate. Because the concept of curvature is basic to the formulation of the contour functional, several curvature approximation methods for discrete curves are presented and evaluated as to efficiency of computation, accuracy of the estimation, and presence of anomalies.

5.5 Experiments and Discussions

5.5.1 Experiments

In this study, we implemented the active contour model using dynamic programming techniques described in [47].

We implemented our algorithm on four sets of CT abdominal images from Department of Oncologic Imaging, National Cancer Centre. The data sets contains 13, 11, 10 and 11 slices of size 512×512 from different patients, which all contain suspected tumor regions. The program is run on a personal computer (Intel Pentium 4, 3.20GHz, 512M RAM) and it takes 15 seconds for 14 iterations on the CT abdominal image.

5.5.2 Simulation Results

In Fig. 5.1, we show the process of deformation of the snake. An initial contour is placed around the tumor region manually (see Fig. 5.1 (b)) and the snake deforms

5.5. Experiments and Discussions

to the liver contour gradually (see Fig. 5.1 (c)–(i)).

We implemented our method on four sets of CT abdominal images, and some samples of the results are shown in Figure 5.2 (slice 2 and 3), Figure 5.3 (slice 4 and 5), and Figure 5.4 (slice 6 and 7), with comparison to the manually traced tumor contours. The segmented tumor can also be shown in the form as in Figure 5.5 and the manually and semi-automatically segmented contours of the whole data set are shown in Figure 5.6 and Figure 5.7, respectively.

We measure our results with an objective quality measuring criterion: relative error of tumor area, which is defined as

$$E = \frac{|A_g - A_m|}{A_g} \quad (5.5.8)$$

where A_g and A_m stand for the tumor area obtained by manual tracing (ground truth) and the estimation method to be evaluated, respectively. We compare our results with that by the WHO criteria, which measures the tumor by multiplying the longest perpendicular diameters [5]. In Table 5.1, Table 5.2, Table 5.3 and Table 5.4, we list the relative error E of our segmentation method for the four cases compared with the WHO criteria.

We also calculate the volume by calculating the number of all the pixels belonging to the segmented object. We compare our results to the ground truth with that of the WHO criteria and the results are shown in Table 5.5, Table 5.6, Table 5.7 and Table 5.8,.

5.5.3 Discussions

From the results shown in Section 5.5.2, we can see that the active contour method yields satisfactory results on our data sets. The boundaries drawn by the active

5.5. Experiments and Discussions

Figure 5.1: Deformation of snake. (a) Original CT abdominal image; (b) CT image with an initial contour, which is a circle; (c)–(f) The snake after 2, 4, 6, 8, 10, 12, 14 iterations, respectively.

5.5. Experiments and Discussions

(a)

(b)

(c)

(d)

Figure 5.2: Results of segmentation by active contour (slice 2 and 3, from top to bottom). Left column: tumor boundary manually traced by experts; Right column: tumor boundary traced by active contour method.

5.5. Experiments and Discussions

(a)

(b)

(c)

(d)

Figure 5.3: Results of segmentation by active contour (slice 4 and 5, from top to bottom). Left column: tumor boundary manually traced by experts; Right column: tumor boundary traced by active contour method.

5.5. Experiments and Discussions

(a)

(b)

(c)

(d)

Figure 5.4: Results of segmentation by active contour (slice 6 and 7, from top to bottom). Left column: tumor boundary manually traced by experts; Right column: tumor boundary traced by active contour method.

5.5. Experiments and Discussions

Figure 5.5: Alternative representation of segmented tumor area (slice 3).

5.5. Experiments and Discussions

Figure 5.6: Manually segmented tumor contours of case 1.

5.5. Experiments and Discussions

Figure 5.7: Semi-automatically segmented tumor contours of case 1.

5.5. Experiments and Discussions

Table 5.1: Relative error of tumor area (E) for Case 1

Slice No	E (Active Contour)	E (WHO)
1	0.013317	0.34374
2	0.029211	0.10224
3	0.05641	0.21813
4	0.011308	0.23797
5	0.039247	0.25796
6	0.058958	0.22772
7	0.053388	0.13176
8	0.018319	0.13012
9	0.086535	0.25505
10	0.30059	0.015911
11	0.20722	0.017268
12	0.12273	0.0045455
13	0.065169	0.31685

5.5. Experiments and Discussions

Table 5.2: Relative error of tumor area (E) for Case 2

Slice No	E (Active Contour)	E (WHO)
1	0.106623	0.27683
2	0.072749	0.23984
3	0.088563	0.28576
4	0.070356	0.25434
5	0.063946	0.27584
6	0.059308	0.28336
7	0.080396	0.18463
8	0.11484	0.10437
9	0.10385	0.16485
10	0.15840	0.12486
11	0.20457	0.18424

Table 5.3: Relative error of tumor area (E) for Case 3

Slice No	E (Active Contour)	E (WHO)
1	0.09285	0.05849
2	0.045728	0.13457
3	0.14839	0.23598
4	0.29374	0.20475
5	0.25387	0.26820
6	0.16395	0.22947
7	0.20584	0.31940
8	0.12843	0.18395
9	0.093286	0.20475
10	0.13574	0.17496

5.5. Experiments and Discussions

Table 5.4: Relative error of tumor area (E) for Case 4

Slice No	E (Active Contour)	E (WHO)
1	0.13958	0.11495
2	0.18463	0.29574
3	0.19432	0.20573
4	0.11394	0.27438
5	0.03957	0.28934
6	0.038579	0.21948
7	0.15396	0.25793
8	0.083275	0.19548
9	0.13857	0.038654
10	0.18473	0.058723
11	0.14938	0.063245

5.5. Experiments and Discussions

Table 5.5: Tumor volume and relative error (E) for Case 1

Method	Ground Truth	Active Contour	WHO
Volume	72849	71140	86647
E	-	0.023459	0.18941

Table 5.6: Tumor volume and relative error (E) for Case 2

Method	Ground Truth	Active Contour	WHO
Volume	61943	58937	71934
E	-	0.048528	0.16129

contour methods are approximately the same as the manually traced ones. The relative error of tumor volume calculated by our method is much smaller compared to that calculated by the WHO criteria according to Table 5.5–Table 5.8, which indicates that our method is much more precise than the commonly used approach in quantitative measure. However, in some cases such as slice 10, 11 and 12 in case 1, our method performs worse than the WHO criteria. This is caused by the noise effect which makes the edges of the tumor unclear. The method finds itself hard to deform to the exact boundaries in these cases. However, this is also hard for experienced radiologists. Another problem with this method is that it needs input from the operator, which will increase the processing time. Research will be carried out to place the initial boundary automatically so that this approach will be fully automatic and further reduce the processing time to a large extent.

Recently, a novel stochastic active contour scheme has been developed by C. Pluempitiwiriyaew *et al* for cardiac MR image segmentation [49]. This scheme

5.5. Experiments and Discussions

Table 5.7: Tumor volume and relative error (E) for Case 3

Method	Ground Truth	Active Contour	WHO
Volume	43965	36221	52674
E	-	0.17614	0.19809

Table 5.8: Tumor volume and relative error (E) for Case 4

Method	Ground Truth	Active Contour	WHO
Volume	48937	52183	54957
E	-	0.066330	0.12302

is designed to overcome some of the unique challenges in cardiac MR images such as problems with low contrast, papillary muscles, and turbulent blood flow and it may be extended to our problem with proper changes.

Chapter 6

3D Reconstruction by Interpolation Methods

6.1 Introduction

Medical imaging systems collect data typically in a slice-by-slice fashion. Typically, the distance between adjacent image elements within a slice is different from the spacing between adjacent image elements in two neighboring slices. In addition, often to minimize dosage, the spacing between slices may not be the same for all slices. For visualization, manipulation, and analysis [12] of such anisotropic data, they often need to be converted into data of isotropic discretization or desired level of discretization in any of the n dimensions.

In general, interpolation techniques can be divided into two categories: scene-based and object-based interpolation [31, 50]. In the first case, the density values of the interpolated scene are directly determined from the density values of the given scene [20–27]. In some scene-based methods, statistical information is used to achieve the minimum estimation error [23–27]. In the second case, some infor-

6.2. Some Scene-Based Interpolation Methods

mation from an object extracted from the given scene is used to guide the interpolation process. The first and mostly used object-based interpolation method is the shape-based interpolation method proposed by Raya and Udupa [28–30]. Instead of interpolating the gray-scale level value or opacity, this kind of methods interpolate the structure information. In comparison with scene-based methods, object-based interpolation methods are able to produce more satisfactory methods, while on the other hand, they tend to be more computationally consuming.

Efforts have also been made to make improvements to the existing interpolation methods [35–37, 51–53], which all employ some preprocessing steps. The extra computational load is outweighed by the improvements in interpolation results. For example, in [36] correspondence is first established between points in consecutive slices, and then this correspondence is used to estimate data between the slices by linear interpolation.

Since in numerous current applications, reconstruction is performed interactively with other processing procedures, for example, in surgical uses when we want to see the inner structure instantaneously, the processing time is a very important factor to evaluate the performance of the methods.

6.2 Some Scene-Based Interpolation Methods

In this section, we describe the scene-based interpolation methods that we use in this study. Suppose for one patient, we have a data set of size $N_1 \times N_2 \times K$, where $N_1 \times N_2$ is the image size and K is the number of slices. We define the whole set of voxels for this patient as V , where $V = \{v = (v_1, v_2, v_3) | 1 \leq v_1 \leq N_1, 1 \leq v_2 \leq N_2, 1 \leq v_3 \leq K\}$, and v is a single voxel. We denote all voxels in the k th slice by V^k , where $V^k = \{v^k = (v_1, v_2, k)\} \subset V$, and v^k is a single

6.2. Some Scene-Based Interpolation Methods

voxel in the k th slice. The corresponding voxel in the l th slice, i.e., a voxel with the same value of v_1 and v_2 is denoted by v^l . The original intensity value function is defined as $f(v), f(v) \in [0, 255]$ and the interpolated intensity value is defined as $g(v), g(v) \in [0, 255]$. Next, we define the different interpolation methods investigated in our experiments.

6.2.1 Linear Interpolation

The intensity value of a voxel v^k is the weighted average of the intensity values of the 2 adjacent voxels. In our case,

$$g(v^k) = 0.5f(v^{k-1}) + 0.5f(v^{k+1}). \quad (6.2.1)$$

6.2.2 Cubic Spline

For this method, a specific spline function defined by Cheney and Kincaid [20] is used as the interpolation kernel. In our case [31],

$$g(v^k) = -0.075f(v^{k-3}) + 0.575f(v^{k-1}) + 0.575f(v^{k+1}) - 0.075f(v^{k+3}). \quad (6.2.2)$$

6.2.3 Modified Cubic Spline

This function is based on a finite impulse response filter, a cubic function that is essentially a truncated sinc function in the spatial domain with a low-pass

6.2. Some Scene-Based Interpolation Methods

frequency response. From [31], we get

$$g(v^k) = -0.0625f(v^{k-3}) + 0.5625f(v^{k-1}) + 0.5625f(v^{k+1}) - 0.0625f(v^{k+3}). \quad (6.2.3)$$

6.2.4 Sinc-Based Methods

These methods are various approximations of the ideal sinc interpolation [33].

1. Dirichlet Apodization

The Dirichlet apodization is the sinc function multiplied by a rectangular window of size W , which is defined as:

$$\text{sinc}_W^D(x) = \frac{\sin(\pi x)}{\pi x} \beta^0\left(\frac{x}{W}\right) \quad (6.2.4)$$

where W is an even integer and $\beta^0(x)$ is given by:

$$\beta^0(x) = \begin{cases} 1 & |x| < 1/2 \\ 1/2 & |x| = 1/2 \\ 0 & |x| > 1/2 \end{cases} \quad (6.2.5)$$

In our case, in order to make the length of the sinc function the same as those of the cubic spline and modified cubic spline, we take $W = 4$ and

$$g(v^k) = -0.2122f(v^{k-3}) + 0.6366f(v^{k-1}) + 0.6366f(v^{k+1}) - 0.2122f(v^{k+3}). \quad (6.2.6)$$

2. Hanning Apodization

6.3. Shape-Based Interpolation

The Hanning apodization is the sinc function multiplied by a Hanning window of size W , which is defined as:

$$\text{sinc}_W^H(x) = \text{sinc}_W^D(x) \left(\frac{1}{2} + \frac{1}{2} \cos \left(\frac{2\pi x}{W} \right) \right) \quad (6.2.7)$$

where W is an even integer. In our case, we take $W = 4$ and

$$g(v^k) = -0.0311f(v^{k-3}) + 0.5434f(v^{k-1}) + 0.5434f(v^{k+1}) - 0.0311f(v^{k+3}). \quad (6.2.8)$$

6.3 Shape-Based Interpolation

6.3.1 Concept of Shape-Based Interpolation

In medical image processing, an essential intermediate step for visualization is segmentation. Often, due to numerous reasons, manual or human assist are needed for segmentation of soft tissues. Clearly, in such situations, the time spent by the user in segmentation is a function of the number of slices covered by the object which is also true with automatic segmentation. If interpolation is done to generate cubic voxels prior to segmentation, which is a common practice, the time requirement rises rapidly to a level where often interactive segmentation becomes impractical. This problem is the major motivation for the proposed interpolation scheme, where interpolation is done after segmentation. Even when automatic segmentation is possible, we expect, at least intuitively, that the information in the original sample points should be more appropriate for segmentation than that in the interpolated points since interpolation may introduce artifacts [29].

6.3. Shape-Based Interpolation

We do the shape-based interpolation by converting the segmented slice images into gray-value images. In these images, the grayness is the shortest distance (within the slice) of the pixel from the boundary of the organ (positive values for inside the organ and negative values for outside). We estimate segmented intermediate slices by interpolating the distance-representing gray-value slices and thresholding at zero. This algorithm is briefly described in Figure 6.1.

6.3.2 Different Distance Functions

In this section, we will introduce four basic distance functions: cityblock distance, chessboard distance, quasi-Euclidean and Euclidean distance. We will give their mathematical representations in the 2D sense.

- *Cityblock Distance*

The cityblock distance between (x_1, y_1) and (x_2, y_2) is

$$D = |x_1 - x_2| + |y_1 - y_2|. \quad (6.3.9)$$

- *Chessboard Distance*

The chessboard distance between (x_1, y_1) and (x_2, y_2) is

$$D = \max(|x_1 - x_2|, |y_1 - y_2|). \quad (6.3.10)$$

- *Quasi-Euclidean Distance*

6.3. Shape-Based Interpolation

Figure 6.1: Shape-based interpolation. Courtesy of Jonathan C. Carr, Information Engineering Division, Engineering Department, University of Cambridge.

6.4. Experiments and Discussions

The quasi-Euclidean distance between (x_1, y_1) and (x_2, y_2) is

$$D = \begin{cases} |x_1 - x_2| + (\sqrt{2} - 1) \times |y_1 - y_2| & \text{if } |x_1 - x_2| > |y_1 - y_2| \\ (\sqrt{2} - 1) \times |x_1 - x_2| + |y_1 - y_2| & \text{otherwise} \end{cases} \quad (6.3.11)$$

- *Euclidean Distance*

The Euclidean distance between (x_1, y_1) and (x_2, y_2) is

$$D = \sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2}. \quad (6.3.12)$$

In Figure 6.2, we give a specific example of distances calculated by the different distance metrics for the 2D case. In Figure 6.3, an example of extension to 3D is given.

6.4 Experiments and Discussions

6.4.1 Experiment 1 (Scene-Based Interpolation)

Experimental Data

In this experiment, we use 4 sets of CT abdominal images of different patients from the Department of Oncologic Imaging, National Cancer Centre of Singapore for evaluation. The sizes of the data sets are as following:

1. Case 1: $512 \times 512 \times 50$, $N_1 = N_2 = 512$, $K = 50$
2. Case 2: $512 \times 512 \times 25$, $N_1 = N_2 = 512$, $K = 25$

6.4. Experiments and Discussions

Figure 6.2: An example of different distance functions (2D).

6.4. Experiments and Discussions

Figure 6.3: An example of different distance functions (3D).

6.4. Experiments and Discussions

3. Case 3: $512 \times 512 \times 25$, $N_1 = N_2 = 512$, $K = 25$
4. Case 4: $512 \times 512 \times 24$, $N_1 = N_2 = 512$, $K = 24$

Criteria for Evaluation

In this study, we interpolate all the slices except the first and the last three, and then compare them to the original slices. We use the signal to noise ratio (SNR) to evaluate the performance of the various interpolation methods. For the k th slice, if the original and interpolated intensity values are $f(v^k)$ and $g(v^k)$ respectively, then the SNR of the k th slice is defined as:

$$SNR = 10 \log \left(\frac{\sum_{v^k \in V^k} (f(v^k))^2}{\sum_{v^k \in V^k} (f(v^k) - g(v^k))^2} \right). \quad (6.4.13)$$

Simulation Results

In Figure 6.4, we plot the SNR of different interpolation methods for the 4 sets of data respectively. In Figure 6.5 and Figure 6.6, we show one sample slice from case 1 and case 2, respectively, obtained by each of the five interpolation methods discussed in Section 6.2.

6.4.2 Experiment 2 (Shape-Based Interpolation)

Experimental Data and Criteria for Evaluation

In this experiment, we use thirteen segmented slices from Chapter 5 as the original data set. We then perform shape-based interpolation using the four distance

6.4. Experiments and Discussions

Figure 6.4: Comparison of SNR of 4 cases, each with 50 slices. (a)–(d) show the SNR of case 1–4, respectively.

6.4. Experiments and Discussions

Figure 6.5: A sample slice obtained by each of the five interpolation methods for Case 1. (a) original; (b) linear; (c) cubic spline; (d) modified cubic spline; (e) Dirichlet Apodization; (f) Hanning Apodization.

6.4. Experiments and Discussions

Figure 6.6: A sample slice obtained by each of the five interpolation methods for Case 2. (a) original; (b) linear; (c) cubic spline; (d) modified cubic spline; (e) Dirichlet Apodization; (f) Hanning Apodization.

6.4. Experiments and Discussions

Figure 6.7: Semi-automatically segmented tumor contours of the whole data set.

transforms described in Section 6.3.2 and linear basis function. We also visualize the tumor volume based on the segmented and interpolated contours.

Simulation Results

The original segmented contours by the active contour method are shown in Figure 6.7 and we give an example of the interpolated contours using the Euclidean Distance transforms in Figure 6.8.

The 3D views of the manually segmented tumor and the computer segmented tumor are shown in Figure 6.9 and Figure 6.10. We also give the 3D visualization

6.4. Experiments and Discussions

Figure 6.8: Interpolated contours of the whole set of segmented tumor contours (Euclidean Distance). From top left, the odd numbered contours are the original ones, and the even numbered contours are the segmented ones.

6.4. Experiments and Discussions

Figure 6.9: 3D visualization of manually segmented tumor.

Figure 6.10: 3D visualization of computer segmented tumor.

of the interpolated set using Euclidean Distance transform in Figure 6.11.

6.4.3 Discussions

From Figure 6.4, we can see that, contrary to what is found in the literature for 1D and 2D cases, linear interpolation performs as well as, and in some cases, even slightly better than all the other methods. This is due to the large distances between consecutive slices in these experiments, which significantly decreases the correlation between adjacent slices. Slice $n - 2$ or $n + 2$ may be totally different from the n th slice, and in these cases, if we use slice $n - 2$ or $n + 2$ to calculate the n th slice, such as we do in the cubic spline, modified cubic spline, Dirichlet

6.4. Experiments and Discussions

Figure 6.11: 3D visualization of the interpolated sets of the computer segmented tumor.

apodization and Hanning apodization, the results are quite different from the original ones. As for the computational load, in linear interpolation, we have to do two multiplications and one addition to calculate each voxel intensity value, while in all the other methods, we have to do four multiplications and three additions. So, if we want to perform interpolation under the condition that the slices are quite far away from each other, linear interpolation would be the best one since it can achieve the same performance as the other methods with about only half the computational load. We also notice that Dirichlet apodization performs worst in all case, which is easy to understand since we only take a 4-point approximation of the sinc function without making any compensation or improvements as in the Hanning apodization. As for the other three methods—cubic spline, modified cubic spline and Hanning apodization—we can hardly tell which one is the best, since there is hardly any difference between their performances. While cubic spline and modified cubic spline are widely used in the 3D image interpolation, Hanning

6.4. Experiments and Discussions

apodization is seldom used and since it performs as well as the other ones, it deserves our further attention. Our future work may also involve deblurring techniques used to improve the quality of the interpolated images.

In Figure 6.4 (d), we can see that there is a sudden drop of SNR for all methods. The SNR for the 10th and 11th slides are much smaller than those of the others. This is because of the fact that these two images are not taken at the right position due to some reasons related to the imaging process. Since we are interpolating under the assumption that all images are equally distanced, failure to get these images at equal distance can cause large errors.

Figure 6.8 shows the result of shape-based interpolation and we can conclude that it saves approximately half of the time used for segmentation, by performing interpolation after, rather than before segmentation. Although the computing time for image distance transform may be quite long, it is outweighed by the time saved from segmentation.

Chapter 7

Conclusions and Recommendations

7.1 Conclusions

In this thesis, we described a novel scheme for the estimation of liver tumor volume from CT abdominal images for clinical uses. We developed a system for automated liver tumor segmentation, reconstruction and volume estimation. Two new segmentation methods have been developed in this study and various interpolation methods which will lead to the 3D reconstruction of the liver tumor have been compared. Shape-based interpolation has also been studied to further reduce the processing time by cutting down the time needed for segmentation.

We first introduced a hybrid method based on region-based segmentation methods and morphological operations, with incorporation of anatomical information. The histogram of the upper left area of the CT abdominal image is first analyzed, and a threshold is selected as the second highest peak value. A certain margin is imposed on the threshold to get the upper and lower threshold for ex-

7.1. Conclusions

traction of liver region. Morphological operations are then performed to smooth the images. Small areas are eliminated by labelling and thresholding, followed by morphological operations to further smooth the image. Fuzzy c-Means clustering is then performed on the extracted liver region for the segmentation of tumor region. Labelling and thresholding are also employed to eliminate small areas which are induced by noises. Morphological operations complete our processing by smoothing the final output. Results show that this method is quite effective in extracting lesions in the center area, while it tends to ignore the lesions near the liver boundary. This method is also tested to be able to handle with multi-lesion cases.

Another method is developed for liver tumor segmentation, which is the active contour model. Initial boundary is manually placed by operators outside the tumor region. The snake deforms to the tumor boundary with the minimization of energy function. Results show that this method is quite efficient in tumor boundary detection and yields good results with respect to relative error of tumor area. The active contours perform worse when the edges of the tumors are not clear and blurs away, and the method finds itself hard to deform to the exact boundaries in these cases. However, this is also hard for experienced radiologists.

Finally, we investigated various interpolation methods on CT abdominal image sets. We investigated 4 interpolation kernels: linear, cubic spline, modified cubic spline and sinc-based methods. We evaluate the respective signal-to-noise ratio (SNR) and results show that linear interpolation performs as well as the other methods based on the SNR criterion, while its computational cost is only about half of the others. We also performed the shape-based interpolation method on our segmented tumor set and found that it ensures a large reduction of the whole processing time, in spite of extra computational load caused by the dis-

7.2. Recommendations for Future Research

tance transform. The reduction of processing time is due to the fact that we now only need to do segmentation for half of the number of images as we would do if interpolation is performed before segmentation.

7.2 Recommendations for Future Research

Future research can be conducted in the following aspects:

The segmentation methods are not robust in some cases and research can be carried out to improve these methods so that they will be able to handle the images covering the whole volume of the liver. This may be achieved by the incorporation of *a priori* information. Additional terms which represent this *a priori* information can be added to the energy function. In [49], C. Pluempitiwiriyaew *et al* developed a novel stochastic active contour scheme for cardiac MR image segmentation [49], which may be extended to our problem with some changes. Since the segmentation using active contour can be viewed as a multi-objective optimization problem, we may also conduct research on the various objectives for our specific problem. Other new methods can also be explored for segmentation of liver tumor, such as live wire method or multiscale filtering, etc.

The evaluation of the segmentation and interpolation results may also be improved. Besides the volumetric measures used in this thesis, we may also evaluate our results by measures which consider the similarity of the resulting shapes.

The liver is divided by the blood vessels into eight segments. For resection of liver cancer or metastases, doctors need to know residual volume of each segment after resection. Surgeons also need to know the geometrical information of tumor and vessels, so that they will not cut the main vessels when doing the resection

7.2. Recommendations for Future Research

(large loss of blood may be fatal in most cases). In order to do this, a system can be developed with the following abilities:

- Segmentation of liver
- Segmentation of lesion (tumor, metastases)
- Segmentation and structural analysis of the hepatic artery, portal vein and hepatic veins
- Volumetric analysis of the liver and designated territories
- Definition of cutting lines for resection
- Risk analysis with calculation of resected or compromised parenchyma

We have studied and explored part of this big problem in this thesis, yet methods still have to be developed for the segmentation of blood vessels as well as 3D reconstruction methods to visualize them. Geometrical knowledge of the blood vessels have to be studied to divide the liver into eight segments. Relative locality knowledge of blood vessels to tumor has also to be studied for volumetric analysis of each liver segment after resection and the decision of cutting lines. Besides, this system imposes a high requirement on visualization of the liver, lesion and blood vessels.

Author's Publications

1. *Rui Lu*, Pina Marziliano and Choon Hua Thng, “Comparison of Scene-Based Interpolation Methods Applied to CT Abdominal Images”, in Proceedings of the 26th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, San Francisco, USA, September 2004.
2. *Rui Lu*, Pina Marziliano and Choon Hua Thng, “Liver Tumor Volume Estimation by Semi-automatic Segmentation Method”, in Proceedings of the 27th Annual International Conference of the IEEE Engineering in Medicine and Biology Society, Shanghai, China, September 2005.

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