

Segmentation of Brain MR Images with ITK Toolkit

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Abstract: Segmentation of nontrivial images is one of the most difficult tasks in image processing. Segmentation accuracy determines the success or failure of computerized analysis procedures. Medical image segmentation has become an important diagnostic tool in the practice of modern medicine. Segmentation of MRI Brain images is the delineation of neuro-anatomical structures such as the Cerebrum, Cerebellum, Hippocampus, etc. as well as abnormalities such as tumors. Although numerous methods have been proposed during the past two decades for brain MRI segmentation, it remains a challenging task. In this paper brain MRI segmentation is demonstrated for delineation of a tumor, ventricles and other anatomical structures using Insight Segmentation and Registration Toolkit (ITK) routines as the foundation. This public software provides callable routines only. It does not provide graphics, visualization, or other interactive tools specific to a given task, such as segmentation. Segmentation of medical images is an important step in forming realistic tissue models. To assist in classifying the relevant literature, three generations of development are identified where each generation adds an additional level of algorithmic complexity. The first generation is composed of the simplest forms of image analysis, the second is characterized by the application of uncertainty models and optimization methods, and the third incorporates knowledge into the segmentation process. The progress toward fully automatic segmentation is discussed and sources of segmentation software from industry and academia are identified, along with databases for segmentation validation. We have implemented a variety of semiautomatic and automatic segmentation routines as well as preprocessing algorithms provided by ITK. This implementation facilitates interactive adjustments of algorithm parameters and their consequences on the segmentation results via an intuitive GUI incorporating the ITK segmentation routines.

Keywords: Brain, Image Segmentation, MRI, ITK, CMake, Tumor and Filter

1. INTRODUCTION

Image segmentation is a process to identify and classify regions of interest from digital images. Typically, digital images are acquired from medical instrumentation as CT (Computer Tomography) or MRI (Magnetic Resonance Image) scanners, digital mammograms etc. Image segmentation plays an important role in medical image processing which enables a variety of clinical applications [10]. It is also a tool to facilitate the detection of abnormalities such as cancerous lesions in the brain. Segmentation of medical images is a challenging task. A variety of different methods have been proposed and implemented in recent years. Although numerous efforts have advanced this technique, there is no single approach that can generally solve the problem of segmentation for the large variety of image modalities existing today [4].

Various segmentation techniques can be classified, for example, as classical techniques such as thresholding, boundary based technique, region based technique, or statistical technique. Depending on the level of interactivity, segmentation can be classified as manual, semiautomatic, or automatic. Manual segmentation is time consuming [2, 6], costly, and non-repeatable. Inconsistencies in the segmented extent of various structures are common among qualified experts. Moreover, it does not use the full multi-dimensional image data. Automatic segmentation methods are sensitive to noise and unexpected situations, leading to errors. Their advantages are a minimum time commitment from the user and results that are highly reproducible, albeit potentially erroneous. These methods are usually problem-specific, and an image-processing expert is needed to determine which

image-processing functions are best suited for a given segmentation task.

Semi-automatic image segmentation combines manual interaction with automated sub-components to solve segmentation problems. Semi-automatic segmentation is faster than a manual strategy with more reproducible results compared to both manual and fully automatic. It uses the complete image data set, and is minimally affected by human inconsistency and error. In addition, the user can harness the power of automated image-processing algorithms without being an image-processing expert

2. BACKGROUND OF THE STUDY

There are multiple medical imaging strategies such as MRI (Magnetic Resonance Imaging), PET (Positron emission Tomography), CT (Computer Tomography), Ultrasound, SPECT (Single Photon Emission Computed Tomography) and many more. This thesis has concentrated on MRI imaging due to the research focus of our laboratory, the Center for Comparative Neuro Imaging.

Magnetic resonance imaging (MRI) is an imaging technique used primarily in medical settings to produce high quality images of soft tissue structures. Unlike conventional X-ray imaging or Computed Tomography, which produce images that show the X-ray attenuation of tissues, MRI measures the amount of hydrogenous materials (water and lipids) in tissues. The nucleus of the hydrogen atom is a spinning charged proton with magnetic properties which the MR imaging strategy utilizes.

2. Two magnetic fields are used in MRI. The first being a strong static magnetic field which causes the hydrogen atoms

in the body to align in a direction parallel to the field. A second magnetic field (radio-frequency pulse) is applied at right angle to the first field causing the hydrogen atoms to change their alignments. When radio-frequency pulse is turned off, the hydrogen atoms return to their alignment along the static magnetic field direction. The time rate of recovery differs with tissue properties. Longitudinal relaxation (T1) depends on the recovery time of the hydrogen atoms to return to the axis of the primary magnetic field. The transverse relaxation time (T2) measures the rate of decay of the hydrogen proton alignment due to the RF pulse.

3. APPROACH

Image segmentation is a process to identify regions of interest from digital images. Image segmentation plays an important role in medical image processing which enables a variety of clinical applications. It is also a tool to facilitate the detection of abnormalities such as cancerous lesions in the brain. Although numerous efforts in recent years have advanced this technique, no single approach solves the problem of segmentation for the large variety of image modalities existing today. Consequently, brain MRI segmentation remains a challenging task. The purpose of this paper is to demonstrate brain MRI segmentation for delineation of tumors, ventricles and other anatomical structures using Insight Segmentation and Registration Toolkit (ITK) routines as the foundation. ITK is an open-source software system to support the Visible Human Project. Visible Human Project is the creation of complete, anatomically detailed, three-dimensional representations of the normal male and female human bodies. Currently under active development, ITK employs leading-edge segmentation and registration algorithms in two, three, and more dimensions. A goal of this thesis is to implement those algorithms to facilitate brain segmentation for a brain cancer research scientist.

4. SEGMENTATION METHODS

Several methods of image segmentation have been proposed in literature [1]. The following figure 1 arranges these methods.

4.1 SINGLE CONTRAST METHODS

4.1.1 Thresholding: Thresholding is the most intuitive approach to segmentation where values of upper and lower thresholds are provided by the user. This method is limited and successful application for clinical use is hindered by the variability of anatomy and image artifacts.

4.1.2 Edge Based Segmentation: Edges are usually detected by rapid changes in intensity values observed while traversing a set of pixels. Operators such as first and second derivatives play significant role in edge detection. Sometimes, insufficient intensity gradients, presence of noise or artifacts, or poor guess of threshold may cause over or under segmentation.

4.1.3 Boundary Tracing: In this method, user selects the pixel on the boundary of the region for outlining purposes. Then the method follows the boundary from this user selected seed point. This method is useful for cases where good definition of an edge boundary exists. This method can cause problems for images with tissue variance.

4.1.4 Seed Growing Segmentation: In this method, user selects a seed or multiple seeds and specifies threshold value.

Using this data, the method examines neighboring pixels of the selected seed(s) and includes them in the region if those neighbors also satisfy the criteria.

4.2 MULTI-SPECTRAL SEGMENTATION

These methods are classified as supervised and un-supervised. Supervised methods require operator input for segmentation. This is done by selecting training pixels or training regions in the images. Un-supervised methods define regions in the image without operator input.

4.3 SUPERVISED METHODS

4.3.1 Pattern Recognition Methods: This is the most common approach for multi-spectral segmentation. There are several pattern recognition techniques and many of them assume particular distribution of the features based upon parametric models. Non-parametric models do not rely on predefined distributions but on the actual distribution of the training samples [9].

4.3.2 Algebraic Methods: For images that clearly identify signature vectors, these methods provide an elegant solution to deal with the partial volume effect, which might have influence on volume measurements. Algebraic approaches can become impractical for images showing complex pathology.

4.4 UNSUPERVISED METHODS

Unsupervised methods, also called “clustering” find the structure in data automatically. A cluster is an area in feature space with high density and can be promising for tumor volume determination. However, the initialization is very important for meaningful clustering and reasonable computation time. These methods are reproducible but may not necessarily arrive at meaningful segmentation and often require computation time.

ITK (Insight Segmentation and Registration Toolkit) has implemented some segmentation methods discussed. ITK is an open-source software system to support Visible Human Project.

5. ITK

Insight Segmentation and Registration Toolkit (ITK) is an open-source software system to support the Visible Human Project. ITK is sponsored by National Library of Medicine at the National Institutes of Health and developed by six principal organizations, three commercial (Kitware, GE Corporate R&D, and Insightful) and three academic (UNC Chapel Hill, University of Utah, and University of Pennsylvania). ITK is currently advancing leading-edge segmentation and registration algorithms in two, three, and more dimensions. ITK does not provide GUI or Visualization. ITK is cross-platform package. A common build environment called CMake is used to manage the compilation process [8]. CMake is a cross-platform open source software system. It was developed by Kitware, as part of the ITK project. CMake is a build process which is independent of the operating system and compiler. Currently it supports UNIX and Windows platforms and produces native build files appropriate to these OS. On Unix CMake produces makefiles and on Windows, it generates projects and workspaces. CMake allows the user to control the software compilation process using simple platform and configuration files (contain pre-defined CMake commands as well as user-defined commands) that are compiler independent. In addition, an automated wrapping process generates interfaces between C++ and interpreted programming languages such as Tcl, Java, and Python. Wrapping process is achieved using

CableSwig. This ITK utility enables developers to create software using a variety of programming languages.

6. ITK SEGMENTATION

Image segmentation plays an important role in medical image processing. The goal of segmentation is to extract one or several regions of interest in an image. Depending on the context, a region of interest can be characterized based on a variety of attributes, such as gray scale level contrast, texture, shape, size etc. Selection of good features is the key to successful segmentation. There are a variety of techniques for segmentation, ranging from simple ones such as thresholding, to more elaborate strategies including region-growing, edge-detection, morphological methods, artificial neural networks and much more. Although numerous methods have been proposed in recent years, there is no single approach that can solve segmentation problems for many existing imaging modalities today [7].

The Insight Toolkit provides a basic set of algorithms that can be used to develop and customize a full segmentation application. The most effective segmentation algorithms can be obtained by carefully customizing combinations of the basic segmentation algorithms and pre-processing and post-processing algorithms implemented in ITK for images of specific modality. The parameters of these algorithms can be tuned for the characteristics of the image modality used as input and the features of the anatomical structure or abnormalities to be segmented [3].

7. THRESHOLD SEGMENTATION

Following section presents the results of applying Connected Threshold Segmentation on Brain MRI to segment tumor and white matter.

7.1. Segmenting Tumor

In following figures, image in figure 2 (a) represents original brain MRI. Figure 2 (b) shows the result of applying curvature flow smoothing with Time Step = 0.125, Number of Iterations = 5. In second row figure 2 (c) was obtained by applying Connected Threshold Segmentation on smoothed image with Lower Threshold = 169, Upper Threshold = 182 and Seed Index (76, 91). Second result in figure 2 (d) was obtained by applying Curvature Flow Smoothing twice, with Time Step = 0.125 each time and Number of Iterations = 5 and 10 respectively. Then Connected Threshold Segmentation was applied with Lower Threshold = 169, Upper Threshold = 182. Dilation was applied to this above result as shown in figure 2 (e). Figure 2 (f) was obtained by applying Edge preserving smoothing (Curvature Anisotropic diffusion with time step = 0.125, conductance = 1, number of iterations = 5) and then applying Connected Threshold to this smoothed result with lower threshold = 50, upper threshold = 90 and Seed Index (76, 91). Figure 2 (g) shows the result of applying dilation to the segmented result in figure 2 (f).

Now we apply Normalization to the image smoothed with curvature anisotropic diffusion, as shown in Figure 2 (h). But as seen from result figure 2 (i), normalization does not contribute to any significant improvement in the result of connected Threshold Segmentation. Hence, hereafter, we have used Normalization in some cases for display purpose only [6].

As we can see here, segmented result does not cross the external boundary of the tumor. Gray matter is not being completely segmented. This illustrates the vulnerability of the region growing methods when the anatomical structures to be

segmented do not have a homogeneous statistical distribution over the image space.

One solution will be to apply level set segmentation to the above result. This result can be dilated so as to cross the internal boundary of the tumor, bring it close enough to the external boundary of the tumor and then apply the level set segmentation such as laplacian or canny edge detection to refine the result.

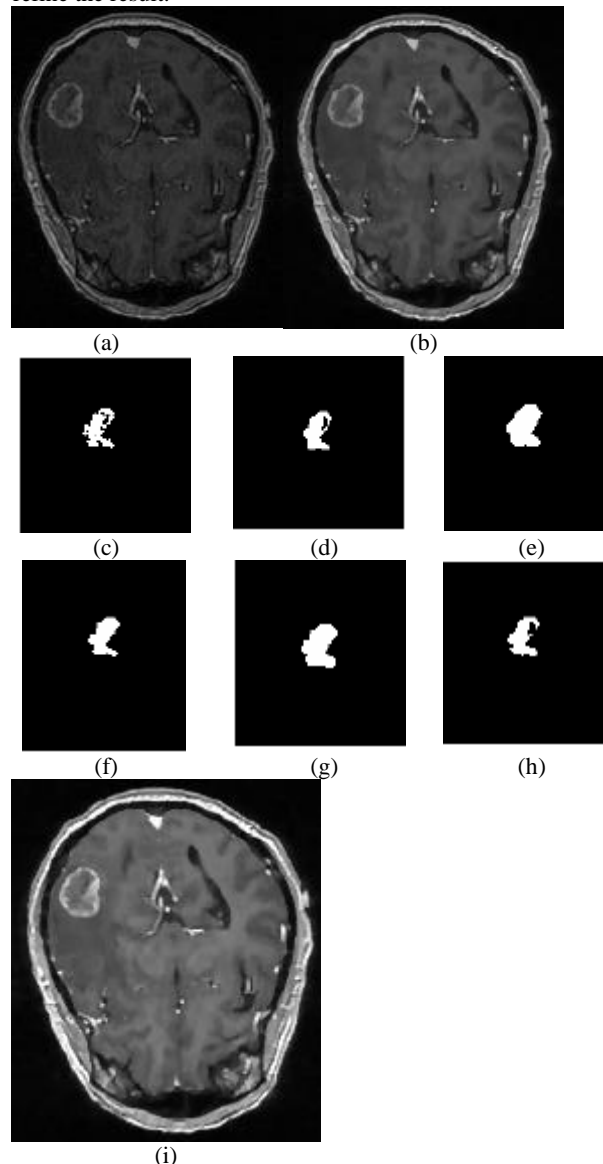


Figure 2 (a) – (h) Segmenting tumor with connected threshold filter

Other level set segmentation algorithms such as shape detection, geodesic active contour may be applied to obtain the desired segmentation.

7.2. Segmenting Brain (White Matter)

Figure 3 (a) shows image smoothed original brain MRI of 256*256. Figure 3 (b) shows brain area segmented with Connected Threshold with lower threshold = 45 and upper threshold = 55 and Seed Index (160,115). Here, smoothing was not applied.

As seen in the results, this filter produces the output with holes. There are different approaches that we can use to fill above holes [5]:

1. Use dilation operation.
2. We can apply flood fill operation using `itk::GrayscaleFillholeImageFilter`

3. If size is enough for characterizing the holes we can use the connected components filter (`itk::ConnectedComponentImageFilter`) and then collect the number of pixels per component in order to identify the labeled regions those need to be set ON to fill the holes.

4. We can use the Connected Threshold Image Filter and use the first pixel of the image as seed point (assuming it is in the exterior of the shape) and segment the "exterior" of brain area.

Then make a logical OR between the exterior and the shape, which will give the negative map of the holes. Negating this map and do an OR between the map and the original shape, you will end up with the shape without holes.

Figure 3 (c) shows the result after applying dilation with X-radius=1, Y-radius=1. Here, most of the holes disappear, but still some holes are left and it changes the segmentation result. Figure 3 (d) shows the result of applying `GrayScaleFillHoleImagefilter` to 3 (b). With this filter, all holes are filled into ON region, including ventricles area.

Figure 3 (e) shows the result of Connected Threshold segmentation with lower threshold = 39 and upper threshold = 56 and figure 3 (f) is the result of applying `GrayScaleFillHole` filter to the result in figure 3 (e).

In all above cases, smoothing was not used. Noise present in the image can reduce the capacity of this filter to grow large regions. When faced with noisy images, it is usually convenient to pre-process the image by using edge-preserving smoothing filters such as Curvature Anisotropic Diffusion Filter, Gradient Anisotropic Diffusion Filter [2].

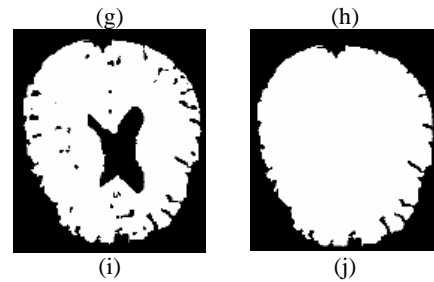
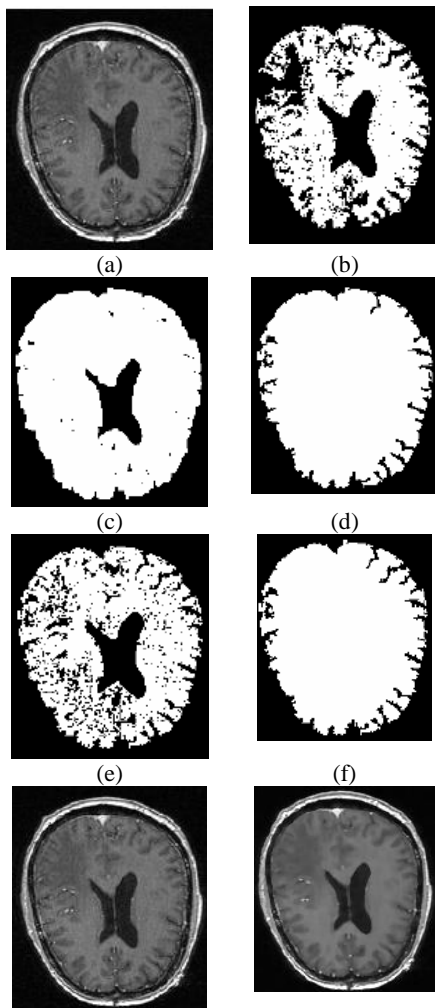


Figure 3 (a) - (j) Segmenting brain with connected threshold filter with smoothing

Here, figure 3 (g) represents original image, figure 3 (h) represents image smoothed with curvature anisotropic Diffusion with No. of Iterations = 5, Time step = 0.125 and Conductance = 1. Figure 3 (i) is the image segmented with Connected Threshold filter with Seed Index (160, 115) and Lower Threshold = 80 and Upper Threshold = 125. This result can be improved with `GrayScaleFillHole` filter as shown in figure 3 (j).

8. IMPLEMENTATION

This section describes the programs developed within this paper and the ITK routines used within the programs. All programs were written in C and C++ compatible on Windows operating systems.

Configuration files (`Cmakelists.txt`) were written and programs compiled and built using `CMake 2.0` and `Microsoft Visual C++ 6.0`. Typical inputs for these programs were 2-D brain slices with the following data characteristics:

- Endian Type = Big Endian
- Element Spacing=(X=1.0156,Y=1.0156)
- Dimension Size = 256 * 256
- Element Type = 16-bit Signed Short

Original brain MRI slices, with details mentioned previously were converted into `MetaImage` format. This format uses an ASCII text `MetaImage` header file and a binary raw data file for each slice. This format was directly compatible with the `ITK Input Reader (itk::ImageFileReader)`. Results (at intermediary times) were written to a file using the `ITK Output Writer (itk::ImageFileWriter)`. Both `ITK` routines handle multiple file I/O file formats.

The actual low level task of reading and writing specific file formats was done by super class `itk::ImageIO`. Input images to the programs were specified with `.mhd` or `.mha` extension. `MetaImageIOFactory` was registered with `objectFactoryBase`. This allowed run-time instantiation of the classes that supported `MetaImage` format, based on the extension specified for an input file.

The IO architecture of the `ITK` makes it possible to avoid explicit specification of the file format used to read or write images. The object factory mechanism enables the `ImageFileReader` and `ImageFileWriter` to determine the file format at run-time. Typically, file formats are chosen based on the filename extension, but the architecture supports arbitrarily complex processes to determine whether a file can be read or written. Alternatively, the user can specify the data file format by explicit instantiation and assignment of the appropriate `itk::ImageIO` subclass. Following example file shows the header files associated with brain MRIs as input.

- ObjectType = Image
- NDims = 2
- BinaryData = True
- BinaryDataByteOrderMSB = True
- Color = 1 0 0 1
- ElementSpacing = 1.01563 1.01563
- DimSize = 256 256
- ElementType = MET_SHORT

➤ ElementDataFile = tumour75.raw

All output files were written as RAW files along with their MetaImage header files that consisted all the information

9. CONCLUSION

Image segmentation plays an important role to facilitate the detection of abnormalities such as cancerous lesions in the brain MRI. Although numerous efforts in recent years have advanced this technique, there is no single approach that can generally solve the problem of segmentation for the large variety of image modalities existing today. We have demonstrated the segmentation of brain MRI for detection of abnormalities as well as ventricles and white matter in the brain. Different basic segmentation filters implemented in ITK were used in pipeline for brain MRI segmentation.

In general, presented results showed that the application of region growing, and combination of region-growing and level set techniques implemented in ITK proved to be efficient for the task of tumor, ventricles and white matter segmentation. Setting the seed points for the fast marching segmentations for initial contour generation provided good results. There was a large improvement concerning quality with level set methods, compared to using only basic segmentation techniques like region growing.

In conclusion, ITK segmentation filters offered a large number of state of the art algorithms implemented in a very consistent and meaningful coding style. With the combination of techniques discussed above, it is important to get some experience in setting the parameters correct in order to get the best results for brain MRI segmentation using the ITK filters.

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