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Image Segmentation and Registration

Neelam Singh
Sacramento State University

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I. INTRODUCTION

The delineation of the boundaries of anatomical structures in medical images can be an important tool in the extraction of diagnostic information from these images. Examples include the delineation of structures in functional imaging so that numerical functional information can be obtained, segmentation of an image so that organ dimensions and volumes can be determined, and segmentation of an image into appropriate anatomical structures so that patient-specific finite element models can be constructed. Although many different approaches to image segmentation have been proposed, only two are in widespread use—manual delineation and segmentation by intensity.

In the case of two-dimensional (planar or section) images manual delineation of the boundary is still the standard method used, even though there is evidence of significant variation between different operators [1]. In the case of 3D imaging, manual delineation of an object boundary is time consuming and tedious, and extraction of a reliable surface is difficult. Nevertheless, manual delineation is often taken as the gold standard, if only because it is recognized that in practice humans are capable of drawing boundaries in situations which challenge many computer based methods. In practice humans may produce sub-optimum boundaries but this may be as much to do with the tedium of drawing an accurate boundary, especially in circumstances where it is known that the boundary does not have to be of exceptionally high accuracy, as with any lack of ability accurately to draw the boundary. There are of course situations where even a human can be uncertain about where to draw a boundary, but in these circumstances, it is usually due to the fact that the image does not carry enough information to identify or suggest where the boundary should be.

The delineation of the boundaries of novel image structures in image guided neurosurgery can be an important tool in the extraction of diagnostic information from these images. Examples include the delineation of structures in functional imaging so that numerical functional information can be obtained, segmentation of an image so that organ dimensions and volumes can be determined, and segmentation of an image into appropriate novel image structures so that patient-specific finite element models can be constructed. Although many different approaches to image segmentation have been proposed, only two are in widespread use manual delineation and segmentation by intensity.

Segmentation by intensity can be effective in a variety of circumstances. It obviously requires that adjacent structures differ in pixel or voxel intensity. One requirement is that the sensitivity of the imaging device does not vary as a function of position. If this condition is not met, then segmented version. voxels representing the same material will differ in intensity, thus defeating the method. A potential additional problem is that if the image is noisy, especially close to the edges of a region of uniform intensity, isolated clusters of voxels will appear and the voxels in the segment selected by a range of intensity values will not be connected. Both of these problems can be addressed. MR images in particular can demonstrate significant nonuniformity. Pham and Prince [21] describe an algorithm that can correct for non-uniformity when segmenting an image into a pre-selected number of regions. This works very well for brain images, where significant structures may have different intensities but it is not too difficult to find other images where this is a less satisfactory approach. MRI image of the knee and the same image segmented using the algorithm of Pham and Prince [21] shows good results. Although segments have been extracted they still need to be separated, typically through the use of morphological operations, and identified. Segmentation by intensity can be effective in a variety of circumstances. It obviously requires that adjacent structures differ in pixel or voxel intensity. One requirement is that the sensitivity of the imaging device does not vary as a function of position. If this condition is not met then voxels representing the same material will differ in intensity, thus defeating the method. A potential additional problem is that if the image is noisy,

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In medical image analysis, segmentation is a difficult process due to the characteristics of the imaging modalities but important problem in biomedical applications.

One such modality that has had a great deal of attention from those researching image segmentation techniques is magnetic resonance imaging (MRI). Automatic brain abnormal tissues segmentation fromMR images is a difficult task that involves various disciplines covering pathology, MRI physics, radiologist's perception, and image analysis based on intensity and shape. There are many issues and challenges associated with brain tumor segmentation. Brain tumors may be of any size, may have a variety of shapes, may appear at any location, and may appear in different image intensities. Manual segmentation is a more difficult and time-consuming task.

$$f_b(r) - m_b(r) = \frac{1}{2}\Delta r(r)\left[\frac{\partial f_b(r)}{\partial r} + \frac{\partial m_b(r)}{\partial r}\right].$$

Moreover, the real time analysis and diagnosis due to fatigue and habituation of physicians can lead to error. Experts typically have to view and analyze multiple images which force them to follow a tedious scanning procedure. This makes an automated brain tumor segmentation method desirable.

Segmentation of Images

The survey of segmentation methods for MR images provides many useful techniques.

A lot of methods for automated segmentation have been proposed in the literature.1-3 Although MR segmentation methods have been quite successful on normal tissues,4-8 the actual methods of MR segmentation are still very much in the development stages for pathological tissues with some success recorded for specific disease processes.9 The challenges associated with automatic brain tumor segmentation have given rise to many different approaches. The two methods do not rely on intensity enhancements provided by the use of contrast agents. A particular limitation of the two methods is that the input images are restricted to the T1, T2, and PD MR Image channels. Additionally, the methods require a training phase prior to segmenting a set of images. Other methods are based on statistical pattern recognition techniques, for example, the method proposed in Ref. 12 and was validated against meningiomas and low-grade gliomas.

Algorithmic View

A method that detects deviations from normal brains using a multi-layer Markov random field framework is proposed.13 Further, an anatomical atlas is used to guide a statistical classification process.14-16 Clark et al. proposed a method for the automatic detection and segmentation of glioblastomas multiforme from a combination of T1, T2, and T2 Flair MRI using classification and an anatomical knowledge database.17 Bonnie et al.18 recently reported results using an interactive tumor segmentation method. Other methods, such as k-nearest neighbors (k-NN) also group pixels based on their similarities in each feature image;19 however, manually selected training data from the various tissue types is required per slice thresholding is an important unsupervised technique for image segmentation to identify and extract a target from its background based on the gray levels of an image. Many threshold selection methods have been proposed in the literature.20 Minimum error thresholding is an optimal threshold selection technique for image segmentation which is derived under normal distribution. Ye22 suggested two ways to implement the scheme. One is to minimize the criterion function and the other is to search a threshold iteratively. Kenong et al.23 and Cheng et al.24 demonstrated the use of minimum error thresholding in medical images. In this work, an attempt is made to detect the abnormality in MRI images by using minimum error thresholding method for the real MRI data obtained for four different diseases viz. Metastases, Meningiomas, Gliomas, Astrocytomas.

The refinement of the optical microscope and development of specific dyes in the late 19th century initiated the detailed examination of the architecture of the brain at the cellular level. Camillo Golgi's black reaction that fortuitously labels only 1% to 5% of the neurons present (

Golgi, 1873), Franz Nissl's staining procedure that labels all cell bodies (Kreutzberg, 1984 2), Carl Weigert's white matter stain (Weigert, 1882), Vittorio Marchi's procedure for staining disintegrating axons (Marchi, 1887 4), and the axonal precious metal stains of Max Bielschowky and Santiago Ramon y Cajal (Bielschowsky, 1903; DeFelipe & Jones, 1988 6) were all used to tease out a wealth of neuroanatomical information in brains of a number of species. Many of these century-old stains are still used alongside modern fluorescence, immunohistochemical, and in situ hybridization "staining" techniques. Microscopes that would be familiar to Cajal are currently used alongside confocal and two-photon microscopes, which provide clarity undreamed of in Cajal's time. In the use of both the modern and classical techniques, an optically transparent sample is an obvious and common requirement. This typically limits the sample being examined to a thin section of a fixed specimen. Thus, the vast majority of knowledge about the cytoarchitecture of the brain arises from in vitro observations of specimens after complex chemical (fixing and staining) and physical (thin slicing) manipulations. Magnetic resonance imaging (MRI) offers the opportunity to obtain in vivo three-dimensional images of optically opaque specimens. Using MRI, the same individual can be imaged repeatedly over time. Thus, time sequences of images can be examined to follow the progression of a disease state or to follow the embryological development of an individual animal.

Structural Systems

The development of structure and function in the nervous system is the product of stereotyped cell divisions and cell movements that generate a complex, interconnected system out of an apparently homogeneous neural tube. In many respects, developmental neurobiology of vertebrates remains in its infancy, with many unanswered basic mechanistic questions. These include: (a) the range of phenotypes that can be adopted by the progeny of a single neuroblast, (b) the mechanisms responsible for assigning cell phenotypes to developing neurons, (c) the patterns of cell migration during neurogenesis, (d) mechanisms controlling the cell migrations, (e) mechanisms underlying the aggregation of cells to form specific recognizable regions of the brain, (f) mechanisms underlying selective cell death, and (g) the establishing of axonal patterns and connections during mammalian brain development. The intrinsic difficulty in addressing mechanistic questions is compounded by the paucity of structural data available on the developing vertebrate brain. Without knowing what is happening, as well as where and when, it is difficult to formulate and evaluate hypotheses about how events come about. The experimental goals of the work described in this chapter are to refine imaging techniques to permit in vivo analyses of axonal patterning, and to create atlases of in vivo three-dimensional magnetic resonance images of the developing brain. This work addresses the fundamental what, when, and where aspects of brain development.

The central theme at the computational-technological-biological interface in this work is to apply newly emerging computational techniques to in vivo MR imaging of the developing brain. This involves major changes in the MRI data-collection/analysis paradigm, so that the data collection and final imaging goals of the investigator are algorithmically incorporated into a set of interactive computational tools. By fashioning these tools into a "teleological pipeline," we are developing a spreadsheet environment for MRI data collection, analysis, rendering, and viewing. By a teleological pipeline we mean computational algorithms and instrumentation, in which the users' goals (i.e., the qualities they wish the final image to possess) guide the data-collection and processing procedures. The users' goals are figuratively entered in one section of the spreadsheet, and, ultimately, the images appear in another section--where they can be evaluated by the user, the goals can be modified, and the process can be repeated. In this way, we are "closing the loop" between the data-collection phase and the image and model production phases of MRI. The teleological pipeline is a robust process of converting goals into computational procedures.

Optimization Problems

Part of the change in paradigm advocated here involves being able to express "what you want" in terms of constrained optimization problems with error metrics, target functions, and other computable quantities. The experience gained in applying goal-directed design in other settings (e.g., making computer animations that are graceful and designing complex very large scale integration [VLSI] circuitry; Barzel & Barr, 1988; Kirk, Fleischer, Watts, & Barr, 1992; Platt & Barr, 1988 8) is being used as a base from which to extend it to MRI. The large number of ways to perform the MRI experiment, coupled with the large number of parameters in any given experiment, make MRI an extremely versatile technique and an ideal venue in which to apply our goal-directed imaging scheme. Its application to MRI will not only greatly increase the efficacy with which data can be collected and analyzed, but will also point the way

to its application in other complex methodologies used in the neurosciences.

At the analysis level, this goal-directed approach will enable one to increase the information extracted from multispectral MRIs via the development of new methods for identifying tissues, volumetrically rendering those different tissues, and creating animations. The same tools will be useful for developing new and faster MRI methods, by specifying low-level goals, such as relationships between individual parts of an imaging sequence and the characteristics of the final image, or by automatically compensating for hardware limitations.

There are two major exports from this research effort: (a) a set of images that will form atlases of brain structure and development and provide information about neuronal connectivity; and (b) a set of integrated software tools that can be applied to data collection in other MRI and light microscopy settings. Novel ways to publish multidimensional images are being explored: videotape, CD-ROM, and electronically, via file transfer protocol (FTP) sites and World Wide Web (WWW) pages; the purpose is to provide a means for data, images, and analysis methods to be readily exchanged. Although MRI data are dealt with in this work, many of the computational aspects will be readily transferable to other imaging modalities. The agenda in this work is to truly integrate sophisticated goal-directed algorithms into the complex experiments of MRI. This effort serves as an exemplar for other neuroscientists who wish to maximize the efficacy of their use of the computer in designing and performing experiments and in analyzing and displaying the results of the experiments, regardless of the nature of the experimental apparatus.

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