Blood Vessel Segmentation in Complex-Valued Magnetic Resonance Images with Snake Active Contour Model

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ABSTRACT

Accurate blood vessel segmentation plays a crucial role in non-invasive blood flow velocity measurement based on complex-valued magnetic resonance images. We propose a specific snake active contour model-based blood vessel segmentation framework for complex-valued magnetic resonance images. The proposed framework combines both magnitude and phase information from a complex-valued image representation to obtain an optimum segmentation result. Magnitude information of the complex-valued image provides a structural localization of the target object, while phase information identifies the existence of flowing matters within the object. Snake active contour model, which models the segmentation procedure as a force-balancing physical system, is being adopted as a framework for this work due to its interactive, dynamic, and customizable characteristics. Two snake-based segmentation models are developed to produce a more accurate segmentation result, namely the Model-constrained Gradient Vector Flow-snake (MC GVF-snake) and Stochastic-snake. MC GVF-snake elaborates a prior knowledge on common physical structure of the target object to restrict and guide the segmentation mechanism, while Stochastic-snake implements the simulated annealing stochastic procedure to produce improved segmentation accuracy. The developed segmentation framework has been evaluated on actual complex-valued MRI images, both in noise-free and noisy simulated conditions. Evaluation results indicate that both of the developed algorithms give an improved segmentation performance as well as increased robustness, in comparison to the conventional snake algorithm.

Keywords: Blood Vessel, Phase-Contrast Magnetic Resonance Imaging, Segmentation, Simulated Annealing, Snake Active Contour Model

INTRODUCTION

Magnetic Resonance Imaging (MRI) has played increasing significant roles in today medical practice. Among the most prominent clinical strength of MRI are its non-hazardous nature and its ability to provide high contrast between various types of tissue. Nowadays the application of MRI has expanded beyond conventional structural mapping into chemically-specified
and flow-related imaging. Advanced applications of MRI require supports of sophisticated signal processing procedure to infer the desired information from typical Magnetic Resonance images. This chapter presents the development of blood vessel segmentation algorithms dedicated to support the quantitative flow imaging based on Phase Contrast Magnetic Resonance Angiography (PC-MRA). PC-MRA requires the consideration of both the magnitude and phase information derived from the MRI natural complex-valued signals, rather than relies solely on the magnitude information as commonly practiced in the MRI application for structural mapping.

MRI is physically based on the Nuclear Magnetic Resonance (NMR) phenomenon discovered at 1946 by Felix Bloch and Edward Purcell. This phenomenon notes the resonance of magnetic systems when triggered with radio waves with frequencies corresponding to its natural magnetic frequencies; that is the gyroscopic precession frequency of the magnetic moment of the nuclei under the influence of an external static magnetic field. By observing the externally measured NMR signals, MRI produces images of the internal physical and chemical characteristics of an object. This is made possible by the spatial encoding principles developed by Paul Lauterbur on 1972, which in turn served as a foundation for the current MRI systems.

The potential of MRI for flow-related imaging is due to its coherent imaging nature. As a coherent imaging system, MRI produces complex-valued signal where magnitude and phase images can be derived. The general form of complex-valued image can be written as:

\[ I(x, y) = |I(x, y)| \exp(j\phi(x, y)) \]  \hspace{1cm} (1)

where \( j = \sqrt{-1} \) is the imaginary number. The magnitude part of equation (1) \(|I(x, y)|\) corresponds to the magnitude image, while the phase part \( \phi(x, y) \) corresponds to the phase image.

The magnitude and phase images of MRI have its own physical and clinical interpretation. MRI magnitude image represents the structural information of the object, while the phase image is related to the internal physical and chemical characteristics. Among the simultaneous use of the MRI magnitude and phase images in clinical applications is the Magnetic Resonance Angiography (MRA) procedure, first proposed by Charles Dumoulin in 1987. This procedure allows imaging and measurement of bulk blood flow in large vessels without the need for contrast agents.

Quantitative flow measurement with MRI is based on the observation of phase shifts acquired by magnetic moments (spins) moving along a magnetic field gradient in comparison to stationary spins. For linear field gradients, the amount of this phase shift is proportional to the velocity of the moving spin. Phase shifts in MRI systems however not only occur from movement of magnetic moments. The originally stationary tissue may also experience phase shift come from chemical shift or external magnetic field inhomogeneity. To measure the net phase shift between moving and stationary spins, NMR signals observation is repeated in a bipolar gradient mode. Measurement in bipolar gradient mode will eliminate the phase shift accounted by another cause than movement of magnetic moments.

As a consequence of the MRI phase image formation, phase shift should lies between the ranges of \( \pm \pi \). Therefore, the calculation of velocity from phase shift information requires a procedure to tune the maximum phase shift measured by the system to the peak velocity expected in the vessel (encoding velocity). Encoding velocity determination is very crucial in the PC-MRA procedure. Wrapping of the velocity information will occur if the encoding velocity is too low. In the other hand, measurement will be prone to error and fail to detect slow movement if encoding velocity is too high. Peak velocity varies under different physiological conditions, and its exact determination prior to the measurement itself is not possible. However, its value can be approximated with various preliminary