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Tissue classification in magnetic resonance images through the hybrid approach of Michigan and Pittsburg genetic algorithm

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ABSTRACT

Magnetic resonance system generates image data, where the contrast is dependent on various parameters like proton density (PD), spin lattice relaxation time (T1), spin–spin relaxation time (T2), chemical shift, flow effect, diffusion, and perfusion. There is a lot of variability in the intensity pattern in the magnetic resonance (MR) image data due to various reasons. For example a T2 weighted image of same patient can be generated by different pulse sequence (Spin Echo, Fast Spin Echo, Inversion recovery, etc.) or on different MR system (1T, 1.5T, 3T, system, etc.) or using different RF coil system. Hence, there is a need for an adaptive scheme for segmentation, which can be modified depending on the imaging scheme and nature of the MR images. This paper proposes a scheme to automatically generate fuzzy rules for MR image segmentation to classify tissue. The scheme is based on hybrid approach of two popular genetic algorithm based machine learning (GBML) techniques, Michigan and Pittsburg approach. The proposed method uses a training data set generated from manual segmented images with the help of an expert in magnetic resonance imaging (MRI). Features from image histogram and spatial neighbourhood of pixels have been used in fuzzy rules. The method is tested for classifying brain T2 weighted 2-D axial images acquired by different pulse sequences into three primary tissue types: white matter (WM), gray matter (GM), and cerebro spinal fluid (CSF). Results were matched with manual segmentation by experts. The performance of our scheme was comparable.

1. Introduction

Image segmentation requirement is important in all MR image analysis tools, used for diagnosis and for planning treatment. These image analysis tools analyze MR images of different contrast characteristics like: T1 weighted (T1), T2 weighted (T2), and proton density (PD). Different contrast images (like T1, T2, and PD) can be acquired using different pulse sequences, which are decided by radiologist, based on region of interest, patient history, type of coil or type of MR system [1,2]. There are variations in the intensity profile of histogram of particular contrast image say T2 weighted acquired using different pulse sequence, or different coil or MR system supplied by different vendor. The same is true for other contrast images also. The intensity/histogram pattern for same contrast image for the same subject under different scanning conditions may be similar, but there are intensity variations for same pixel in the acquired images. This is visible, in shift of peaks and valleys in the histogram. With these intensity variations under different acquisition conditions, it is difficult to obtain anatomical segmentation boundaries based on intensity threshold alone and needs an adaptive segmentation procedure.

Thresholding for MR image segmentation is the simplest approach. Extensive surveys discussing various aspects of threshold are reported in the literature [3,4]. Threshold selection algorithms have been compared with the help of experimental results on a set of real life images or on a set of histograms [5,6]. There are good examples, which show that separating object and background regions with the help of first order and second order statistics give good results for a large class of MR images [7]. Normally the threshold is applied on the intensity values only.

However, dynamic range of soft tissue contrast is widespread in MR images. Moreover the transition across boundaries is gradual, which poses special challenge for segmentation of anatomical boundaries. Also other problems encountered are due to potential sources of errors, such as image noise, intensity non-uniformity, and factors related to image weightings. Any algorithm for segmentation of MR images should adequately address these problems.

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