A New Model Based Method to Automatic MR Brain Image Segmentation

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Introduction

In this work, we present a fully automatic method for the segmentation of brain tissue involving MR images. A major objective of this approach is to eliminate the requirement of direct human inputs as was reported by Peng et al. [1], the so-called supervised method. The supervised method often uses the classification approach, such as reported by Peng et al. [1] who used a statistical decision model of the maximum a posterior probability and Markov random field for a prior probability (MAP-MRF) framework with a spatial Gaussian mixture model (SGMM) for the estimation of a posterior probability. One critical step of this approach is the parameters learned in SGMM. These parameters are associated with the mixture center locations and their corresponding average regional intensities. Traditionally, these parameters are learned from training sets that are usually provided by direct human inputs [1]. In the current work, the direct human inputs are replaced by the SPM brain atlas [2].

Methods

a. Tissue classification: The tissue classification was conducted in a way similar to that of the supervised method. This method is to search the optimal label of each pixel in the images such that $\omega(x, y) = \arg\max(P(\vec{X}(x, y)|\omega(x, y))P(\omega(x, y))$, where $\omega(x, y)$ is the label at the pixel (x, y), $\vec{X}(x, y) = [x, y, I(x, y)]$ is a 3-component vector, and $I(x,y)$ is the image intensity. In the SGMM, we have separated the tissue *i* into N_i components or sub-regions, and the center of sub-region r_{ij} is corresponding to the spatial mean vector. An intuitive observation is that, in a small area of the image, the intensity variation of the sub-regions within one tissue type should be less than that between tissues. Thus, the best estimated mean intensity, $\mu^I{}_{ij}$, should also result in the minimum intensity variation in a small area of the image. The mathematic formulation of this observation can be expressed as $(\mu^I)^* = \underset{\mu^I}{\operatorname{argmin}} \sum_i \sum_{j \in R_i} f(\mu^I{}_{ij})$, where $f(\mu^I{}_{ij}) = \sum_{m \in G(r_{ij})} (\mu^I{}_m - \mu^I{}_{ij})^2$ describes the intensity variation of the sub-regions within tissue *i*. $G(r_{ij})$ denotes a set of sub-regions that are connected to the sub-regions within tissue *i*.

b. Segmentation procedure: Our algorithm consists of the following major steps: **1)** Co-register the SPM brain atlas with the target MR images to construct the referenced brain images, **2)** Normalize the referenced brain imaging intensity to the level of the MR brain images, **3)** Use expectation maximization (EM) algorithm [3] or modified k-mean (MKM) algorithm [1] to learn the SGMM parameters from the referenced brain atlas slice by slice and set the learned parameters as current parameters, **4)** Repeat the following procedures for a prior set number of iterations: **a)** Use iterated conditional modes (ICM) algorithm to determine the label of each slice of the target images according to the current parameters, **b)** Use EM algorithm or MKM algorithm to modify the current parameters according to the latest labels, **c)** Modify the current parameters by minimizing the intensity variation of the local regions within the same tissue.

Results

We tested the new method on two brain volumes. One is 1.5 Tesla simulated brain volume images [4] with matrix size of 181x217x181, 8-bit quantization, voxel size 1x1x1 mm^3, noise level 9% and inhomogeneity levels 40% (the worst case). The other is *in vivo* brain images from IBSR [5] with matrix size of 256x256x128, 16-bit quantization, and voxel size 1.17x1.17x1.5mm^3, obtained from 1.5 Tesla MR Scanners. Fig. 1 illustrates the GM segmentation results of slice 101 from the simulated data. It clearly demonstrates that the new method outperforms the supervised methods [1], and the improvement is most obvious on the bottom part of images illustrated in Fig. 1 (c) and (d). Fig. 2 illustrates the WM segmentation results of slice 22 from the *in vivo* brain images. Note that the new method achieves significant improvement (from 72.5% to 89.4%). The improvement on the simulated data and *in vivo* data is attributed to the fact that the learned SGMM parameters are more accurate and reliable due to the sub-region similarity criterion. Furthermore, by implementing the brain atlas, the new method can be fully automatic.

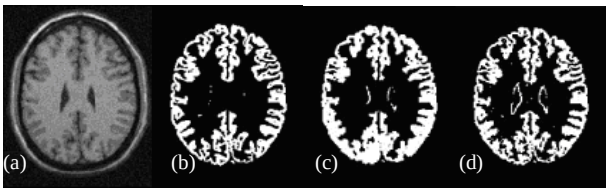

Fig.1. Comparison of GM Segmentation using simulated data: (a) Original Data (slice 101); (b) GM from Gold standard; (c) GM result using supervised method (86.5%); (d) GM result using the new method (90.0%)

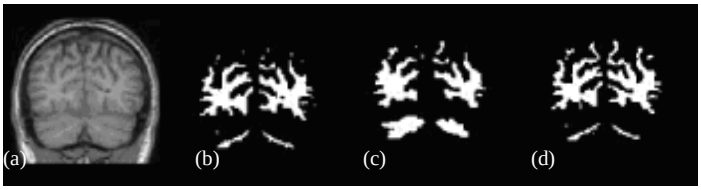

Fig.2. Comparison of WM Segmentation using *in vivo* data from IBSR: (a) Original data (slice 22); (b) WM from Gold standard; (c) WM result using supervised method (72.5%); (d) WM result using the new method (89.4%).

Discussion

We present a novel automatic method to segment the MR brain images without human intervention or input. The method is based on a statistical model incorporating the MAP-MRF framework with sub-region similarity criterion. The SGMM parameters are learned from the referenced brain atlas reconstructed from a digital brain atlas in an automatic manner. We have demonstrated that this method worked well for a simulated data and an *in vivo* data at 1.5T. The results are superior to that of the supervised method [1]. Further work will focus on the validation of high-field images that are believed to pose severe intensity inhomogeneity and the improvement of the computational speed for parameters learning.

Reference

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