MULTILEVEL SEGMENTATION AND CLASSICATION OF MS LESIONS

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Abstract

This paper focuses on the segmentation and classification of multiple sclerosis lesions in magnetic resonance images. As MRI is the primary tool used in the diagnosis of multiple sclerosis, there is substantial interest in developing an algorithm that will detect lesions from such images. We present a flexible framework in which segmentation and classification are integrated. We assume that we are given a training set of MRI images which contains manually labeled regions of MS lesions. The algorithm we used combines two effective techniques from the computer vision literature: graph-based bottom-up methods and top-down generative models. Results on synthetic data obtained from the McGill Brainweb simulator and real data acquired at 3T are presented.

Introduction

Multiple sclerosis (MS) is a demyelinating disease of the central nervous system (CNS). With MS, the body's immune system attacks myelin, which protects the nerve fibers in the CNS. The damaged myelin leads to scar tissue (sclerosis). Even though the causes of MS remain unknown and there is no cure as of today, much is known about the mechanisms involved in the disease process and several therapies have proven helpful. In order to better understand MS, magnetic resonance imaging (MRI) is often used during the diagnostic process. MRI is the best imaging technology for detecting the presence of MS lesions in different parts of the CNS. Presently, to fully diagnosis and quantify MS lesions from MRI images, it is common to have human experts manually delineate the lesions from the data. However, it is an extremely time consuming task and very often have significant intra and inter-observer variability. Therefore, there is a need to have a fully automatic detection of MS lesion. However, it is well known that lesions are relatively small, exhibit a wide variety of shapes, may have significant differences in location across patients, and have varying intensities and textures.

Methods

We present a framework in which segmentation and classification are integrated in a flexible manner. In particular, we will adopt the approach of [1]. We assume that we are given a training set of MRI images which contains manually labeled regions of MS lesions. Our algorithm combines two effective computer vision algorithms, namely a graph-based bottom-up method and a top-down generative model. Graph-based bottom-up methods are based on the concept of spectral clustering. Such algorithms are able to give quick answers but are very memory intensive and do not always give meaningful results. Top-down generative models are guaranteed to get an answer based on the posterior probability but are very computationally expensive and hard to design and train. The framework allows for different users to specify different types of features, e.g. intensity, spatial location, shape, and input channels to be used for classification. The algorithm is summarized as follows: **1)** Based on the training set where each voxel corresponds to each node, generate the probabilities $P(m_i, m_j)$, prior probability that nodes v_i and v_j have model (class) labels m_i and m_j, and $P(s_i \mid m_i)$, the conditional probability of an observed feature s_i at the node v_i for the model m_i. **2)** At level $t = 0$, initialize the graph G^0 with each voxel being a node v_i^0 with 6-neighbor connectivity, the feature being the intensity $s_i^0 =$ Intensity at voxel v_i^0, and the weight $W_{ij}^0 = \exp(-\theta \mid s_i^0 - s_j^0 \mid)$, where θ is a user-defined parameter. **3)** Choose representative set R^t such that $\forall v_i \in V^t$, with V^t being the entire set of nodes and $0 < \beta < 1$, $\sum_{v_j \in R^t} W_{ij}^t \geq \beta \sum_{v_j \in V^t} W_{ij}^t$. **4)** Construct the graph at the next level $t+1$, $G^{t+1} = (V^{t+1}, W^{t+1})$ by the following: ***a)*** Set $V^{t+1} = R^t$. ***b)*** Compute interpolation matrix $P_{ij}^t = W_{ij}^t / \sum_{v_k^{t+1} \in V^{t+1}} W_{ik}^t$ where $v_i^t \in V^t$ and $v_j^{t+1} \in V^{t+1}$. ***c)*** Compute the affinity at coarser level, $W^{t+1} = P^{tT} W^t P^t$. ***d)*** Compute the feature of node $v_j^{t+1} \in V^{t+1}$, $s_i^{t+1} = \sum_{v_i^t \in V^t} P_{ij}^t s_i^t / \sum_{v_i^t \in V^t} P_{ij}^t$. ***e)*** Use the model-based probabilities to modify the affinity. For $v_i^{t+1}, v_j^{t+1} \in V^{t+1}$, $\tilde{W}_{ij}^{t+1} = W_{ij}^{t+1} P(X_{ij} \mid s_i^{t+1}, s_j^{t+1})$ and set $W^{t+1} = \tilde{W}^{t+1}$. **5)** Set $t \leftarrow t+1$ and repeat steps **2)-4)** until $\mid V^t \mid = 1$ or $W^t = 0$ or $t = T$, where T is a user defined value. **6)** Classify each voxel $v_{i_0}^0$ by $m_{i_0}^* = \text{mode}\{m_{i_0}^0, m_{i_0}^1, \ldots, m_{i_0}^{T-1}, m_{i_0}^T\}$.

Results

BrainWeb: We first test our algorithm on the McGill BrainWeb dataset. We trained our algorithm on noise level 3%with RF level 0%. Notice that the false positive rate is lower at noise levels 5 and 7% than at noise level 3%. This is expected as the overlap (true positive) decreases from 3% to 7%, the false positive rate will increase.

Noise level with RF 0%	Overlap	False Positive (fp)	Similarity	Noise level with RF 0%	Overlap	False Positive	Similarity
3%	0.9707	0.5060	0.7839	5%	0.8417	0.2186	0.8170
7%	0.5215	0.1102	0.6392	9%	0.2823	0.5869	0.3020

Table 1: Classification measures on the BrainWeb dataset

Real Data: We now present the results of our algorithm and compare it to the manually marked ground truth data. In the ground truth data, lesions are marked in red, whereas it will be marked as light blue in the classification results given by the algorithm.

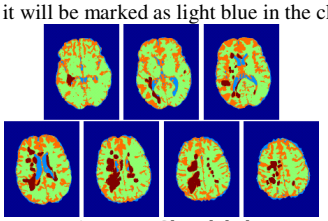

Figure 1a Class labels

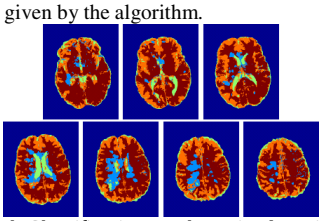

Figure 1b Classification results trained on right side of volume, overlap 0.61, fp 0.41 and similarity 0.60.

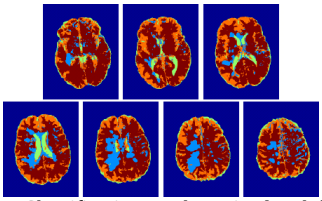

Figure 1c Classification results trained on left side of volume, overlap 0.76, fp 0.67 and similarity 0.62.

Discussion and Conclusions

According to [2], the state-of-the-art algorithms have similarity of 0.6, which our proposed algorithm achieves without any extensive preprocessing, and with a currently limited amount of training data. We are also going to use this framework to analyze a series of MRI images of the same subject taken over a period of time. In this case, the manually marked data of a previous time can be used as the training set and latter time points being the testing set. Adding prior information about the position of the lesions is also being investigated. The proposed framework is fully flexible and allows for different users to specify different types of features, eg intensity, spatial location, shape, to be used for classification.

References

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