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MRI segmentation fusion for brain tumor detection

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ABSTRACT

The process of manually generating precise segmentations of brain tumors from magnetic resonance images (MRI) is time-consuming and error-prone. We present a new algorithm, Potential Field Segmentation (PFS), and propose the use of ensemble approaches that combine the results generated by PFS and other methods to achieve a fused segmentation. For the PFS method, we build on our recently proposed clustering algorithm, Potential Field Clustering, which is based on an analogy with the concept of potential field in Physics. We view the intensity of a pixel in an MRI as a "mass" that creates a potential field. Specifically, for each pixel in the MRI, the potential field is computed and, if smaller than an adaptive potential threshold, the pixel is associated with the tumor region. This "small potential" segmentation criterion is intuitively valid because tumor pixels have larger "mass" and thus the potential of surrounding regions is also much larger than in other regions of smaller or no "mass". We evaluate the performance of the different methods, including the ensemble approaches, on the publicly available Brain Tumor Image Segmentation (BRATS) MRI benchmark database.

1. Introduction

The Internet of Things consists of a large number of diverse and spatially distributed sensors that collect and/or generate data. The fusion of such heterogeneous data facilitates the discovery of important patterns and the subsequent understanding of the problem or situation that is being monitored. In particular, clustering algorithms combine heterogeneous data into different groups or "clusters" and thus allow for the categorization/classification of the data. In this paper we consider the problem of clustering of image pixels based on their associated heterogeneous data values, i.e., visual intensities, and the fusion of the multiple alternative segmentations generated by different clustering methods, for the purpose of automatic brain tumor segmentation from magnetic resonance images (MRI).

In the medical imaging domain, delineating the extent of tissue abnormalities that appear in an image is a very common but critical task. However, doing this task manually is very time-consuming and error-prone. E.g., a study [1] found average variations of 16%–40% between individuals performing the same brain tumor segmentation and average variations of 5%–35% within individuals performing the segmentation three times at one-month intervals. As a result, the automatic segmentation of tissue abnormalities from medical images is a critical component of next generation computer-aided diagnosis technologies. The objective is to develop automatic segmentation algorithms that can achieve results that are comparable to those generated by medical experts, e.g., a neuroradiologist.

MRI exploits the physical properties of the nuclear spin of hydrogen to generate a digital representation of brain tissue. Because the human body is mostly made up of water (the brain in particular is about 85% water), hydrogen, which is composed of a single proton, is the most abundant element. Under normal circumstances, the nuclear spin of hydrogen is randomly orientated. However, when placed in a strong magnetic field, such as that generated by an MRI scanner, the nuclear spin aligns with the magnetic field. If a radio wave frequency (RF) that matches the hydrogen nuclear spin natural oscillation frequency is applied, the nuclear spin moves out of alignment away from the magnetic field, a phenomenon known as resonance. If the RF source is switched off the nuclear spin realigns with the magnetic field, a phenomenon known as relaxation, and causes a signal (also RF) to be emitted. Different tissues relax at different rates and different types of relaxation times (T1, T2) are used as components of the signal. For instance, high water content, which is a common manifestation of a disease, appears as bright areas in a T2 MRI.

In general, image segmentation is a hard problem for computers that requires both low-level and high-level object-specific knowledge. This has resulted in a situation where most previous work on

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automated brain tumor segmentation is based on machine learning, both supervised [2–10] and unsupervised [11–19]. Among the supervised methods, approaches include using Support Vector machines [4,6], Random Forests [2], Bayesian classifier [7], fractal features [8], outlier detection [9] and Markov Random Fields [10]. The limiting factor of supervised learning methods is the amount of expert input that is required in the form of, e.g., a priori information, hand-specified information on a set of training images, etc.

Unsupervised learning can be formulated as a search for patterns in unlabeled data. With the unsupervised methods, the general routine is to establish local feature correspondences between sets of feature points in an input image and solve an optimization problem based on an objective function with particular constraints. However, some unsupervised methods such as [15,16] are not yet fully automatic and require manual human interaction.

Among the unsupervised methods, clustering methods are very popular and differ from classification methods such as discriminant analysis in that classification involves a *known* number of groups and in that the operational objective is to assign a new observation to one of these clusters. On the other hand, cluster analysis makes no assumption about the number of clusters and ideally seeks to find the optimal number of clusters based on some objective function. It is known that the final assignment of observations depends, to some extent, on the initial partition [20]. Because of its conceptual simplicity *K*-means is the best known and most commonly used clustering algorithm, which is reflected in the large number of methods, e.g., [11,18,19,21], that are based on it or variations thereof. However, its performance depends heavily on the number of initial cluster centers and on the selection of the initial cluster centers.

In [21] the Electrostatic Force Clustering algorithm [22], a variation of *K*-means, is employed for tumor localization in MRI. The algorithm, which is based on an analogy with the laws of electrostatics, is said to always converge to the same solution independently of different initial conditions, i.e., initial cluster centers. The direction of movement of the cluster centers is determined by the electrostatic force that affects them. When an electrostatic balance/equilibrium is obtained, the centers stop moving. Accurate localization (coarse detection) of the center of a tumor region is important, because it is typically a requisite landmark for the subsequent fine tumor detection process of identifying the precise boundaries of the tumor, e.g., the segmentation step.

In [21], after the center localization step, a region growing segmentation algorithm is employed with the seed initialized to the center found. In a region growing segmentation, starting from the initial seed point, each neighboring pixel (8-connected) is examined and it is determined whether or not the pixel should be added to the tumor region. This process iterates recursively on each newly added pixel. The criterion that is used to determine whether or not a neighboring pixel belongs to the tumor region is based on the intensity of the pixel. In this paper, we refer to this combination of region growing segmentation with electrostatic force clustering for seed initialization [21,22] as the FOR method. A good choice of initial seed point is an important issue that has a critical impact on the segmentation performance of region growing. Thus, the closer the initial seed point is to the true tumor center, the better the resulting segmentation. As we observed in [23], the localization (and subsequent segmentation) performance of this algorithm is highly dependent on the value of a step size parameter α.

Given a set of instances represented by points $\{\mathbf{r}_1, \ldots, \mathbf{r}_n\}$, where $\mathbf{r}_i \in \mathbb{R}^d$, in the Electrostatic Force Clustering algorithm [21,22], the points are assumed to be electrical charges, each with a position $\mathbf{r}_i$ and a negative charge w_i. A set of K cluster centers $\{\mathbf{c}_1, \ldots, \mathbf{c}_K\}$, where $\mathbf{c}_i \in \mathbb{R}^d$, is randomly initialized. Each cluster center $\mathbf{c}_i$ is associated with the subset $\mathcal{S} \subset \{\mathbf{r}_1, \ldots, \mathbf{r}_n\}$ of points that are the closest to it in the d-dimensional space. The corresponding total charge associated with $\mathbf{c}_i$ is $W_i = \sum_{\mathbf{r}_j \in \mathcal{S}} w_j$. The cluster centers are allowed to move according to the laws of electrostatics. That is, their direction of movement is determined by the electrostatic force that affects them in the space. At each step, the total force affecting $\mathbf{c}_i$ is

$$\mathbf{f}_i = \sum_{\mathbf{r}_j} \frac{W_i w_j}{r_{ij}^2} \frac{(\mathbf{c}_i - \mathbf{r}_j)}{r_{ij}} + \sum_{\mathbf{c}_j, i \neq j} \frac{W_i W_j}{r_{ij}^2} \frac{(\mathbf{c}_i - \mathbf{c}_j)}{r_{ij}} \tag{1}$$

where, in the first summation, r_{ij} is the distance $\| \mathbf{c}_i - \mathbf{r}_j \|$ and, in the second summation, r_{ij} is the distance $\| \mathbf{c}_i - \mathbf{c}_j \|$. At each step, the new position of each $\mathbf{c}_i$ is

$$\mathbf{c}_i^{(t+1)} = \mathbf{c}_i^{(t)} + \alpha \frac{\mathbf{f}_i}{\| \mathbf{f}_i \|} \tag{2}$$

where $\mathbf{c}_i^{(t+1)}$ is the next center position, $\mathbf{c}_i^{(t)}$ is the previous center position, α is a fixed step size and $\|\mathbf{f}_i\|$ is a force unit vector with the direction of movement.

In [21], this clustering algorithm is used for tumor localization in MRI. More specifically, the points $\{\mathbf{r}_1, \ldots, \mathbf{r}_n\}$ correspond to the image pixels, each with a position $\mathbf{r}_i \in \mathbb{R}^2$ and a negative charge w_i that is proportional to the intensity of the pixel. A number $K > 3$ of cluster centers are randomly initialized and the algorithm iterates according to Eqs. (1) and (2). After reaching equilibrium, the next step is to identify which of the K centers (or clusters) overlaps with the tumor, which can be estimated by simply selecting the center with the largest total charge, i.e., largest W_i.

In [23] we applied the potential-*K*-means method [24] to the tumor center localization problem. We viewed the intensity of a pixel as equal to its "workload" and employed the potential-*K*-means method [24], which generates a balanced distribution of the pixels into clusters of approximately equal total intensity. This balancing requirement introduced a search bias that tended to generate either small clusters of higher intensity pixels, which overlap with the tumor area, or large clusters of lower intensity pixels. In [25], we proposed Potential Field Clustering, which is based on an analogy with the concept of potential field in Physics, and also employed it for tumor center localization. The center of a tumor was localized and, as in [21], then used as the initial seed in a region growing segmentation algorithm. In this paper, we refer to this combination of region growing segmentation with Potential Field Clustering [25] for seed initialization, as the PFC method.

For a given MRI, let $\mathcal{S}_1, \mathcal{S}_2, \ldots, \mathcal{S}_n$ be the segmented images generated by n different segmentation algorithms. Each of the n segmentation algorithms is capturing the same MRI but, because they are using different segmentation criteria and focusing on different characteristics/properties, the resulting segmented images $\mathcal{S}_1, \mathcal{S}_2, \ldots, \mathcal{S}_n$ also have different characteristics/properties and segmentation results. However, because they use the same input, i.e., same MRI image, they also contain redundant and complementary information about the observed tissue abnormality. The different but complementary information from the n segmented images can then be fused into a single fused segmented image $\mathcal{S}_{fused}$ by employing a particular fusion rule that combines, e.g., pixel-level information, from the n segmented images.

In this paper we build on our previous work on Potential Field Clustering [25] and develop a stand-alone brain tumor segmentation algorithm, Potential Field Segmentation (PFS). We also propose the use of an ensemble of segmentation methods that includes PFS, FOR, and PFC to achieve a consensus segmentation that combines data from the multiple alternative segmentation results. That is, the segmented images $\mathcal{S}_{PFS}, \mathcal{S}_{FOR}, \mathcal{S}_{PFC}$ are fused into a single fused image by using different fusing rules. The rest of this paper is organized as follows. The proposed PFS method, as well as the ensemble approaches, are presented in Sections 2 and 3 respec-