Hierarchical Random Walker for Multimodal Brain Tumor Segmentation

Yang Xiao, Jie Hu

School of biomedical engineering, Southern Medical University, Guangzhou, China
genq@163.com

Abstract. In this text, a Random Walker (RW) based method is proposed for brain tumor MR images segmentation with interaction. Not only the method is designed to achieve a final segmentation result, but also it is a convenient tool for users to modify their results iteratively. To overcome the shortcoming of typical RW algorithm, we extend RW to feature space for soft clustering, and then carry out pixel-wise segmentation in image space. Proposed method is performed on multimodal brain MR images, including T2-weighted, contrast enhanced T1-weighted, and FLAIR sequences.

Keywords: image segmentation, brain tumor, Random Walker, interactive, hierarchical

1 Introduction

Segmentation of brain tumor image is very important. Because the inter-patient variation of tumor shape, position, texture, and size is large, a robust fully-automatic method is difficult to design. In addition, intervention is needed when automatic result is evaluated and validated. Therefore, we focus on interactive algorithms.

Since the Graph Cuts (GC) algorithm is brought to attention [1], a family of interactive segmentation methods are proposed and of interest for recent decade, such as Random Walker (RW) [2] and Shortest Path (SP) [3], which provide another chance to modify the segmentation results when automatic implementation is unavailable or incorrect, especially on medical images. In [4], these popular interactive algorithms are unified into a common optimization framework. However, RW is distinguished from others due to its particular soft segmentation. In next section, RW will be discussed, and our improvement of typical algorithm and its application for multimodal brain tumor MR will be illustrated.

2 Method

2.1 Typical Random Walker

The RW algorithm is formulated on a weighted graph and optimized by solving a Dirichlet problem. The objective function is given by

$$\begin{aligned} &\min_{x} \sum_{e_{i,j} \in E} w_{i,j} (x_i - x_j)^2, \\ &\text{s.t. } x(F) = 1,\ x(B) = 0, \end{aligned} \tag{1}$$

where x is the target soft label, and w is similarity measure between pixel i and j, and the constraints are set by interaction.
Furthermore, similarity measure w is often defined as

$$w_{i,j} = \exp(-\beta (\nabla I_{i,j})^2), \tag{2}$$

where $\nabla I_{i,j}$ denotes absolute distance in feature space between pixel i and j, and β is a parameter given by designer.

2.2 RW in feature space

Similarly, the discrete feature space is defined as an edge-weighted graph, and the objective function of clustering is given by

$$\begin{aligned} &\min_{\mu} \sum_{e_{i,j} \in E} s_{i,j} (\mu_i - \mu_j)^2, \\ &\text{s.t. } \mu(F) = 1,\ \mu(B) = 0, \end{aligned} \tag{3}$$

where μ represents clustering label, as well as s is similarity measure of distribution density between sample i and j in feature space, which is defined by

$$s_{i,j} = \exp(-\alpha (\nabla P_{i,j})^2), \tag{4}$$

where $\nabla P_{i,j}$ is defined as variation of distribution density in feature space, and α is a parameter given by designer.
In typical RW, similarity measure is defined by its negative correlativity to absolute distance in feature space, which neglects prior label information provided by user. To mine the prior information from the seeds as much as possible, we extend RW to feature space as a soft semi-supervised clustering. When the clustering labels are obtained, we will re-define the similarity measure as in (2) by relative distance between labels as follow,

$$w_{i,j} = \exp(-\beta (\mu_i - \mu_j)^2). \tag{5}$$

2.3 Proposed Method

The whole workflow of proposed method is illustrated in Fig. 1. In the pre-processing step, T2, CET1, and FLAIR sequences are filtered by Gaussian kernel. To initialize the hierarchical RW, the user has to select two groups of seeds which locate tumor and edema respectively, and the interface for interaction, where the user can input seeds in images of any modal, is shown in Fig. 2.

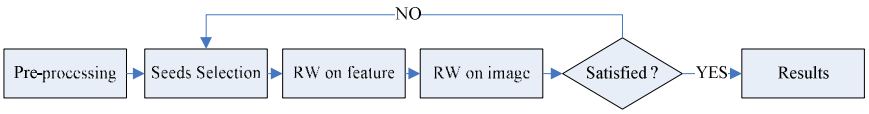

Fig. 1. Flow diagram of proposed method.

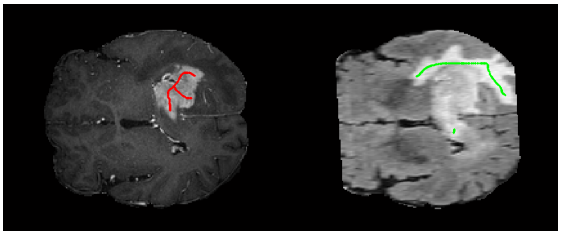

Fig. 2. Interface for selecting seeds.

After the initialization, the core algorithm of proposed method, which is hierarchical RW, is performed, and then results are displayed in the interface for user's iterative modification.

RW is carried out in T2-FLAIR intensity space, as described in last sub-section, to identify the abnormal (tumor and edema), and in T2-T1C intensity space to identify the tumor respectively. In Fig. 3, the joint distribution density and results of clustering is shown.

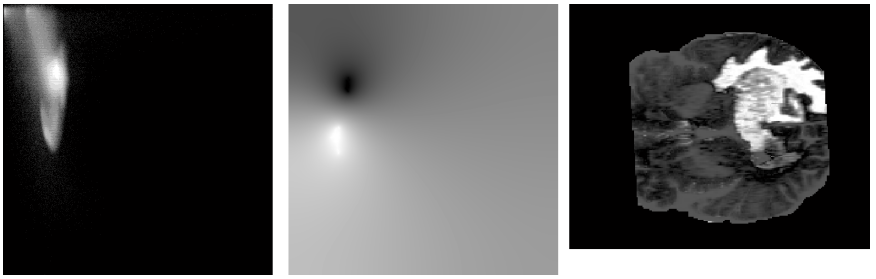

Fig. 3. From left to right: density in T2-FLAIR space; soft clustering labels; and images labeled by clustering result.

The labels of clustering are utilized to calculate similarity measure of pixel-pair according to (5), and typical RW in image space is employed to obtain segmentation labels, as shown in Fig. 4. If the segmentation is not accepted, the user could iteratively revise the result until satisfied.

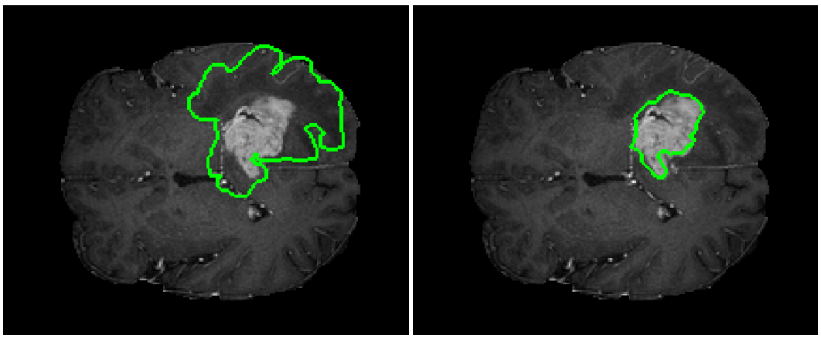

Fig. 4. Illustration of segmentation results in some slice: edema (left) and tumor (right).

3 Results

The proposed method was applied to 80 sets of brain tumor MR images, of which 12 groups failed due to high space complexity of RW. With enough interaction, a user could gain any segmentation result by an interactive segmentation algorithm, so we evaluate the results acquired from single interaction without any modification. The performance of our method is illustrated in Table 1 and Table 2 where 7 segmentation performance metrics are introduced.

Table 1. The mean of evaluation metrics.

Mean

	Dice		Jaccard		Specificity		Sensitivity		Avg Dist.		Hausdorff Dist.		Kappa
Edema	0.25	0.53	0.17	0.41	0.82	0.82	0.39	0.65	8.24	4.91	37.38	30.89	0.18

Table 2. The standard deviation of evaluation metrics.

Standard Deviation

	Dice		Jaccard		Specificity		Sensitivity		Avg Dist.		Hausdorff Dist.		Kappa
Edema	0.21	0.15	0.17	0.16	0.00	0.00	0.22	0.15	25.97	18.16	51.21	51.48	0.18

4 Discussion and Conclusion

We presented a hierarchical RW method which assists user to locate tumor and edema interactively in dozens of seconds. The improved algorithm performed better than typical one, while the feature space is multi-dimensional.

The RW is optimized by solving a large sparse equation, which needs adequate memory resource, and when the size of image is huge, a technique for linear equation is necessary.

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