Brain tumor segmentation based on GMM and active contour method with a model-aware edge map

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We present a method for automatic segmentation of heterogeneous brain tumors. Our method will take about 30 minutes to process one volume in Matlab.

1 Theory background

Our method combines the model of gray distribution of pixels (Gaussian Mixture Models, GMM) with the edge information between two difference classes of tissue in the brain. High detection precision can be achieved. The core of our method is based on the following three models.

1.1 Gaussian Mixture Model(GMM)

We model five classes of data in brain: brain white matter, brain gray matter, brain csf, tumor and edema.

Denote the parameters of Gaussian component [1] $\varphi_i = \{\phi_i, \mu_i, \Sigma_i\}$, where $\mu_i$is mean of vector and Σ_i is the covariance matrix. The ϕ_i parameter is called the mixing coefficient and describes the relative weight of component i in the complete model. The complete model can be written $\psi = \{k, \varphi_i, \cdots, \varphi_k\}$, where k is the number of component in the data. A mixture model on d-dimension data x is written:

$$P(x;\Psi) = \sum_{i=1}^{k} \phi_i \, p(x;\mu_i,\Sigma_i)$$

$$= \sum_{i=1}^{k} \phi_i \frac{\exp\left(-\frac{1}{2}(x-\mu_i)^T|\Sigma_i|^{-1}(x-\mu_i)\right)}{(2\pi)^{d/2}|\Sigma_i|^{1/2}} \quad (1)$$

The standard expectation-maximization algorithm is used to estimate the parameters of each class mixture model in a maximum likelihood formulation.

1.2 Probability distance model between two different tissues

We define a likelihood function $P(\{s_u\}|\{m_u\})$ for the probability of the observed statistics $\{s_u\}$ conditioned on model variables $\{m_u\}$ of pixels {u}. Denote b_1= white matter, b_2=gray matter, b_3=csf, b_4=edema, b_5 =tumor, According to the characteristic brain MRI images , we assume

$$p = (m_2|s_1, s_2 - s_1, m_1) = p(m_2|s_2 - s_1, m_1) \quad (2)$$

To characterize an edge between normal brain tissues and abnormal brain tissues (edema) we can deduce the following term (the edge between edema and tumor can be derived similarly).

$$P(m_1 = \text{normal brain}, m_2 = \text{abnormal brain}|s_1, s_2)$$

$$= \sum_{i=1}^{3}\sum_{j=4}^{5} p(\,(m_1 = b_i, m_2 = b_j|s_1, s_2)$$

$$= \sum_{i=1}^{3}\sum_{j=4}^{5} p(\,(m_2 = b_j|s_1, s_2 - s_1, m_1 = b_{i,})p(m_1 = b_i|s_1)$$

$$= \sum_{i=1}^{3}(\sum_{j=4}^{5} p(\,m_2 = b_j|s_2 - s_1, m_1 = b_{i,}))\frac{p(s_1|m_1 = b_i)p(m_1 = b_i)}{\sum_{k=1}^{5} p(s_1\,|m_1 = b_k)p(m_1 = b_k)}$$

$$= \sum_{i=1}^{3}\frac{\sum_{j=4}^{5} p(s_2 - s_1|m_2 = b_j, m_1 = b_i)p(m_2 = b_j|m_1 = b_i)}{\sum_{j=1}^{5} p(s_{2-}\,s_1|m_j = b_j, m_1 = b_i)p(m_j = b_j)}\frac{p(s_1|m_1 = b_i)p(m_1 = b_i)}{\sum_{k=1}^{5} p(s_1\,|m_1 = b_k)p(m_1 = b_k)} \quad (3)$$

1.3 Active contour model

The traditional deformable active contour model [2] is a curve X(S) = [x(s),y(s)],s $\in$[0,1], that move within the image to minimize an energy function. The curve dynamically changes the shape of an initial contour in response to internal and external forces. The internal forces provide the smoothness of the contour. While the external forces push the curve more toward the desired features, such as boundaries. The object contour is extracted when the energy function is minimized. The energy is defined as

$$E = \int_0^1 \frac{1}{2}\left[\alpha|x'(s)|^2 + \beta\left|x''(s)\right|^2 + E_{ext}x(s)\right) ds \quad (4)$$

where, $x'(s)$ and $x''(s)$ are first and second derivatives of $x(s)$with respect to s. The parameter α controls the tension of the curve and β controls its rigidity. E_{ext} is the

external energy which is calculated from the image data. To minimize the energy function, the snake must satisfy the Euler equation:

$$\alpha x''(s) - \beta x''''(s) - \nabla E_{ext} = 0 \quad (5)$$

According gradient vector flow snake was proposed by Xu and Prince [3], we define a new static external force field called GVF field:

$$F_{ext} = v(x,y) = [u(x,y), v(x,y)] \quad (6)$$

where u and v are the grey changes on x-axis and y-axis of the image ly. F_{ext} can be computed by minimizing the following energy function:

$$E = \iint \mu\left(u_x^2 + u_y^2 + v_x^2 + v_x^2\right) + |\nabla f|^2 |v - \nabla f|^2 dxdy$$

where, $u_x, u_{y,} v_x, v_y$ are derivative of x-axis and y-axis respectively. f(x,y) is the edge map (using probability distance model between two different tissues). μ is a regularization parameter governing the tradeoff between the first term and the second term in the formula [4].

2 Algorithm implementation

2.1 Acquiring rough localization information of tumor and edema

On the training data, we run Expectation Maximization for the GMM on each class of data with free means, variances, and mixing proportions. These means are labeled and saved for the testing data.

For the testing data, firstly, we use Graph-based Segmentation to get some super-voxels in the volumes [5]. Secondly, every voxel can be classified by EM for GMM with fixed means, and labeled according to the labeled means. Thirdly, every super-pixel can be classified by using maxing vote's method. Finally, we chose some special super-pixels whose 50% pixels are almost tumor or edema.

2.2 Seeking edges of between different tissues based on probability distance model

We compute the probability distance for every pixel according to (3). A model-aware edge map can be got. The pixel-pair-class likelihoods, $p\left(s_2 - s_1 \middle| m_2 = b_j, m_1 = b_i\right)$ are computed against GMM.

2.3 Acquiring high precision boundary based on snake method

Based on the rough location information achieved in step (1), we can get an initial contour of the object. And combining with the edges from step (2), precise boundaries

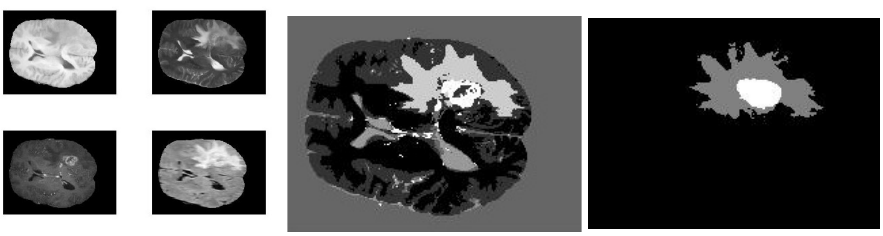
between tumor and edema, and edema and normal brain tissues are located using active contour method.

3 Experiment results

We only process the true data, the whole result can be found on the web. We pick some data and list them as table 1.The figures are raw data, segmentation result with GMM with fixed means and segmentation result with model-aware Snake.

Table 1. Segmentation performance on part of the training data

Subjcet	Average Dist 1	Average Dist 2	Dice 1	Dice 2	Hausdroff Dist 1	Hausdroff Dist 2	Cohen's Kappa	Sensitivity 1	Sensitivity 2	Specificity 1
averages	17.573	0	0.348	0.307	131.772	114.957	0.156	0.367	0.327	0.999
BRATS_LG0008	0	0	0.199	0.83	193.891	180.73	0.16	0.281	0.935	0.998
BRATS_LG0002	123.01	0	0.602	0.322	134.994	143.156	0.353	0.51	0.246	0.997
BRATS_HG0015	0	0	0.716	0.875	0	141.032	0.623	0.572	0.81	1
BRATS_HG0008	0	0	0.728	0.823	113.214	125.41	0.602	0.601	0.751	0.999
BRATS_HG0006	0	0	0.329	0.786	176.529	0	0.348	0.208	0.81	0.999
BRATS_HG0003	0	0	0.699	0.912	146.58	130.088	0.554	0.544	0.92	1
BRATS_HG0002	0	0	0.834	0.537	157.197	84.94	0.341	0.93	0.756	0.998



4 Reference

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