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Model-driven, probabilistic level set based segmentation of magnetic resonance images of the brain

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***Abstract*— Accurate segmentation of magnetic resonance (MR) images of the brain to differentiate features such as soft tissue, tumor, edema and necrosis is critical for both diagnosis and treatment purposes. Region-based formulations of geometric active contour models are popular choices for segmentation of MR and other medical images. Most of the traditional region-based formulations model local region intensity by assuming a piecewise constant approximation. However, the piecewise constant approximation rarely holds true for medical images such as MR images due to the presence of noise and bias field, which invariably results in a poor segmentation of the image. To overcome this problem, we have developed a probabilistic region-based active contour model for automatic segmentation of MR images of the brain. In our approach, a mixture of Gaussian distributions is used to accurately model the arbitrarily shaped local region intensity distribution. Prior spatial information derived from probabilistic atlases is also integrated into the level set evolution framework for guiding the segmentation process. Our experiments with a series of publicly available brain MR images show that the proposed active contour model gives stable and accurate segmentation results when compared to the traditional region based formulations.**

I. INTRODUCTION

Magnetic Resonance (MR) Imaging is routinely used to image the anatomical structures within the brain and has the ability to produce high contrast volumetric images. Accurate segmentation of MR images to differentiate features such as soft tissue, tumor, edema and necrosis is critical for both diagnosis and treatment purposes. However, segmentation of brain MR images is a challenging task given the variable and complex nature of tumor presentation, the abundant noise, and intensity inhomogeneities due to bias field. Numerous image processing techniques have been proposed for medical image segmentation with varying stability and accuracy. Active contours, also known as "snakes" are widely employed for medical image segmentation and tracking. Active contours are energy minimizing curves that iteratively evolve until they overlay on an object boundary in the image. The energy functional is usually composed of two terms: an internal energy term, which defines local constraints on smoothness and tautness of the curve, and an external energy term, which drives the evolution of the curve towards features such as edges to delineate objects of interest.

Active contour models can be categorized into two main types: *parametric (explicit)* and *geometric (implicit)*. Parametric models are the classical snake models [1] defined as $C(s) = (x(s), y(s)) \in \Omega, s \in [0, 1]$, where Ω is the image domain and s is the parameterization defining the coordinates of the curve. These classical snakes evolve using a Lagrangian formulation until an object boundary is delineated. However, these models have a major drawback that they are highly dependent on the chosen parameterization of the initial curve, which makes it crucial to obtain prior knowledge and define a reasonable initial curve for the model to give meaningful results. Geometric active contours on the other hand, are based on level set theory of curve initialization and evolution.

The underlying concept of geometric active contours is to implicitly evolve a higher dimensional level set embedding function $\Phi : \Omega \rightarrow R$ whose zero level set $C : \Phi = 0$ represents dynamic shapes and surfaces [2]. The evolving curve C partitions the image into two regions: C_{in}, which is enclosed by $\Phi > 0$ and C_{out} , which is the region outside, i.e., where $\Phi < 0$. The curve C evolves following $\partial_t C = F.N$ where F is derived from an energy functional and signifies the speed of evolution, and N denotes the exterior unit normal vector to the evolving curve C. To deal with cusps, corners and automatic topological changes, curve evolution can be handled using the level set method proposed by Oshar and Sethian [3]. The associated evolution of the level set function can then be represented by $\partial_t \Phi = F.|\nabla \Phi|$. Classical geometrical active contour models use the image gradient to drive the evolution of the curve [1]. Unfortunately, these models are highly sensitive to noise, which makes them unsuitable for medical images as these images are usually noisy and contain obscure, ill-defined boundaries.

To overcome these limitations, region based segmentation models based on local region statistics have been proposed. Most of these formulations are variants of the piecewise constant Mumford-Shah functional [4]. One of the most widely used region based models is that of Chan and Vese [5], commonly known as active contours without edges. Several variations of this model have been proposed with impressive results. However, most of these models assume piecewise-constant approximation (or in general, a Gaussian distribution) for modeling local region image intensity. Such an assumption of homogeneous intensity regions with distinct means is rarely accurate in brain MR images. Fur-

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ther, these models use only intensity information for image segmentation. For structures like the brain, the approximate location of anatomical structures is very well defined a priori and can be utilized to improve the segmentation process. In this paper, we propose a new region-based active contour model that uses a mixture of Gaussians to model the intensity distribution in the image and integrates spatial prior information obtained from probabilistic atlas maps into the level set evolution framework.

II. DESCRIPTION OF THE MODEL

A. Mixture Model

Mixture models [6] are widely used due to their ability to form smooth approximations and to model arbitrarily shaped class densities. In the proposed approach, we model the intensity distribution in the image partitions using a Gaussian mixture model to form a close approximation to the actual intensity distribution in the image [7]. A Gaussian mixture model can be represented as a weighted sum of M component Gaussian densities, $P(X \mid \lambda) = \sum_{i=1}^{M} w_i g(X \mid \mu_i, \Sigma_i)$ where $X = \{x_1, x_2, ...x_n\}$ is a set of N observations from a D dimensional space, $w_i, i = 1, ..., M$, represent mixture weights or prior probabilities of each component satisfying $\sum_{i=1}^{M} w_i = 1; g(x_j \mid \mu_j, \Sigma_j)$ are D-variate Gaussian components and denote the probability of observation x_j coming from the i^{th} component. Each Gaussian component can be represented as: $g(x_j \mid \mu_i, \Sigma_i) = \frac{1}{(2\pi)^{D/2}|\Sigma_i|^{1/2}} exp\{-\frac{1}{2}(x_j - \mu_i)'\Sigma_i^{-1}(x_j - \mu_i)\}$ where μ_i, Σ_i are the mean and covariance matrices of the individual components. Hence, the parameters of the mixture model are given by $\lambda = \{w_i, \mu_i, \Sigma_i\}, i = 1, .., M$. The model parameters can be estimated by maximizing the overall likelihood of the observations X coming from the model λ. Maximum likelihood expression is a non-linear function of the parameters λ and, therefore, a closed form solution for direct maximization is not possible. However, Maximum Likelihood (ML) parameter estimates can be found iteratively using the popular Expectation Maximization (EM) algorithm [8].

B. Active Contour

Let C denote the evolving curve on the image domain Ω; C_{in} denote the image region bounded by C, and C_{out} the image region outside C. In the proposed active contour model, we minimize the following energy functional

$$F(C) = \mu.Length(C) + v.Area(C_{in}) + F_{ext} \qquad (1)$$

where, $\mu, v \geq 0$ are fixed parameters. The first two terms are regularization terms that enforce local constraints on the curve, while F_{ext} denotes the external force on the curve C. We define F_{ext} via a Bayesian approach of minimizing the expected loss incurred due to pixel misclassification. We define a loss matrix L, where each element L_{ij} corresponds to the loss incurred if a pixel belonging to the i^{th} class is misclassified as that belonging to the j^{th} class. In this paper, we consider a two-class classification problem and the loss matrix is defined as $L = \begin{bmatrix} L_{11} & L_{12} \\ L_{21} & L_{22} \end{bmatrix}$. The expected loss is defined as,

$$F_{ext} = E[L] = \sum_k \sum_j \iint\limits_{(x,y)\in C_j} L_{ij} \times P((x,y), C_k) dxdy$$

where R_j denotes an image region j. Therefore, for a two-class classification problem ($C_{in} = C_1, C_{out} = C_2$),

$$F_{ext} = \iint\limits_{C_{in}} L_{21} P((x,y), C_{out}) dxdy + \iint\limits_{C_{out}} L_{12} P((x,y), C_{in}) dxdy$$

And, $P((x_j, y_j), C_k) = P((x_j, y_j) \mid C_k) P(C_k)$, where $P(C_k)$ denotes the prior probability of class C_k obtained from the probabilistic atlas maps, $P((x_j, y_j) \mid C_k)$ is the probability that pixel (x_j, y_j) should belong to the class C_k and is represented using the mixture model components as $P((x_j, y_j) \mid C_k) = \sum_{i=1}^{M} w_i g((x_j, y_j) \mid \mu_i, \Sigma_i)$, where $g((x_j, y_j) \mid \mu_i, \Sigma_i)$ is a D-variate Gaussian distribution with μ_i, Σ_i as the mean and the covariance matrix. The energy functional (1) can be represented as

$$F(C, \lambda_1, \lambda_2) = \mu.Length(C) + v.Area(C_{in}) + \iint\limits_{(x,y)\in C_{out}} L_{12} \sum_{i=1}^{M_1} w_i g((x,y) \mid \mu_i, \Sigma_i) P(C_{in}) dxdy + \iint\limits_{(x,y)\in C_{in}} L_{21} \sum_{j=1}^{M_2} w_j g((x,y) \mid \mu_j, \Sigma_j) P(C_{out}) dxdy \qquad (2)$$

C. Level Set Formulation

In the level set formulation [3], a curve C defined on the image domain Ω can be represented by the zero level set $\Phi(x,y) = 0$ of a higher dimensional function called a Lipschitz function $\Phi : \Omega \to R$ such that

$$\Phi(x,y) = \begin{cases} = 0 & \text{at } C \\ > 0 & \text{inside } C, \\ < 0 & \text{outside } C \end{cases} \qquad (x,y) \in \Omega \qquad (3)$$

Defining the level set function $\Phi(x,y)$ enables representation of an unknown curve C, regions C_{in} and C_{out} in terms of the evolving function $\Phi(x,y)$ [9]. Using the Heaviside function H and Dirac delta function δ, defined as:

$$H(z) = \begin{cases} 1 & \text{if z} > 0 \\ 0 & \text{if z} < 0 \end{cases}, \qquad \delta(z) = \frac{d}{dz} H(z) \qquad (4)$$

the energy functional $F(C, \lambda_1, \lambda_2)$ can now be represented as a function of $\Phi, \lambda_1, \lambda_2$ [10]:

$$F(\Phi, \lambda_1, \lambda_2) = \mu \int\limits_{\Omega} \delta(\Phi) |\nabla \Phi| dxdy + v \int\limits_{\Omega} H(\Phi) dxdy + \iint\limits_{\Omega} L_{12} \sum_{i=1}^{M_1} w_i g((x,y) | \mu_i, \Sigma_i) P(C_{in}) (1 - H(\Phi)) dxdy + \iint\limits_{\Omega} L_{21} \sum_{j=1}^{M_2} w_j g((x,y) | \mu_j, \Sigma_j) P(C_{out}) (H(\Phi)) dxdy \qquad (5)$$

We use slightly regularized versions of Heaviside and Dirac functions denoted as H_ϵ and δ_ϵ described in [9] for computing the associated Euler-Lagrange equation. Let us denote by F_ϵ the associated regularized energy functional, defined by

$$F_\epsilon(\Phi,\lambda_1,\lambda_2) = \mu \int_\Omega \delta_\epsilon(\Phi)|\nabla\Phi|dxdy + v\int_\Omega H_\epsilon(\Phi)dxdy+$$
$$\iint_\Omega L_{12}\sum_{i=1}^{M_1} w_i g((x,y)|\mu_i,\Sigma_i)P(C_{in})(1-H_\epsilon(\Phi))dxdy+$$
$$\iint_\Omega L_{21}\sum_{j=1}^{M_2} w_j g((x,y)|\mu_j,\Sigma_j)P(C_{out})(H_\epsilon(\Phi))dxdy \quad (6)$$

Minimizing the regularized energy functional (6) with respect to Φ gives the associated Euler-Lagrange equation. Parametrization by an artificial time $t \geq 0$ gives the following update equation of $\Phi(x,y,t)$ in the descent direction:

$$\frac{\partial\Phi(x,y,t)}{\partial t} = \delta_\epsilon(\Phi)\Big[\mu\cdot div\Big(\frac{\nabla\Phi}{|\nabla\Phi|}\Big) - v$$
$$+L_{12}\sum_{i=1}^{M_1} w_i g((x,y)|\mu_i\Sigma_i)\times P(C_{in})$$
$$-L_{21}\sum_{j=1}^{M_2} w_j g((x,y)|\mu_j,\Sigma_j)\times P(C_{out})\Big] \quad (7)$$

The initial contour is defined by $\Phi(x,y,0) = \Phi_0(x,y)$.

D. Numerical Implementation

We used regularization of $H(\Phi)$ using $C^2(\bar{\Omega})$ functions for computing the associated Euler-Lagrange equation, as proposed in [9],

$$H_\epsilon(z) = \begin{cases} 1 & \text{if } z > \epsilon \\ 0 & \text{if } z < -\epsilon \\ \frac{1}{2}\Big[1+\frac{z}{\epsilon}+\frac{1}{\pi}sin(\frac{\pi z}{\epsilon})\Big] & \text{if } |z| \leq \epsilon \end{cases}$$

To obtain a discrete form of the update equation (7) of $\Phi(x,y,t)$, we use a finite difference implicit scheme for discretization of the divergence operator as proposed in [11] and then use an iterative process [12]. The principal steps of the algorithm are:

- Initialize $\Phi_0(x,y)$ at iteration n = 0.
- Compute mixture model parameters λ_1,λ_2 using the EM algorithm.
- Solve (7) in $\Phi_n(x,y)$ to obtain $\Phi_{n+1}(x,y)$.
- Check for convergence, otherwise repeat for iteration = n+1.

The loss matrix L was defined as a 2x2 matrix in which the off-diagonal elements were assigned the same loss value of 1. However, for multi-class segmentation problems, L can be defined such that the individual loss values are different and this could depend upon the context in which the segmentation is being performed.

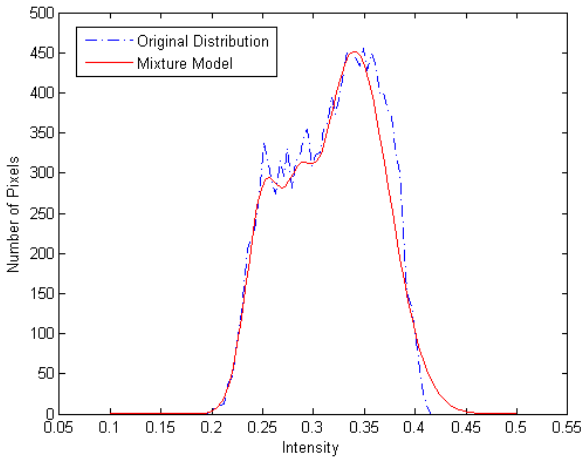

Fig. 1. Histogram of the original white matter intensity distribution *(blue curve)* and the modeled intensity distribution using mixture models with $M = 3$ components *(red curve)*

III. EXPERIMENTAL VALIDATION

We tested the proposed model on a series of publicly available MR images. We used the International Consortium for Brain Mapping (ICBM) atlases obtained from the Laboratory of Neuro Imaging, University of California at Los Angeles (LONI) as prior spatial probability atlas maps for this study (http://www.loni.ucla.edu/Atlases). The probabilistic atlases were registered to MR images using an elastic image registration algorithm as proposed in [13].

Fig. 1 illustrates the ability of the mixture models to accurately model the local region intensity distribution. The blue curve shows the original intensity distribution inside the white matter region of the MR image (the original image is illustrated in the first row of Fig 2) and the red curve shows the modeled intensity distribution using $M = 3$ mixture components. From Fig. 1, it is evident that the local region intensity distribution may not be a Gaussian distribution, and hence cannot be accurately modeled using a piecewise constant approximation, resulting in pixel missclassification.

Fig. 2 illustrates the segmentation results of the gray matter (2^{nd} column) and white matter regions (3^{rd} column) obtained from our proposed model on three publicly available MR images. We also show the comparison of our model with the Chan and Vese piecewise constant model (4^{th} column) [5] in segmenting the white matter region. Qualitatively speaking, from Fig. 2, it is evident that the proposed model produces better segmentation results than the Chan and Vese model [5].

IV. CONCLUSION

In this paper, we have proposed a model driven, probabilistic active contour method for automatic segmentation of brain MR images. The salient features of the proposed model are the use of mixture models to accurately model the local region intensity distributions in different parts of the image, and the use of prior spatial information derived

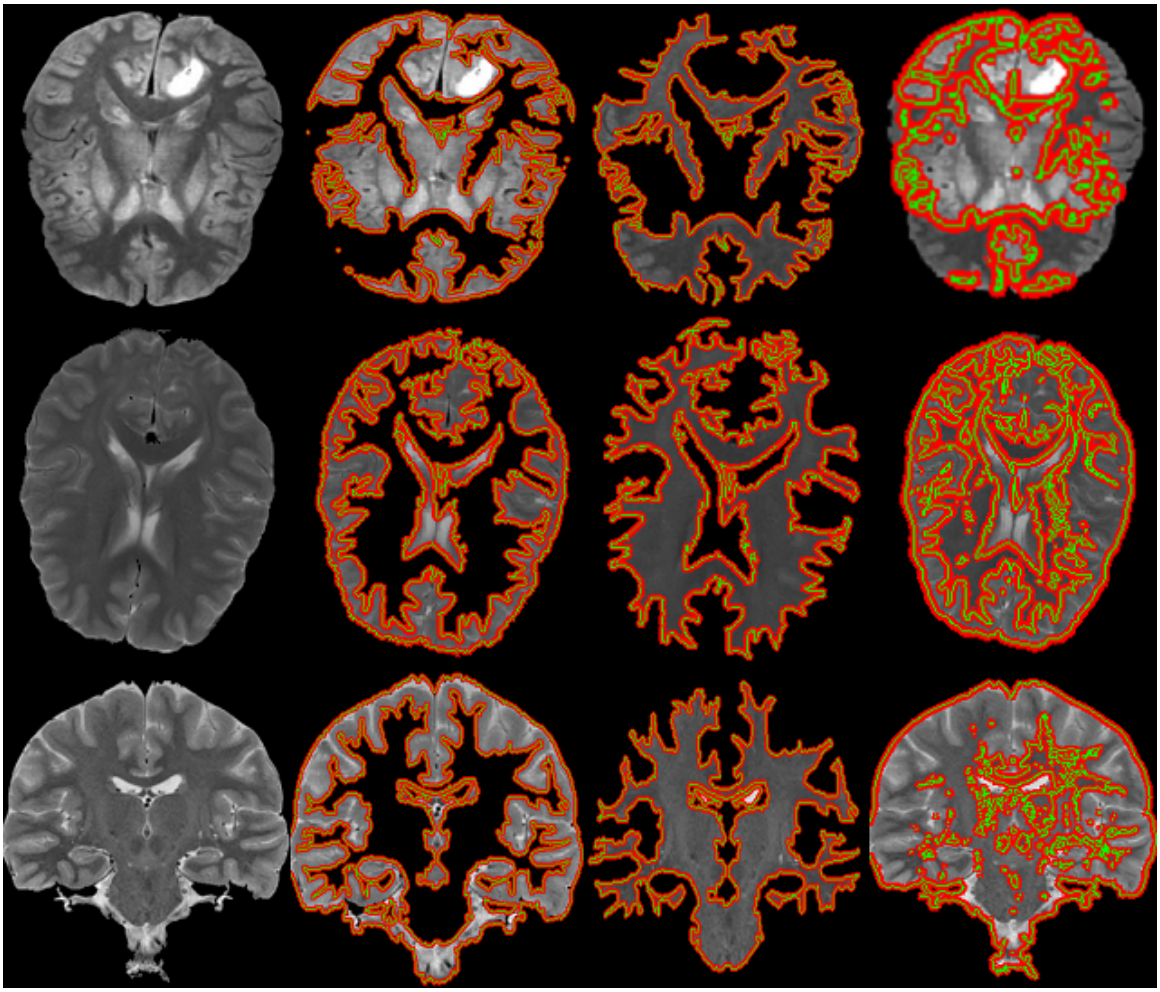

Fig. 2. Segmentation results of the proposed active contour model on a set of MR images showing original image (1^{st} column), segmented gray matter(2^{nd} column), and segmented white matter(3^{rd} column). The 4^{th} column shows the segmentation result obtained from the Chan-Vese model by assuming a piece-wise constant approximation.

from probabilistic atlases to guide the segmentation process. As compared with the piecewise constant region-based active contour models, the proposed method results in stable and more accurate segmentation results. The use of prior spatial information from probabilistic atlases enables our model to accurately segment low contrast brain structures from the surrounding tissue. As a part of the future work, we plan to use quantitative measures (such as the Jaccard similarity coefficient) to evaluate the effectiveness of the proposed model in accurately segmenting brain MR images on a larger data set.

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