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Original paper

Interactive breast mass segmentation using a convex active contour model with optimal threshold values

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ABSTRACT

Introduction: A convex active contour model requires a predefined threshold value to determine the global solution for the best contour to use when doing mass segmentation. Fixed thresholds or manual tuning of threshold values for optimum mass boundary delineation are impracticable.

Introduction: A proposed method is presented to determine an optimized mass-specific threshold value for the convex active contour derived from the probability matrix of the mass with the particle swarm optimization method. We compared our results with the Chan–Vese segmentation and a published global segmentation model on masses detected on direct digital mammograms.

Methods and materials: The regional term of the convex active contour model maximizes the posterior partitioning probability for binary segmentation. Suppose the probability matrix is binary thresholded using the particle swarm optimization to obtain a value T_1, we define the optimal threshold value for the global minimizer of the convex active contour as the mean intensity of all pixels whose probabilities are greater than T_1.

Results: The mean Jaccard similarity indices were 0.89 ± 0.07 for the proposed/Chan–Vese method and 0.88 ± 0.06 for the proposed/published segmentation model. The mean Euclidean distance between Fourier descriptors of the segmented areas was 0.05 ± 0.03 for the proposed/Chan–Vese method and 0.06 ± 0.04 for the proposed/published segmentation model.

Conclusions: This efficient method avoids problems of initial level set contour placement and contour re-initialization. Moreover, optimum segmentation results are realized for all masses improving on the fixed threshold value of 0.5 proposed elsewhere.

1. Introduction

Projection X-ray images of the breast are routinely used to diagnose breast diseases, including those presenting with masses. These mammographic masses are often superimposed on anatomical structures which create local minima within the mass regions, and can result in mass margins having incomplete or missing boundary information. This has led to reported significant inter-observer variability in manual delineation of mass boundaries amongst experts [1,2], and in choosing lexicon for describing mass margin, density and shape of mammographic masses amongst resident radiologists [3]. Consequently, the task of mass boundary delineation is still challenging and in some cases can produce unsuitable segmentation solutions.

In recent years, interactive segmentation algorithms have been proposed to assist radiologists in delineating mass boundaries, hopefully, to achieve realistic segmentation solutions which accurately represent the physical attributes of these masses and thus, decrease the statistical significance of the variability associated with manual delineation. The initialization of these algorithms requires some user-specified seeds to indicate the search area for the mass boundary. Some of these methods seek to partition an image into meaningful regions with information both from the entire image and from the anatomical information provided by the user, while adhering to certain pre-defined criteria.

The geometric active contour model [4] is one such interactive segmentation algorithm widely employed in boundary delineation of anatomical structures in medical image analysis. It minimizes energy functionals, derived from the statistical distribution of the gray level intensities or image gradients, of the image to produce closed and smoothed contours depicting the boundaries of these structures.

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Region-based models utilize statistical information obtained from regions inside and outside an initial contour to evolve the contour towards the desired boundary. The Chan–Vese region-based active contour model [5] is one of the methods widely used for image segmentation. To deal with topological changes, the initial contour is embedded in the level set of a function in higher dimensions. Its energy functional is non-convex, and it is derived from the local statistical distribution of the gray level intensities within a narrow band of pixels. Hence, the energy functional is minimized with the gradient descent method which is susceptible to local minima within the search path. Zhang et al. [6] proposed a region-based active contour model to delineate objects with weak or blurred edges. Their model is known as the 'active contours with selective local or global segmentation model'. Zhang et al. formulated the statistical information, inside and outside the initial contour, as a signed pressure force function for curve propagation while regularizing the level set function with a Gaussian smoothing kernel. Direct digital mammograms exhibit intensity inhomogeneity, consequently, masses with ill-defined margins and local minima within the mass region. Delineation of direct digital mass lesions with these algorithms, produces segmentation results which are dependent on the placement of the initial level set contours [7].

Bresson et al. [8] proposed a region-based active contour model whose energy functional is convex. It is derived from the global statistical distribution of the gray level intensities of the image. This model allows for the implementation of a global minimization algorithm, based on the dual formulation of the total variation (TV), to search for a global minimum of the active contour rather than using the gradient descent method. The segmentation results are independent of the placements of the initial level set contours, and do not require the implementation of the contour re-initialization process as level sets are not involved in their method of curve evolution.

Medical image analysis methods have exploited spatial prior probabilistic atlases as guides or confidence maps, to segment magnetic resonance images of the brain [9] and prostate [10] with the active contour segmentation model. In mammography, such a map is difficult to establish because breast tissues vary greatly in texture, shape and size. Nonetheless, algorithms such as the random walker method can provide mass-specific confidence maps which can be incorporated into other segmentation algorithms to improve their competence in delineating ill-defined mass boundaries [11].

Nguyen et al. [12] combined the probabilistic matrix from the random walker segmentation method with a convex energy functional to derive a robust interactive segmentation model. They modeled the convex energy functional as a linear mixture of Gaussian distributions, and expressed the probability matrix as a binary classifier to propagate the contour whenever the statistical models of the foreground and the background are similar. However, in their implementation, the user fixes the threshold value of the global minimum for the convex energy functional. In mass lesion segmentation, a fixed threshold value for the global minima of a database of direct digital mass lesions is not feasible because the gray level intensity distributions of the background tissues surrounding most masses are heterogeneous. This approach may underestimate or overestimate the optimum threshold values of these masses and, consequently, lead to unsuitable segmentation outcomes. Furthermore, hand tuning each threshold value for optimum mass boundary delineation is impractically time consuming. The concentric morphology model of a mass describes a mass lesion as possessing a highlighted focal region surrounded with successively less intense concentric layers.

This study proposes an interactive segmentation model to derive a reliable estimate of the mass-specific threshold value from the morphological characteristics of the mass lesion for the global minimizer of its convex energy functional. Our method assumes that the statistical properties of the highlighted focal region represent the statistical model of the ground truth label. Subsequently, the mass-specific threshold value for the global minimizer can be derived from the threshold value that maximizes the between-class variance of the highlighted focal region and the non-mass region of the probability matrix of the mass lesion. Our approach defines the mass-specific value as the mean pixel gray level of all pixels whose probability of belonging to the highlighted focal region is greater than the threshold value. The main contribution of this paper lies in extracting reliable information from the probability matrix to provide a mass-dependent reliable estimate of the threshold value for each global minimizer.

2. Mathematical background

2.1. Maximum likelihood active contour model for binary segmentation

The binary partition of the image domain Ω into Ω_1 and Ω_2 by an evolving curve, C, can be achieved by maximizing the posterior partitioning probability for binary segmentation. Assuming that all pixel intensities are independently distributed and all prior probabilities are equally likely, the binary partition can be formulated as the minimization of the following energy functional:

$$E(\Omega_1,\Omega_2,p_1,p_2) = -\sum_{i=1}^{2}\int_{\Omega_i} log(p_i((I(x,y)|\Omega_i)))dxdy + \mu length(C) \quad (1)$$

where $I(x,y)$ is the value of the gray intensity value at pixel position (x,y) in region Ω_i, $p_i((I(x,y)|\Omega_i))$ the likelihood of a pixel (x,y) in Ω_i having the value $I(x,y)$, and $\mu > 0$ is a constant.

Assuming that the gray level pixel values, $I(x,y)$, are drawn from a Gaussian distribution, then:

$$p_i((I(x,y)|\Omega_i)) = \frac{1}{\sqrt{2\pi}\sigma_i}\exp -\frac{(I(x,y)-\mu_i)^2}{2\sigma_i} \quad (2)$$

where σ_i^2 and μ_i are the variance and mean of Ω_i, respectively.

Suppose the curve, C, is embedded in the level set function, $\phi(x,y)$, such that the regularized Heaviside function, H_ϵ, is the characteristic function separating the foreground and background. Then, optimum partition is obtained by solving the following gradient descent flow:

$$\frac{\partial\phi}{\partial t} = H'_\epsilon(\phi)\left[div\left(\frac{\nabla\phi}{|\nabla\phi|}\right) + log(\sigma_2) - log(\sigma_1) + \left(\frac{(I(x,y)-\mu_2)^2}{2\sigma_2^2}\right) - \left(\frac{(I(x,y)-\mu_1)^2}{2\sigma_1^2}\right)\right] \quad (3)$$

2.2. Convex energy functional modeled with the posterior partitioning probability for binary segmentation

The steady state solution of Eq. (3) is given as:

$$\frac{\partial\phi}{\partial t} = div\left(\frac{\nabla\phi}{|\nabla\phi|}\right) + \lambda\left(log(\sigma_2) - log(\sigma_1) + \left(\frac{(I(x,y)-\mu_2)^2}{2\sigma_2^2}\right) - \left(\frac{(I(x,y)-\mu_1)^2}{2\sigma_1^2}\right)\right) \quad (4)$$

This is the gradient descent flow of the energy functional:

$$E(\phi,\sigma_1,\sigma_2,\mu_1,\mu_2) = \int_\Omega |\nabla\phi| dxdy + \lambda\int_\Omega r(x,y,\sigma_1,\sigma_2,\mu_1,\mu_2)\phi dxdy \quad (5)$$

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