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RESEARCH ARTICLE

Medical Image Segmentation Using Combined Level Set and Saliency Analysis

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ABSTRACT In the realm of computer vision, image segmentation has become a crucial task with widespread applications, particularly in medical imaging. Although there have been significant advancements in image segmentation methods, challenges persist in accurately delineating intricate structures within noisy and varied medical images. In this study, we have developed a novel segmentation model that combines the distance regularized level set evolution (DRLSE) model with a local gradient flow-based image (LGFI) and saliency maps. This innovative fusion addresses the limitations of existing methods and offers robust and precise solutions for medical image segmentation. We provide comprehensive mathematical formulations and demonstrate the effectiveness of the proposed model across diverse medical images. Through quantitative and qualitative analyses of the brain tumor segmentation (BraTS) 2019 dataset, we have demonstrated the superior accuracy, robustness, and computational efficiency of the proposed model in comparison with the state-of-the-art methods. This research marks a significant step toward enhancing medical image analysis, with potential applications in diagnostics and healthcare practices.

INDEX TERMS Active contour, biomedical image processing, distance regularized, gradient-flow, image segmentation, saliency.

I. INTRODUCTION

In recent years, image segmentation has emerged as a pivotal task in the field of computer vision, finding extensive applications in diverse domains including medical imaging, autonomous vehicles, object recognition, robotics, and virtual and augmented reality [1]. The accurate and efficient segmentation of objects from images plays a fundamental role in various real-world applications, enabling detailed analysis, diagnosis, and understanding of complex visual data. Among these applications, medical image segmentation holds a special significance owing to its crucial role in medical diagnosis, treatment planning, and disease monitoring [2], [3].

Despite substantial progress in image segmentation techniques, challenges persist, particularly when dealing with

the intricate structures and diverse textures found in medical images. Traditional methods, such as thresholding [4], histogram-based clustering, region growing [5], K-means clustering [6], and watershed [7], often face difficulties in accurately delineating objects due to noise, intensity variations, and indistinct boundaries. To tackle these challenges, sophisticated models have been developed, such as active contours [8], conditional and Markov random fields [9], sparsity-based [10], graph cuts [11], and deep learning [12] models. These methods incorporate intricate mathematical formulations and machine learning algorithms.

Graph cut methods were effective for image segmentation by finding a global minimum contour based on user-defined constraints [1], [11]. This results in the segmentation being highly dependent on the initial input and often requires iterative adjustments if the assumptions aren't initially met. While effective under correct assumptions, these methods need user interaction to refine the constraints and achieve accurate

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segmentation. One prominent category of segmentation methods involves active contour model (ACM) approaches, wherein the evolution of curves or surfaces is employed to capture object boundaries. ACMs offer sub-pixel accuracy, closed contours, and topology adaptability, effectively partitioning images into non-overlapping regions by minimizing the energy functional for image segmentation [8]. However, despite various ACMs integrating image information, real-world images are frequently influenced by adverse factors, such as intensity inhomogeneity and noise. Consequently, the application of ACMs for image segmentation remains a topic that warrants further exploration.

ACMs can be classified into two categories: parametric and geometric models. Parametric models, such as the original snake model introduced by Kass et al. [8], employ predefined shapes and offer computational efficiency. However, they may lack the flexibility required to capture intricate and complex shapes. In contrast, geometric ACMs, such as level set methods, guide the evolving curves toward the target boundaries using geometric measurement parameters. Geometric ACMs have two main subcategories: edge- [13], [14], [15], [16] and region-based models [17], [18], [19], [20], [21], [22], [23], [24]. Edge-based models are designed to detect and connect edges within an image, effectively outlining object boundaries. However, these models struggle in the presence of noise and may miss objects with ambiguous edges. On the contrary, region-based models consider both the interior and edges of an object, making them valuable for objects with varying intensity levels or noisy images. However, they can be sensitive to the initial conditions and may not perform well on objects with unclear boundaries.

To address these challenges, many hybrid models have been proposed recently [25], [26], [27], [28], [29]. These models fuse different approaches, aiming to capitalize on the strengths of both edge- and region-based models while mitigating their individual weaknesses. Although powerful, the implementation and optimization of hybrid models can be complex. Ultimately, the selection of a segmentation model depends on the specific applications and characteristics of the image in question. Often, a combination of models tailored to the unique demands of the task at hand may be necessary to achieve the most accurate and reliable results. In the context of medical image segmentation, several methods have been proposed to tackle the unique challenges posed by medical images, including the presence of noise, variability in object shapes, and diverse tissue textures [30]. Techniques such as region-based methods and deep learning approaches have been extensively explored. While deep learning methods, especially convolutional neural networks (CNNs), have achieved remarkable success in various computer vision tasks, their application to medical image segmentation often requires a substantial amount of labeled data and computational resources, which may not always be readily available [31]. Moreover, due to the intricate nature of medical images, effectively modeling ACMs in this domain is particularly challenging. ACMs

heavily rely on edge detection and linkage, making them susceptible to noise and uncertainties in the boundary definitions within medical images. This vulnerability poses a significant obstacle to the successful application of ACMs in medical image segmentation tasks.

The pursuit of resilient autonomous segmentation techniques aimed at enhancing segmentation efficiency and minimizing inter-observer discrepancies among clinicians has gained considerable research momentum. Nonetheless, this process faces challenges, primarily stemming from the intricate nature of medical images such as those from a magnetic resonance imaging (MRI) scan. Biased conditions, including intensity inhomogeneity, low contrast, and noise, often compromise the quality of medical images—such as MRI and computed tomography (CT) images—as observed in recent studies [32]. Such issues can blur the boundaries between unhealthy and healthy tissues, creating significant challenges in the segmentation process, introducing ambiguity, and making accurate delineation difficult [33].

The distance regularized level set evolution (DRLSE) model has demonstrated notable success in various image segmentation tasks due to its ability to handle topological changes and effectively capture intricate object boundaries [15]. To enhance the stability of the level set function (LSF), the DRLSE model introduces a distance regularization term that mitigates deviations between the LSF and standard signed distance function during curve evolution. Unlike other models, the DRLSE eliminates constant reinitialization, addressing a significant drawback. However, it lacks self-adjustment during energy minimization and is sensitive to the initial contours.

The bias correction (BC) model [34], designed to correct the unevenly distributed intensity in medical images, offers precise results with less segmentation time than the traditional PS model but is comparatively less efficient and accurate. Local binary fitting (LBF) [19] and region-scalable fitting (RSF) [20] models utilize kernel functions to guide level set motion, avoiding periodic reinitialization and enhancing efficiency. However, these models are sensitive to initial contours and can potentially become trapped in local minima. The local image fit (LIF) model [35] incorporates Gaussian filtering and local image information for faster segmentation than RSF but remains susceptible to initial contour variations.

Attempts to handle nonconvex energy functions have led to complex methods, such as translating nonconvex functions into convex ones [36]; although these are effective, their practical implementation is challenging. Another approach in [37] involves numerical approximation to approximate optimal solutions for relaxed problems but does not guarantee obtaining the global minimizer of the minimal partition problem. These diverse methods represent ongoing efforts to improve the segmentation efficiency and accuracy of ACMs. However, saliency incorporates human visual attention cues, allowing the segmentation model to prioritize the relevant regions in an image, thereby improving the precision of the segmentation results. Techniques such as constructing

facial saliency maps [38] and employing saliency-SVM models [39] have significantly enhanced image segmentation accuracy. The fusion of regional saliency with the random walk method [40] and its integration with ACMs [41] further refines the segmentation outcomes. Additionally, the saliency-driven region edge-based top-down level set evolution model (SDREL) [42] incorporates a saliency map into a global ACM, enabling the efficient segmentation of grayscale and color images. SDREL demonstrates remarkable performance and rapidly evolves contours toward object boundaries. However, challenges persist in handling images with distorted intensities, which are common in real-world and medical imaging, and some ACMs remain sensitive to noise and initialization. Despite these challenges, ongoing research on saliency-based segmentation holds the promise of transformative advancements in image analysis [41], [43], [44], [45], [46], [47], [48]. While prior saliency-based ACMs have shown promising results for images with strong boundaries and intensity homogeneity, they are typically designed for specific types of images and struggle to generalize across diverse medical imaging modalities.

In this study, we develop a novel image segmentation model that enhances the DRLSE model by combining it with a local gradient flow-based image (LGFI) [49] and saliency maps. Through the synergistic combination of these components, our proposed model effectively addresses the limitations of existing methods and offers a robust and accurate solution for medical image segmentation. In the following sections, we delve into the mathematical formulations, implementation details, experimental setup, and results, showcasing the efficacy of our approach across a diverse range of medical images. Through a comprehensive evaluation and comparison with the state-of-the-art methods, our proposed model demonstrates superior performance in terms of accuracy, robustness, and computational efficiency.

The remainder of this paper is organized as follows. Section II provides a review of the DRLSE model to establish the context for the proposed model. Section III presents the mathematical formulations of our proposed model, wherein the LSF is initialized by integrating edge information using DRLSE and saliency. The contour evolution is achieved by combining DRLSE and LGFI. Section IV presents simulation results and compares our proposed model with the state-of-the-art methods using synthetic, real, and multiple medical images. Additionally, we conduct quantitative and qualitative analyses of the brain tumor segmentation (BraTS) 2019 dataset to demonstrate the superiority of our proposed model. Finally, in Section V, we conclude the discourse, summarize the contributions, and suggest potential avenues for future research.

II. RELATED WORK

This section serves as a foundational component of this paper, offering a review of the DRLSE model to establish the context for the research presented herein. In [15], a meticulous formulation of the DRLSE model, representing an enhanced

version of the traditional edge-based level set method, was introduced. The authors introduced a penalty term, denoted as $R_p(\Phi)$, into the energy function, referred to as the regularization term for the level set, and defined it as follows:

$$R_p(\Phi) = \int_{\Omega} p(|\nabla\Phi(x)|) dx \quad (1)$$

where Φ and ∇ denote the LSF and the gradient operator. This compelled the curve to evolve closely along the signed distance function, eliminating the necessity for an expensive reinitialization procedure during the contour evolution process. In this context, the potential functional, $p(s)$, displays two minima at $s = 1$ and $s = 0$, respectively, and is defined as follows:

$$p(s) = \begin{cases} \frac{1}{(2\pi)^2} (1 - \cos(2\pi s)), & \text{if } s \leq 1 \\ \frac{1}{2}(s-1)^2, & \text{if } s \geq 1 \end{cases} \quad (2)$$

Further, the gradient flow of (1) is given as:

$$\frac{\partial\Phi}{\partial t} = \mu \operatorname{div}(d_p(|\nabla\Phi|) \nabla\Phi), \quad (3)$$

where μ denotes scaling constant, $\operatorname{div}(\cdot)$ represents the divergence operator, and $d_p(s) = p'(s)/s$, and $(\cdot)'$ signifies the derivative.

The total energy function of DRLSE is given as

$$\begin{aligned} E_{\text{DRLSE}}(\Phi) &= \mu R_p(\Phi) + \lambda L_g(\Phi) + \alpha A_g(\Phi) \\ &= \mu \int_{\Omega} p(|\nabla\Phi(x)|) dx \\ &\quad + \lambda \int_{\Omega} g(x) \delta_{\varepsilon}(\Phi(x)) |\nabla\Phi(x)| dx \\ &\quad + \alpha \int_{\Omega} g(x) H_{\varepsilon}(-\Phi(x)) dx \end{aligned} \quad (4)$$

where $\lambda > 0$ and $\alpha \in \mathbb{R}$ are the coefficients governing the edge and area terms. The term $A_g(\Phi)$ calculates the weighted area of region where $x : \Phi(x) < 0$, amplifying the motion of the zero-level contour throughout LSF. Concurrently, $L_g(\Phi)$ evaluates the line integral of the function $g(\cdot)$ along the zero-level contour of Φ . Notably, in (4), the function g serves as the edge indicator, H_{ε} denotes the smooth approximation of Heaviside function, and δ_{ε} represents the smooth approximation of Dirac delta function; these are defined as:

$$g = \frac{1}{1 + |\nabla G_{\sigma} * I|^2}, \quad (5)$$

$$H_{\varepsilon}(\Phi) = \frac{1}{2} \left[1 + \left(\frac{2}{\pi} \right) \arctan \left(\frac{\Phi}{\varepsilon} \right) \right], \quad (6)$$

$$\delta_{\varepsilon}(\Phi) = H'_{\varepsilon}(\Phi) = \frac{\varepsilon}{\pi(\Phi^2 + \varepsilon^2)} \quad (7)$$

where G is the Gaussian Kernel with standard deviation σ and ε balances the smoothness. Finally, (4) is minimized and

the gradient flow of DRLSE is expressed as (8).

$$\frac{\partial E_{\text{DRLSE}}(\Phi)}{\partial t} = \mu \operatorname{div} (d_p(|\nabla \Phi|) \nabla \Phi) + \lambda \delta_\varepsilon(\Phi) \operatorname{div} \left(g \frac{\nabla \Phi}{|\nabla \Phi|} \right) + \alpha g \delta_\varepsilon(\Phi) \quad (8)$$

The DRLSE model offers several advantages in image segmentation tasks, including its ability to ensure smoothness and continuity in segmented regions while implicitly representing curves. This makes it well-suited for applications with complex geometries and topological changes. It operates within a variational framework, providing a solid mathematical foundation and allowing the incorporation of geometric constraints.

Despite these strengths, the DRLSE model has certain limitations. It is sensitive to initial placements, computationally intensive, and can struggle with intensity variations, potentially leading to leakage into adjacent regions. To enhance its performance, we introduce saliency in the initialization of the LSF, ensuring robustness to initialization. Additionally, we incorporate the LGFI into its energy function, thus strengthening its resistance to leakage into adjacent regions. These modifications refine the DRLSE model, making it more reliable and precise for use in challenging segmentation tasks.

III. METHODOLOGY

This section presents a detailed methodology for medical image segmentation using the DRLSE model [15] with LGFI [49] and a saliency map. This integrated approach offers several advantages, such as combining edge-based contour evolution, local intensity analysis, and region-of-interest, highlighting the need for robust and accurate medical image segmentation.

Let $I : \Omega \rightarrow \mathbb{R}^2$ be an input image and a LSF $\Phi(x, y)$ with an initial contour $\Gamma_0 : (x, y) \in \Omega | \Phi(x, y) = 0$. The variables x and y denote points in I . In addition, we define $\Omega_0 : x \in \Omega | \Phi(x, y) = 0$ as the zero-level set, $\Omega_{\text{in}} : \Omega | \Phi(x, y) < 0$ as the domain's inside Ω_0 , and $\Omega_{\text{ex}} : \Omega | \Phi(x, y) > 0$ as the domain's outside Ω_0 .

A. SALIENCY

To highlight salient regions within the medical image and guide the subsequent segmentation process, we utilize the Itti-Koch model [50] to compute a saliency map, denoted as $S(x, y)$. This map emphasizes areas of interest based on intensity and color contrasts, providing crucial insights into the regions of diagnostic significance. It is computed as a weighted combination of the intensity channel and color channels:

$$S(x, y) = \lambda_I I_{\text{ch}}(x, y) + \lambda_C C_{\text{ch}}(x, y), \quad (9)$$

where λ_I and λ_C are weighting parameters that control the influence of intensity and color contrasts, respectively. The intensity channel, I_{ch} , and color channels, C_{ch} , together contribute to the overall saliency map, providing a more

comprehensive representation of regions of interest in the image. I_{ch} emphasizes intensity variations, while C_{ch} captures color contrasts, making the saliency map suitable for a wider range of medical imaging scenarios. I_{ch} is computed as:

$$I_{\text{ch}}(x, y) = G_{\sigma_I}(I(x, y) - G_{\sigma_G}(I(x, y)))^2 \quad (10)$$

where G_{σ_I} and G_{σ_G} represent Gaussian smoothing with standard deviation σ_I and σ_G , respectively. This operation highlights regions with significant intensity variations, such as edges and texture details. C_{ch} is computed as the square of the differences in color components:

$$C_{\text{ch}}(x, y) = G_{\sigma_C} \left(\sum_{c=1}^3 (I(x, y, c) - G_{\sigma_G}(I(x, y, c)))^2 \right) \quad (11)$$

where c represents red, green, and blue color components of the image (for color images) and G_{σ_C} denotes Gaussian smoothing with standard deviation σ_C . $C_{\text{ch}}(x, y)$ is calculated to capture color contrasts in the image, emphasizing regions with significant color variations. This is particularly relevant in certain medical imaging contexts where color information is important. It is worth noting that if the image is grayscale, (9) can be simplified to:

$$S(x, y) = \lambda_I I_{\text{ch}}(x, y) \quad (12)$$

B. INITIALIZATION OF LSF

The LSF, denoted as $\Phi(x, y, t)$, is a key component of the segmentation process. It is initialized using a combination of the DRLSE model, which incorporates edge information, $e(x, y)$, from the Canny edge detector, and binary saliency information, $B(x, y)$, derived from the computed saliency map given in (9):

$$\Gamma_0(x, y) = e(x, y) \cup B(x, y). \quad (13)$$

Here, $B(x, y)$ is obtained by applying a threshold γ_S to the saliency map $S(x, y)$:

$$B(x, y) = \begin{cases} 1, & \text{if } S(x, y) > \gamma_S \\ 0, & \text{Otherwise.} \end{cases} \quad (14)$$

Next, a signed distance function, denoted as d , is constructed based on Γ_0 to initialize $\Phi(x, y, 0)$:

$$\Phi(x, y, 0) = d(\Gamma_0) - d(1 - \Gamma_0). \quad (15)$$

The interior of the initial contour is assigned negative values, while the exterior is assigned positive values. Subsequently, the LSF is then normalized to the range $[-1, 1]$:

$$\Phi(x, y, 0) = \frac{\Phi(x, y, 0)}{\max |\Phi(x, y, 0)|} \quad (16)$$

C. CONTOUR EVOLUTION USING DRLSE AND LGFI

The segmentation process involves iteratively evolving Φ to refine the contour. This is achieved through the combination of DRLSE and LGFI and the LSF is updated as follows:

$$\Phi(x, y, t + \Delta t) = \Phi(x, y, t) + \Delta t E(x, y, t) \quad (17)$$

where Δt denote the time step and $E(x, y, t)$ represents the combined external force, which is the combination of energies of the DRLCE and LGFI:

$$E(x, y, t) = E_{\text{DRLCE}}(x, y, t) + E_{\text{LGFI}}(x, y, t). \quad (18)$$

Here, $E_{\text{DRLCE}}(x, y, t)$ denotes the sum of the internal and external energy terms:

$$E_{\text{DRLCE}}(x, y, t) = E_{\text{in}}(x, y, t) + E_{\text{ex}}(x, y, t). \quad (19)$$

The internal energy term, $E_{\text{in}}(x, y, t)$, enforces contour smoothness using the curvature, $L(\Phi(x, y, t))$, of Φ :

$$\begin{aligned} E_{\text{in}}(x, y, t) &= \lambda L(\Phi(x, y, t)) \\ &= \lambda \int_{\Omega} \int_{\Omega} \delta_{\varepsilon}(\Phi(x, y, t)) |\nabla \Phi(x, y, t)| dx dy \end{aligned} \quad (20)$$

where λ is a weight parameter. The external energy term, $E_{\text{ex}}(x, y, t)$, encourages the contour to evolve toward image features:

$$\begin{aligned} E_{\text{ex}}(x, y, t) &= \alpha A(\Phi(x, y, t)) \\ &= \alpha \int_{\Omega} \int_{\Omega} (H_{\varepsilon}(-\Phi(x, y, t)) - \mu) dx dy \end{aligned} \quad (21)$$

where α and μ denote weight parameter and regularization constant, respectively. In contrast to the approach outlined in (8), $E_{\text{in}}(x, y, t)$ and $E_{\text{ex}}(x, y, t)$ in the proposed method, as described in (20) and (21), do not employ the edge indicator function. Instead, the edge is estimated, as elaborated in Section III-B.

Further, the LGFI, which enhances segmentation based on local intensity characteristics, was integrated into the segmentation process. This integration enhances adaptability of the proposed algorithm to varying image conditions and focuses on regions of clinical importance. The LGFI energy term, $E_{\text{LGFI}}(x, y, t)$, is computed as follows:

$$E_{\text{LGFI}}(x, y, t) = \int_{\Omega} \int_{\Omega} |I(x, y) - I_{\text{LGFI}}(x, y, t)|^2 dx dy \quad (22)$$

where $I_{\text{LGFI}}(x, y, t)$ represents the local mean and is computed as:

$$I_{\text{LGFI}}(x, y, t) = \frac{1}{N} \sum_{i=-k}^k \sum_{j=-k}^k G_{\sigma_k}(I(x+i, y+j, t)), \quad (23)$$

where G_{σ_k} denotes the Gaussian smoothing with standard deviation σ_k , N represents the number of pixels in I , and k signifies the size of a truncated Gaussian window covering a

$(2k+1) \times (2k+1)$ pixel neighborhood. Finally, the LGFI energy is adjusted based on the sign of $\Phi(x, y, t)$:

$$E_{\text{LGFI}}(x, y, t) = \begin{cases} E_{\text{LGFI}}(x, y, t) & \text{if } \Phi(x, y, t) \geq 0 \\ -E_{\text{LGFI}}(x, y, t) & \text{if } \Phi(x, y, t) < 0, \end{cases} \quad (24)$$

Hence, the proposed energy function $E(x, y, t)$ in (18) can be rewritten as:

$$\begin{aligned} E(x, y, t) &= \lambda \int_{\Omega} \int_{\Omega} \delta_{\varepsilon}(\Phi(x, y, t)) |\nabla \Phi(x, y, t)| dx dy \\ &+ \alpha \int_{\Omega} \int_{\Omega} (H_{\varepsilon}(-\Phi(x, y, t)) - \mu) dx dy \\ &+ \int_{\Omega} \int_{\Omega} |I(x, y) - I_{\text{LGFI}}(x, y, t)|^2 dx dy \end{aligned} \quad (25)$$

Further, to minimize (25) with respect to Φ , the derivative of (25) can be written using the calculus of variations as:

$$\begin{aligned} \frac{\partial E(x, y, t)}{\partial \Phi} &= \lambda \delta_{\varepsilon}(\Phi(x, y, t)) \text{div} \left(\frac{\nabla \Phi(x, y, t)}{|\nabla \Phi(x, y, t)|} \right) \\ &+ \alpha (\delta_{\varepsilon}(\Phi(x, y, t)) |\nabla I(x, y)| - \mu) \\ &+ (I(x, y) - I_{\text{LGFI}}(x, y, t)). \end{aligned} \quad (26)$$

The integration of a threshold parameter, denoted as γ , is crucial to control the evolution of Φ , ensuring its proper progression during the iterative process. Mathematically, this can be expressed as:

$$\left| \frac{\partial \Phi(\Delta t)}{\partial t} \right| = |\Phi(t+1) - \Phi(t)| < \gamma, \quad (27)$$

where $\Phi(t+1)$ and $\Phi(t)$ represent the LSF at time steps $t+1$ and t respectively, and Δt represents the time interval parameter. This condition is essential as it prevents Φ from reaching a state where it no longer converges, thereby ensuring the stability and accuracy of the segmentation process.

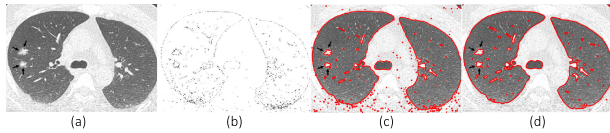
IV. EXPERIMENTAL RESULTS

In this section, experimental results obtained using various ACMs, including CV [18], LBF [19], LIF [35], variational level-set approach for bias correction and segmentation (VLSBCS) [21], and SDRLE [42] were chosen for comparative experiments. These models were evaluated on diverse images, including synthetic, natural, and medical images, to assess their segmentation performance in terms of CPU running time and the number of iterations. All models were implemented using MATLAB 2022b and executed on a system with an Intel Core i7 3.6GHz CPU, 8GB RAM, and a 64-bit Windows 11 operating system. During the experiments, the proposed model utilized the fixed parameters, listed in Table 1, while the parameters for the other models were obtained from the literature. To determine the model parameters in Table 1, we averaged results from empirical experiments on a set of images, finding negligible

TABLE 1. Parameters of the proposed model.

Parameter	Symbol	Value
Saliency weight constants	λ_I, λ_C	0.7, 0.3
Internal energy weight constant	λ	5
External energy weight constant	α	0.2
Regularization constant	μ	0.2
Heaviside constant	ε	1.5
Standard deviations	$\sigma_I, \sigma_C, \sigma_G, \sigma_k$	0.3, 12, 8, 2
Stopping Threshold	γ	$N \times 0.005$
Time step	Δt	1

* N is the number of pixels in I .

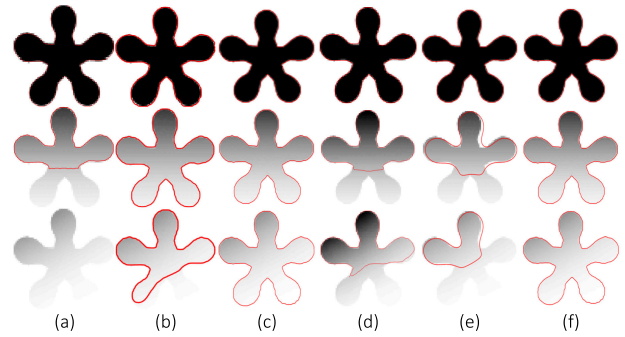
**FIGURE 1.** Effect of saliency on COVID CT scan image segmentation from [51]. (a) Original image, (b) Saliency map, (c) Segmentation without saliency, and (d) Segmentation with saliency.

differences in accuracy and runtime between the averaged and optimized parameters.

Fig. 1 provides a visual representation of the impact of integrating saliency information into the initialization of the proposed model. In this experiment, the input image was a CT scan of the Coronavirus disease (COVID) lung from [51], as depicted in Fig. 1(a). Fig. 1(b) illustrates the saliency map generated as discussed in Section III-A. The segmentation obtained without incorporating saliency (achieved by initializing λ_I and λ_C to zero), is displayed in Fig. 1(c), while the resulting segmentation, enhanced by the integration of saliency information is shown in Fig. 1(d). The clear contrast between the two segmentation outcomes underscores the significant improvement in reliability and accuracy achieved by leveraging the saliency information within the proposed model, emphasizing its effectiveness in enhancing the segmentation results.

Fig. 2 presents a comparative analysis of the segmentation outcomes for a synthetic image with varying intensities using various ACMs alongside the proposed model. The experiment began with a homogeneous image (row 1) and gradually introduced intensity alterations, making manual segmentation challenging (rows 2 and 3). The figure displays the segmentation results from CV, LBF, LIF, VLSBCS, SDRLE, and proposed models. Notably, the proposed and LIF models consistently delivered superior segmentation, regardless of intensity variations. While the CV, LBF, VLSBCS, and SDRLE models performed reasonably well on homogeneous image (row 1), their segmentation accuracy declined with increased intensity inhomogeneity.

Table 2 presents a comprehensive analysis of the computational complexities of various segmentation models, including CV, LBF, LIF, VLSBCS, and SDRLE, alongside the proposed approach, applied to the images illustrated in Fig. 2. The convergence rates of these models differ,

**FIGURE 2.** Segmentation of a synthetic image with intensity variation using (a) CV, (b) LBF, (c) LIF, (d) VLSBCS, (e) SDRLE, and (f) proposed model.**TABLE 2.** Number of iterations and run time for Fig. 2.

Model		Row 1	Row 2	Row 3
CV [18]	Iterations	57	474	3000
	Runtime (s)	0.81	3.42	17.21
LBF [19]	Iterations	110	320	100
	Runtime (s)	6.19	16.3	5.42
LIF [35]	Iterations	50	140	190
	Runtime (s)	2.57	6.25	8.16
VLSBCS [21]	Iterations	20	30	40
	Runtime (s)	1.78	2.89	7.31
SDRLE [42]	Iterations	7	10	11
	Runtime (s)	1.22	0.63	0.76
Proposed	Iterations	2	3	5
	Runtime (s)	0.21	0.37	0.49

influencing the number of iterations required and, subsequently, the runtime. Notably, the proposed model exhibited exceptional efficiency, achieving remarkably low runtimes of 0.21s, 0.37s, and 0.49s with 2, 3, and 5 iterations for segmenting the images in rows 1-3 of Fig. 2. In contrast, the CV, SDRLE, VLSBCS, LIF, and LBF models took 0.81s, 1.22s, 1.78s, 2.57s, and 6.19s, respectively, to accurately segment the homogenous image in Row 1. Although the SDRLE model exhibited relatively faster runtime among the comparison models, only the LIF model achieved reasonably accurate segmentation within an acceptable time frame. The distinctive feature of our proposed model lies in its utilization of saliency during initialization, enabling rapid convergence and significantly reducing the overall runtime, setting it apart from traditional comparative models.

Fig. 3 presents images with multiple objects, showcasing intensity variations in both the foreground and background. The segmentation results are displayed for the CV, LBF, LIF, VLSBCS, SDRLE, and the proposed method in columns one through six, respectively. These results clearly highlight the limitations of previous methods: the CV method fails to achieve accurate segmentation in the presence of inhomogeneity, and the LBF and LIF methods are sensitive to the initial contour position, leading to inaccurate results. While the VLSBCS and SDRLE methods perform well and achieve accurate results in some cases, the proposed method consistently outperforms them, delivering precise segmentation outcomes across all images. Similar to Table 2, Table 3

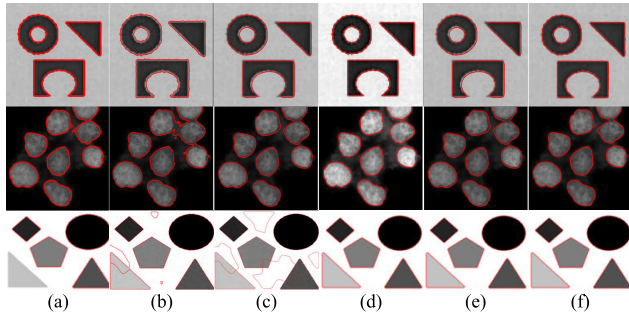


FIGURE 3. Segmentation of images with multiple objects. (a) CV, (b) LBF, (c) LIF, (d) VLSBCS, (e) SDRLE, and (f) proposed model.

provides the comprehensive analysis of the computational complexities in terms of maximum iteration and runtime required for the segmentation models to segment the images in Fig. 3.

In Fig. 4, an experiment demonstrating image segmentation under various noise conditions is presented. The top rows (row 1 and row 3) display the segmentation outcomes of two noise-free images. In contrast, row 2 and row 4 exhibit the segmentation results of images subjected to noise, with variances of 0.1 and 0.04 respectively, both having a zero mean. This comparison provides valuable insights into the robustness of the proposed model, demonstrating its efficacy even in the presence of noise.

Fig. 5 provides comprehensive insights into the performance of various segmentation models applied to a diverse set of medical images sourced from multiple datasets, including CT scans, MRIs, and X-rays. These images intricately detail COVID-19 affected lungs, brain structures, human cells, blood vessels, and the complex hand anatomy. The comparative nature of the figure is particularly striking because it presents the segmentation results obtained using five different models: CV, LBF, LIF, SDRLE, and the proposed model. The CV model relies on global image features and struggles with intensity inhomogeneities. LBF, which leverages local image information, copes better with local details but depends on the initial contour position. LIF utilizes local means and variances but struggles to select an optimal local window size. VLSBCS is sensitive to the initial contour position and can provide good segmentation for small intensity changes in the image, but fails under severe intensity changes. Although SDREL leverages global image data, its edge-based approach often includes unwanted elements, limiting its versatility in medical segmentation.

Each segmented region clearly illustrates the distinctive capabilities of the proposed approach compared to traditional methods. Notably, the proposed model outperforms its counterparts by seamlessly segmenting all types of medical images, irrespective of the complexity and intricacy inherent in these diverse datasets. Fig. 5 serves as a testament to the robustness of the proposed model, demonstrating its ability to handle a wide array of medical imaging scenarios with precision and accuracy. By successfully delineating

TABLE 3. Number of iterations and run time for Fig. 3.

Model		Image 1	Image 2	Image 3
CV [18]	Iterations	200	200	200
	Runtime (s)	3.427	2.43	2.936
LBF [19]	Iterations	110	320	500
	Runtime (s)	6.19	16.3	21.42
LIF [35]	Iterations	50	140	200
	Runtime (s)	2.57	6.25	8.29
VLSBCS [21]	Iterations	50	50	100
	Runtime (s)	12.78	5.14	14.87
SDRLE [42]	Iterations	5	15	20
	Runtime (s)	0.549	1.35	2.76
Proposed	Iterations	5	15	15
	Runtime (s)	0.41	0.57	0.49

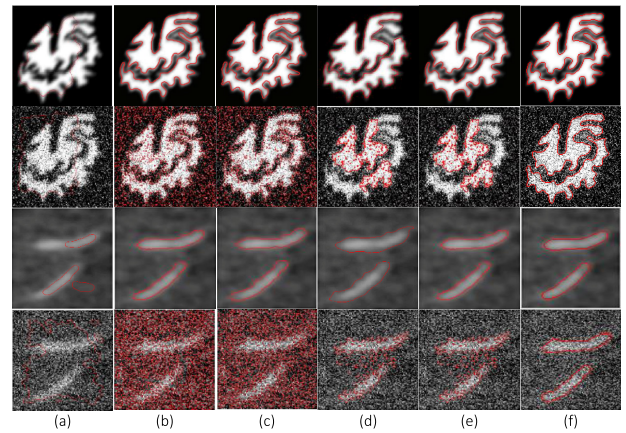


FIGURE 4. Segmentation of images under noise conditions using (a) CV, (b) LBF, (c) LIF, (d) VLSBCS, (e) SDRLE, and (f) proposed model.

TABLE 4. Average metric and run time comparison for BraTs dataset [52].

Model	DI	JI	Runtime (s)
LBF [19]	0.811	0.771	18.78
LIF [35]	0.792	0.759	30.04
VLSBCS [21]	0.795	0.783	7.98
SDRLE [42]	0.759	0.725	4.48
Proposed	0.968	0.957	2.55

vital structures within the COVID-19 affected organs and various anatomical elements, the proposed model is a promising solution for medical image segmentation, offering potential applications in diagnostics, research, and healthcare practices.

Moreover, the precision of the segmentation outcomes can be rigorously evaluated using quantitative image segmentation assessment metrics. Commonly employed techniques for segmentation evaluation include the Dice Index (DI) and Jaccard Similarity Index (Jaccard Index, JI). The DI quantifies the overlap between the segmented region (S_{SR} , produced by a segmentation model) and the ground truth region (S_{GT} , manually annotated or known reference region). Similarly, the JI quantifies the similarity between S_{SR} and S_{GT} . The DI and JI are calculated using the following

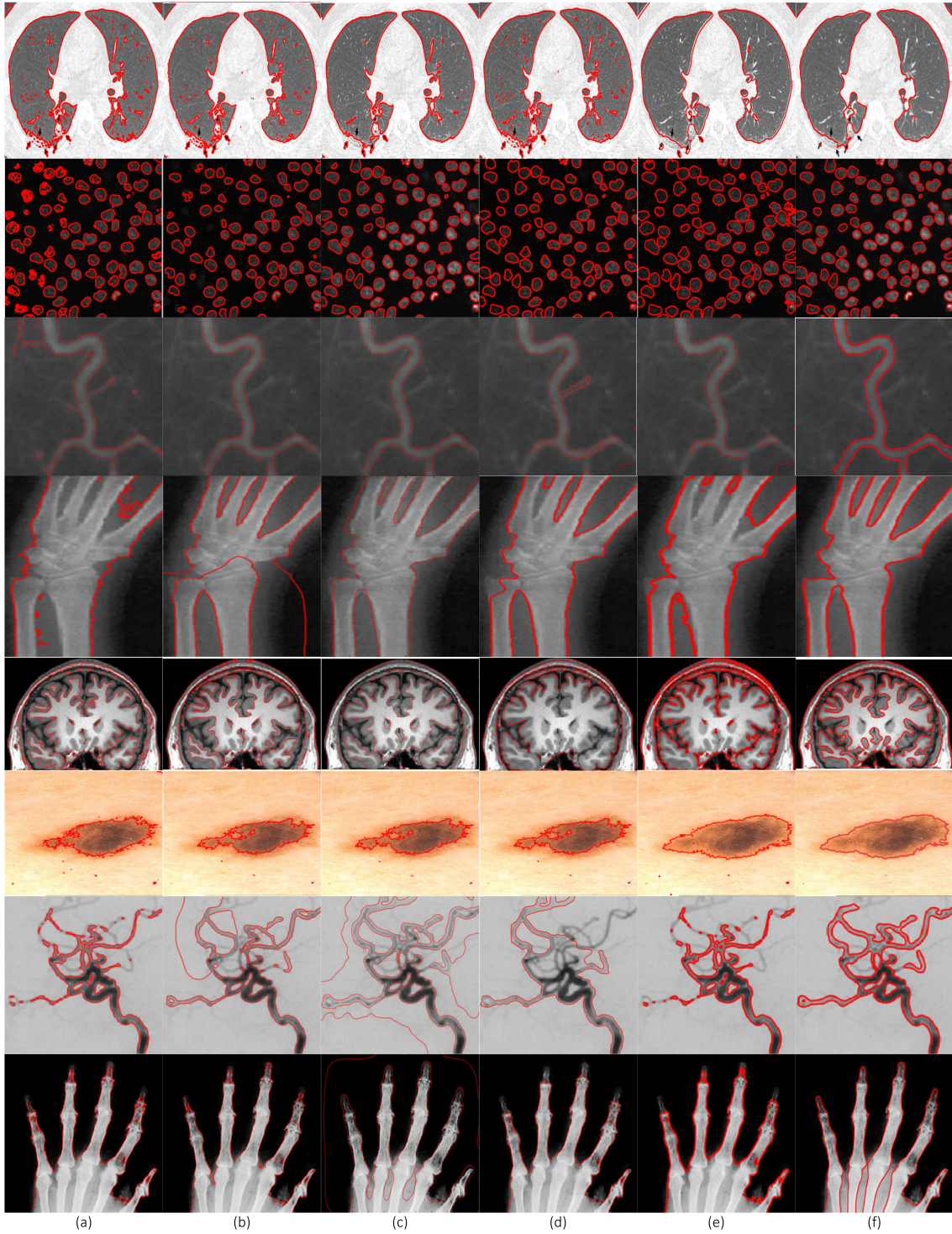


FIGURE 5. Segmentation of different medical images using (a) CV, (b) LBF, (c) LIF, (d) VLSBCS, (e) SDRLE, and (f) proposed model.

formulas:

$$DI_{SR,GT} = 2 \frac{|S_{SR} \cap S_{GT}|}{|S_{SR}| + |S_{GT}|}, \quad (28)$$

$$JI_{SR,GT} = \frac{|S_{SR} \cap S_{GT}|}{|S_{SR} \cup S_{GT}|}. \quad (29)$$

The DI and JI ranges from 0 to 1, where 1 indicates a perfect overlap between the S_{SR} and S_{GT} , and 0 indicates no overlap at all. A higher DI and JI signify a better agreement between the segmented result and the ground truth, indicating a more accurate segmentation. These evaluation methods ensure a consistent and fair comparison among all the models

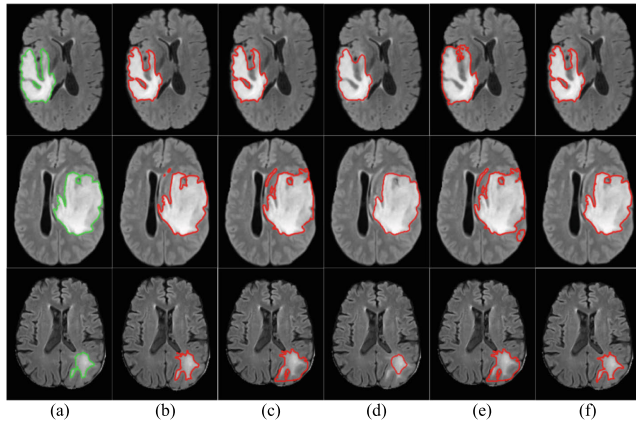


FIGURE 6. Segmentation of three brain MRIs from [52] using ACMs. (a) Ground truth, (b) LBF, (c) LIF, (d) VLSBCS, (e) SDRLE, and (f) Proposed model. These results highlight the proposed model's precision and reliability as compared to the prior ACMs.

discussed earlier and were applied to the BraTS 2019 [52] dataset for precise measurement and analysis.

Table 4 displays the average DI, JI, and runtime required for the segmentation of the 335 MRIs sourced from the BraTS dataset [52]. This figure provides a clear comparison between the performance of the proposed model and the previously evaluated models. The analyses in Table 4 demonstrate that the proposed model achieves the highest DI and JI values with significantly lower processing time.

For a more detailed examination, Fig. 6 presents the segmentation outcomes for three specific MRIs extracted from the BraTS 2019 dataset [52]. Fig. 6(a) displays the ground truth images, serving as the benchmark against which the accuracy of various segmentation methods is measured. The subsequent columns, Fig. 6(b)–(f), show the results obtained from LBF, LIF, VLSBCS, SDRLE, and the proposed model, respectively. The superiority of the proposed model is evident from this detailed visual exploration. Fig. 6 illustrates the superior performance of the proposed model, which captures tumor regions with remarkable accuracy. These results underscore the robustness and exceptional capabilities of the proposed model, demonstrating its ability to handle diverse medical imaging datasets and achieve precise and reliable segmentation outcomes.

Furthermore, Fig. 7 displays the segmentation results obtained using the deep learning models and the proposed model. The most popular model for semantic segmentation is U-Net [53], [54], [55], known for using 3D convolutions on entire 3D images rather than 2D slices. In this study, two deep learning models—Dual-gated Recurrent UNet (DRU) [54] and UNet Deep Weight Prior (UDWP) [55]—are tested on the BraTS dataset [52] using 20 training images and a fixed test sample of 50 images. The results in Fig. 7 show that the proposed model achieves similar accuracies to those of the deep learning models. Deep learning models require extensive datasets for high accuracy in image segmentation due to their complexity and ability to learn intricate patterns.

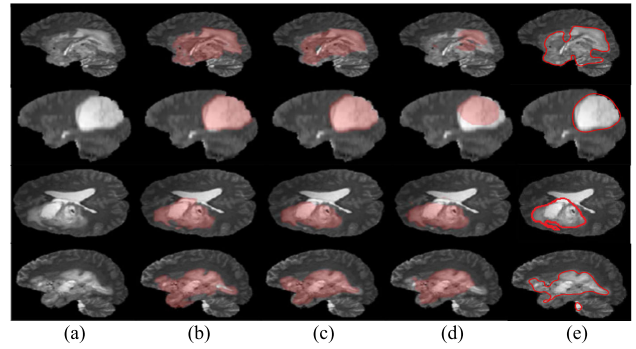


FIGURE 7. Segmentation and comparison of the proposed model and deep learning models on the three brain MRIs from [52]. (a) Original image, (b) Ground truth, (c) UDWP, (d) DRU, and (e) Proposed model.

Large annotated datasets help these models discern subtle variations, capture nuanced features, and generalize well to new data, thereby improving prediction accuracy and mitigating overfitting. These observations highlight the effectiveness of the proposed model alongside established deep learning approaches.

V. CONCLUSION

This study introduces an innovative approach to medical image segmentation by enhancing the DRLSE model through the integration of the LGFI and saliency maps. Through comprehensive experiments and comparisons with existing methods, the proposed model demonstrates remarkable accuracy, robustness, and computational efficiency in diverse medical imaging scenarios. By effectively addressing challenges related to intensity variations, noise, and ambiguous boundaries, the proposed model offers a reliable solution for accurate medical image segmentation.

The significance of this study lies in its potential to revolutionize medical diagnostics and research. By providing a precise delineation of intricate structures within medical images, the proposed model facilitates a more accurate analysis, enabling clinicians to make informed decisions. Moreover, its computational efficiency makes it practical for real-time applications, thereby enhancing the speed and reliability of medical image processing.

Future work should focus on refining the integration of saliency maps and exploring additional enhancements to address the specific challenges posed by certain medical imaging modalities. Additionally, the application of the proposed model to real-time clinical environments and its integration into medical imaging systems can be investigated to assess its practical utility in healthcare practices.

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