

Unsupervised Skin Lesion Segmentation via Structural Entropy Minimization on Multi-Scale Superpixel Graphs

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Abstract—Skin lesion segmentation is a fundamental task in dermoscopic image analysis. The complex features of pixels in the lesion region impede the lesion segmentation accuracy, and existing deep learning-based methods often lack interpretability to this problem. In this work, we propose a novel unsupervised Skin Lesion Segmentation framework based on structural entropy and isolation forest outlier Detection, namely SLED. Specifically, skin lesions are segmented by minimizing the structural entropy of a superpixel graph constructed from the dermoscopic image. Then, we characterize the consistency of healthy skin features and devise a novel multi-scale segmentation mechanism by outlier detection, which enhances the segmentation accuracy by leveraging the superpixel features from multiple scales. We conduct experiments on four skin lesion benchmarks and compare SLED with nine representative unsupervised segmentation methods. Experimental results demonstrate the superiority of the proposed framework. Additionally, some case studies are analyzed to demonstrate the effectiveness of SLED.

Index Terms—skin lesion segmentation, structural entropy, medical image analysis

I. INTRODUCTION

Skin lesion segmentation of dermoscopic images is essential for skin cancer diagnosis [1]. Accurate segmentation of skin lesions from the surrounding skin is challenging because skin lesions, especially melanoma ones, vary in color, texture, shape, size, and location. Moreover, low contrast between the lesion and healthy skin, changing illumination, and the existence of artifacts like hairs, blood vessels, and color calibration charts make this task even harder.

A large amount of unsupervised skin lesion segmentation methods have been proposed by researchers in recent years, including thresholding-based methods [2], region-based methods [3], saliency-based methods [4], and clustering-based methods [5]. They segment skin lesions without labeled datasets, relieving medical experts from the laborious work of data labeling. However, the fine-grained characteristics of lesion skins and healthy skins are under-explored. Figure 1 illustrates examples of skin lesions from the PH2 dataset [6]. On the one hand, the features like color and texture of pixels within the lesion

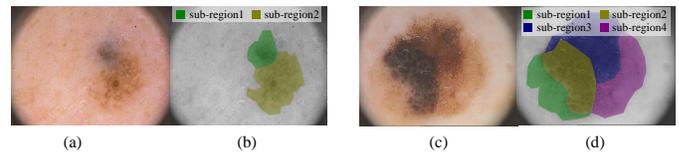


Fig. 1. Examples of skin lesion dermoscopic images. (a) Example lesion 1; (b) The segmentation regions of (a), which contains two sub-regions; (c) Example lesion 2; (d) The segmentation regions of (c), which contains four sub-regions.

regions are diverse, and the lesion region can be further divided into some unspecified number of sub-regions as shown in Figures 1(b) and 1(d). Ignoring the diversity in a fine-grained level of those pixels leads to sub-optimal segmentation results. On the other hand, the features of pixels in healthy skin are generally consistent, which is one of the most important prior information for skin lesion segmentation. Existing methods fail to fully and effectively utilize this prior, thus being unable to accurately segment the margin between the lesion region and healthy skin.

Regarding the diversity of pixel features in the lesion region, some works directly segment the dermoscopic image into two regions, *i.e.*, the lesion region and healthy skin [2], [3]. They ignore the fine-grained level distinction within the lesion region, which can lead to inaccurate segmentation of pixels at lesion borders. Other works segment dermoscopic images into a proper number of regions [5], and then classify regions into the lesion region and healthy skin. Though being better at distinguishing the fine-grained features, they require a pre-defined number of sub-regions, which lacks generalization ability to new scenarios. Regarding the consistent healthy skin prior, RSSLS [7] utilizes reconstruction error-based saliency to segment skin lesions. With the detected background, *i.e.*, the healthy skin, the whole image is reconstructed based on the background, forming the saliency map. However, the background detection process is complex and imprecise, inducing noise into the segmentation procedure.

In this work, we propose a novel unsupervised Skin Lesion

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segmentation framework via structural entropy (SE) and outlier Detection, namely SLED, which adaptively determines the number of segments by SE minimization, and utilizes the consistent healthy skin prior through isolation forest outlier detection. The basic idea is that we take image segmentation as the graph partition problem where graphs are constructed to incorporate both color features and spatial position of pixels (or superpixels). First, we segment the dermoscopic image into a proper number of regions by minimizing the SE of a graph constructed from the image without the need to know the number of sub-regions a priori, which is critical as shown in Figure 1 the number of sub-regions of a lesion is unknown and unpredictable. The nodes of the graph are pre-segmented superpixels and edge weights are the similarity between superpixels. Modules in the graph partition obtained by SE minimization represent the regions. Second, we distinguish these regions into the lesion region and healthy skin by maximizing the between-class variance, forming a single-scale segmentation. Third, we integrate single-scale segmentation results from different superpixel scales into multi-scale segmentation. To achieve this integration, we train isolation forest models using superpixels in the healthy skin regions from single-scale segmentation results and generate a multi-scale outlier score map by combining outlier scores from different scales. The consistency of pixel features in healthy skin helps isolation forest models to distinguish the lesion region from healthy skin with higher outlier scores. Thresholding on the multi-scale score map gives the multi-scale segmentation. Source code is available on Github¹.

We comprehensively evaluate our framework with state-of-the-art unsupervised segmentation methods and several clustering-based methods on four popular skin lesion segmentation datasets. The results show that our framework is more accurate in skin lesion segmentation. We also test the performance of several outlier detection methods, finding that isolation forest best models healthy skin in dermoscopic images. The main contributions of this paper are summarized as follows: (1) An unsupervised skin lesion segmentation framework guided by iteratively refined structural entropy is proposed, which adaptively determines the number of segments in the segmentation process. (2) We characterize the fact that features in healthy skin are consistent and devise a novel multi-scale segmentation mechanism via isolation forest outlier detection method. (3) Comprehensive experiments on four popular skin lesion segmentation datasets demonstrate that our framework achieves new state-of-the-art performance among unsupervised skin lesion segmentation methods.

II. RELATED WORK

A. Unsupervised Skin Lesion Segmentation

Compared to supervised methods, unsupervised skin lesion segmentation methods avoid the laborious work of lesion labeling, and have attracted great interest in recent years. Here we briefly review existing unsupervised skin lesion

segmentation methods, including thresholding-based, region-based, saliency-based, and clustering-based approaches.

Histogram thresholding is a simple yet effective way for skin lesion segmentation. The thresholding histograms are constructed in different ways, such as principle component analysis (PCA) on color bands [8] and carefully chosen color bands [2]. More specialized thresholding techniques are also designed for skin lesion segmentation, including weighted thresholding [9] and adaptive thresholding [10]. Region-based methods iteratively merge image regions until the desired lesion region is found. In [3], a simple region merging method that merges superpixels into two regions, i.e., the lesion region and healthy skin, is proposed. In [11], a superpixel region labeling method via continuity classification for skin lesion segmentation is proposed. Saliency detection-based methods treat skin lesions in dermoscopic images as the salient object. They construct a saliency map by assigning each pixel a saliency score, and segment the lesion region by thresholding on the saliency map. The saliency scores are defined by reconstruction errors [7], color and brightness prior [12], color channel volume [4] in unsupervised manners, or lists of regional contrast and regional property in a supervised manner [13]. Clustering-based methods group pixels or superpixels into regions and then classify them to find the skin lesion. Ahn *et al.* [5] proposed a spatial guided self-supervised clustering network (SGSCN) for skin lesion and liver tumor segmentation that iteratively determines the number of segments. Zhang *et al.* [14] proposed a deep hyperspherical clustering method based on the theory of belief functions to achieve unsupervised skin lesion segmentation. In the single-scale segmentation step of our framework, we group superpixels by minimizing SE and classify regions by maximizing the between-class variance.

B. Unsupervised Image Segmentation

Apart from methods specifically designed for skin lesion segmentation, there exist a large number of unsupervised image segmentation methods for more general usage. Classical image segmentation methods group pixels into meaningful regions. Representative methods include K -means and spectral clustering [15]. More recent works utilize the power of deep learning such as convolutional neural networks (CNNs) to learn vision features. Kanazaki *et al.* [16] proposed a CNN-based model to group spatially continuous pixels of similar features to facilitate unsupervised natural image segmentation. In order to perform the segmentation of the target region, there are several other research lines in unsupervised image segmentation related to skin lesion segmentation, which focuses on different scenarios. The first line is unsupervised salient object detection, which aims at localizing and segmenting salient objects simultaneously without manual annotations. Yan *et al.* [17] pointed out the unreliability of usually used noisy labels generated by traditional unsupervised salient object detection methods and proposed unsupervised domain adaptive salient object detection which learns from synthetic labels with higher quality. Zhou *et al.* [18] proposed a texture-guided saliency distilling unsupervised salient object detection model through

¹<https://github.com/SELGroup/SLED>

a confidence-aware saliency distilling strategy that assigns scores to samples based on confidence, and a boundary-aware texture matching strategy which refines boundaries by matching textures. The second line is unsupervised foreground extraction, which aims for a binary partition of an image with a foreground containing identifiable objects and a background with remaining regions. Yu *et al.* [19] presented deep region competition (DRC) to solve the foreground extraction problem by reconciling energy-based prior with generative image modeling in the form of mixture of experts. Ding *et al.* [20] pointed out two kinds of trivial solutions in the image compositional generation process when performing foreground extraction, and solved trivial solutions with the proposed ComGAN model. For the task of skin lesion segmentation, lesions can be taken as salient objects or image foregrounds, so both methods belonging to these two research lines can be used to tackle the task of skin lesion segmentation.

C. Structural Entropy

SE [21] is first proposed to measure the complexity of the hierarchical structure of graphs through associated encoding trees, which is naturally a node clustering method. As the SE of a graph G is the minimum overall number of bits required to determine the codewords of the graph nodes, it measures the uncertainty embedded in G . SE has been successfully applied in the field of bioinformatics [22], reinforcement learning [23], [24], and graph neural networks [25]–[27]. In this work, we use the two-dimensional SE, *i.e.*, SE of a graph by a partition, to perform skin lesion segmentation. Without confusion, SE in the following sections means two-dimensional SE.

Let $G = (V, E, \mathbf{W})$ be an undirected weighted graph, where $V = \{v_1, \dots, v_N\}$ is the node set, E is the edge set, and $\mathbf{W} \in \mathbb{R}^{N \times N}$ is the edge weight matrix. A graph partition \mathcal{P} defined on G can be formulated as $\mathcal{P} = \{X_1, X_2, \dots, X_L\}$, where X_i is the i -th module containing a subset nodes of V . Given a graph G and its graph partition \mathcal{P} , the SE of G given by \mathcal{P} is defined as:

$$\mathcal{H}^{\mathcal{P}}(G) = - \sum_{X \in \mathcal{P}} \sum_{v_i \in X} \frac{g_i}{\text{vol}(G)} \log_2 \frac{d_i}{\text{vol}(X)} - \sum_{X \in \mathcal{P}} \frac{\text{cut}(X)}{\text{vol}(G)} \log_2 \frac{\text{vol}(X)}{\text{vol}(G)}, \quad (1)$$

where d_i is the degree of node v_i , g_i is the weight sum of edges connecting v_i and other nodes, $\text{vol}(X)$ and $\text{vol}(G)$ are volumes, *i.e.*, the sum of the node degrees, in module X and graph G , respectively, and $\text{cut}(X)$ is the cut of X , *i.e.*, the weight sum of edges between nodes in and not in module X .

III. METHODOLOGY

In this section, we present SLED, a novel unsupervised skin lesion segmentation framework based on SE and outlier detection. The overview of SLED is depicted in Figure 2. SLED composes of three components: superpixel graph construction, SE guided segmentation, and multi-scale segmentation mechanism by outlier detection. Different scale superpixels are grouped by SE to form single-scale segmentation

TABLE I
DEFINITION OF NOTATIONS.

Symbol	Domain	Description
G	-	Superpixel graph
V, E, \mathbf{W}	-	Node set, edge set, edge weight matrix
v	-	graph node/superpixel
\mathcal{P}	-	Graph partition (image segmentation)
L	\mathbb{Z}	Number of modules/regions
X, Y	-	Modules in graph partition (regions in images)
$\mathcal{H}^{\mathcal{P}}(G)$	-	SE of G given by \mathcal{P}
$\text{cut}(X)$	\mathbb{R}	Cut of X (weight sum of edges connected to nodes in X)
$\text{vol}(X)$	\mathbb{R}	Volume of X (degree sum of nodes in X)
σ_B^2	\mathbb{Z}	Between class variance of regions
o	\mathbb{R}	Outlier score of a superpixel
O	$\mathbb{Z}^{N \times N}$	Outlier score map
ϵ	\mathbb{N}	superpixel scale

results, which are then integrated by the outlier detection-based multi-scale mechanism to generate the final segmentation.

A. Basic Notations

In this paper, superpixel graphs are constructed from images to perform segmentation, so some notations refer to elements both in graphs and images. In particular, v denotes both a graph node and a superpixel, \mathcal{P} denotes both a graph partition and an image segmentation, and X and Y denote both modules in graph partition and regions in images. We list some important notations in Table I.

B. Superpixel Graph Construction

Graph-based segmentation methods [15], [28] integrate the information of both color features and spatial position of pixels (or superpixels) in the procedure of graph construction. This gives graph-based methods the ability to segment images accurately and keep the spatial continuity of segments in the meantime. Among the graph-based methods, SE-based methods give a high-quality graph partition by SE minimization. Furthermore, SE-based methods adaptively determine the number of modules in the partition, which are segments corresponding to sub-regions in images in the case of skin lesion segmentation. This gives SE-based methods the advantage of accurate segmentation of pixels at lesion borders.

We construct a graph $G = (V, E, \mathbf{W})$ based on the image, where the nodes in $V = \{v_1, \dots, v_N\}$ correspond to superpixels of image segmented by SLIC algorithm [29], the edges in E connect spatially close superpixels, and the weight matrix \mathbf{W} measures the similarities among superpixels. To utilize the spatial information of superpixels, we only connect the nodes whose spatial distance is smaller than a threshold r . For nodes v_i and v_j with edge connected, the similarity weight $\mathbf{W}_{i,j}$ is computed as follows:

$$\mathbf{W}_{i,j} = \exp\left(\frac{-d(v_i, v_j)^2}{\sigma_i \sigma_j}\right), \quad (2)$$

where $d(v_i, v_j)$ is the mean color distance between v_i and v_j , σ_i and σ_j are the local scaling parameters for nodes [30]. We

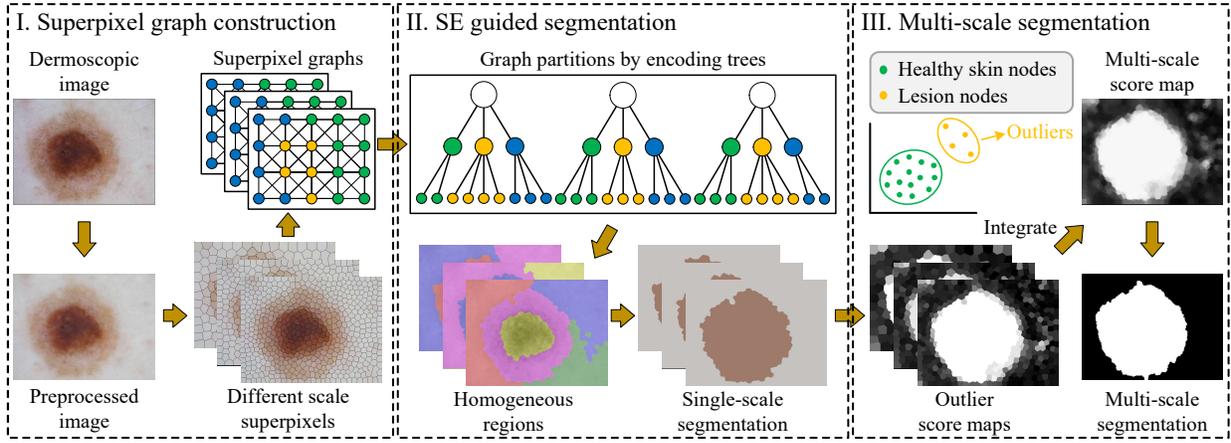


Fig. 2. Overview of SLED.

then sparsify this graph into a K -nearest neighbor graph by retaining K most significant edges for each node, which avoids the complex dense graphs for subsequent SE minimization.

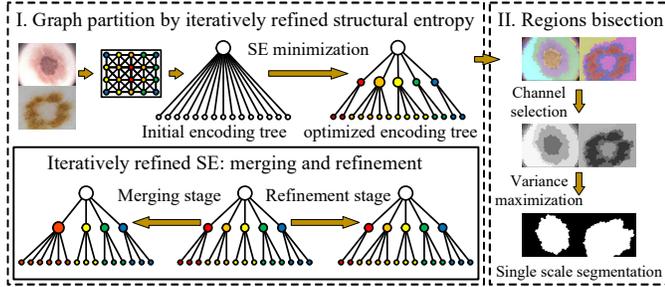


Fig. 3. Illustration of SE guided segmentation.

C. Structural Entropy Guided Segmentation

After superpixel graphs construction, images are segmented into regions through SE minimization on these graphs. The procedure of SE guided segmentation is depicted in Figure 3. We aim to partition the graph into several modules by SE minimization. Since nodes in modules represent the superpixels of the image, those modules thus represent homogeneous regions of the image. As such, we can simply classify those regions to be either lesion regions or healthy skin regions to predict accurate lesion boundaries.

We minimize the SE of G to obtain a high-quality graph partition $\mathcal{P} = \{X_1, X_2, \dots, X_L\}$. Greedily applying the merging operator [21] on the encoding tree gives the SE minimized encoding tree and corresponding graph partition with adaptively determined L modules. However, the partition result by greedy merging can be sub-optimum. We propose the iteratively refined structural entropy for better results. It composes a merging stage and a refinement stage, as illustrated in Algorithm 1. In the merging stage, we merge nodes to maximize the decreasing amount of SE to obtain the encoding tree with multiple modules. And then in the refinement stage,

we greedily adjust nodes into different modules to achieve better SE scores.

Algorithm 1 Iteratively refined structural entropy

Input: A graph $G = (V, E, \mathbf{W})$

Output: Encoding tree \mathcal{T} and corresponding partition \mathcal{P}

- 1: Initialize \mathcal{T} containing all graph nodes as tree leaves
- 2: // Merging stage
- 3: **repeat**
- 4: Merge a chosen module pair (X, Y) into $X \cup Y$ condition on $\operatorname{argmax}_{X, Y} \{\Delta \mathcal{H}_{X, Y}^{\mathcal{M}}\}$ via Eq. (3)
- 5: Update $\Delta \mathcal{H}^{\mathcal{M}}$ for node pairs connected to X or Y
- 6: **until** $\Delta \mathcal{H}^{\mathcal{M}} < 0$ for all module pairs
- 7: // Refinement stage
- 8: **repeat**
- 9: **for** each node $v_i \in V$ **do**
- 10: Remove node v_i from the original module X
- 11: Insert node v_i into a chosen module Y condition on $\operatorname{argmax}_Y \{\Delta \mathcal{H}_{X, v_i}^{\mathcal{R}} - \Delta \mathcal{H}_{Y, v_i}^{\mathcal{L}}\}$ via Eqs. (4) and (5)
- 12: Update the cut and the volume of each module
- 13: **end for**
- 14: **until** $\mathcal{H}^{\mathcal{P}}(G)$ converges

In the merging stage, we apply the merging operator on the initial encoding tree which contains all graph nodes as tree leaves to obtain the encoding tree by merging. For an encoding tree \mathcal{T} with modules X and Y contained, the decrease amount of SE after merging X and Y is given by:

$$\begin{aligned} \Delta \mathcal{H}_{X, Y}^{\mathcal{M}} = & \frac{1}{\operatorname{vol}(G)} [(\operatorname{vol}(X) - \operatorname{cut}(X)) \log_2 \operatorname{vol}(X) \\ & + (\operatorname{vol}(Y) - \operatorname{cut}(Y)) \log_2 \operatorname{vol}(Y) \\ & - (\operatorname{vol}(X \cup Y) - \operatorname{cut}(X \cup Y)) \log_2 \operatorname{vol}(X \cup Y) \\ & + (\operatorname{cut}(X) + \operatorname{cut}(Y) - \operatorname{cut}(X \cup Y)) \log_2 \operatorname{vol}(G)], \end{aligned} \quad (3)$$

where \mathcal{M} denotes modules Merging, $X \cup Y$ is a module merged from X and Y , containing nodes from either X or Y , $\operatorname{vol}(X)$ and $\operatorname{vol}(G)$ are the volume of X and G , and $\operatorname{cut}(X)$

is the cut of X , as defined in Section II-C. Merging operator merges X and Y into $X \cup Y$ if $\Delta\mathcal{H}_{X,Y}^M > 0$.

In the refinement stage, we iteratively refine the encoding tree from the merging stage to obtain the encoding tree by refinement. For graph node v_i , the decrease amount of SE by removing v_i from the original module X is given by:

$$\Delta\mathcal{H}_{X,v_i}^{\mathcal{R}} = \frac{\text{vol}(X) - \text{cut}(X)}{\text{vol}(G)} \log_2 \frac{\text{vol}(X)}{\text{vol}(G)} - \frac{\text{vol}(X \setminus \{v_i\}) - \text{cut}(X \setminus \{v_i\})}{\text{vol}(G)} \log_2 \frac{\text{vol}(X \setminus \{v_i\})}{\text{vol}(G)}, \quad (4)$$

where \mathcal{R} denotes node Removing, $X \setminus \{v_i\}$ means removing node v_i from module X , and the increase amount of SE by inserting node v_i into another module Y is given by:

$$\Delta\mathcal{H}_{Y,v_i}^{\mathcal{I}} = -\frac{\text{vol}(Y) - \text{cut}(Y)}{\text{vol}(G)} \log_2 \frac{\text{vol}(Y)}{\text{vol}(G)} + \frac{\text{vol}(Y \cup \{v_i\}) - \text{cut}(Y \cup \{v_i\})}{\text{vol}(G)} \log_2 \frac{\text{vol}(Y \cup \{v_i\})}{\text{vol}(G)}, \quad (5)$$

where \mathcal{I} denotes node Inserting, $Y \cup \{v_i\}$ denotes inserting node i into module Y . It should be noted that the constructed graph G contains no self-loop, thus $g_i = d_i$ for graph node v_i . In each iteration, we remove nodes from the original modules and find modules that minimize SE the most.

In the merging stage, the merging operator is performed iff $\Delta\mathcal{H}_{X,Y}^M > 0$, so $\mathcal{H}^P(G)$ decreases after each merging iteration and converges when no such module pair exists. In the refinement stage, node v_i transfers from module X to a module Y with largest $\Delta\mathcal{H}_{X,v_i}^{\mathcal{R}} - \Delta\mathcal{H}_{Y,v_i}^{\mathcal{I}}$ in each iteration, so $\mathcal{H}^P(G)$ decreases or stays constant after each refinement iteration, and converges when no improvement can be made.

The time complexity of the merging stage is $O(N \log^2 N)$ [21]. In the refinement stage, calculating $\Delta\mathcal{H}_{X,v_i}^{\mathcal{R}}$ and $\Delta\mathcal{H}_{Y,v_i}^{\mathcal{I}}$ for each node v_i and every possible module Y take time of $O(NL)$ for each iteration. Also, updating the cut and the volume of each module take time of $O(NL)$ for each iteration. Thus, the total time complexity of Algorithm 1 is $O(N \log^2 N + NLT)$, where N , L , and T denote the number of nodes, modules, and iterations, respectively.

Homogeneous Regions Bisection. Hereafter, we classify those segmented regions into the lesion region and healthy skin. We adopt the between-class variance maximization method, which is a widely used criterion in skin lesion segmentation [2]. Specifically, we choose a color channel c from the image, obtain a gray image, and use the intensity of the gray image to classify the regions into classes C_0 and C_1 . To better separate the regions, the channel c is chosen from the RGB channels with maximum σ_B^2 after bisection. For each region X_i , the occurrence probability ω_{X_i} and the mean intensity μ_{X_i} are represented as:

$$\omega_{X_i} = \frac{\|X_i\|}{M}, \quad (6)$$

and

$$\mu_{X_i} = \frac{\sum_{\text{pixel}_j \in X_i} I_j}{\|X_i\|}, \quad (7)$$

respectively, where I_j is the intensity of pixel j , $\|X_i\|$ is the number of pixels in region X_i , and M is the total number of pixels in the image. The between-class variance of regions is given by:

$$\sigma_B^2 = \omega_0(\mu_0 - \mu_T)^2 + \omega_1(\mu_1 - \mu_T)^2, \quad (8)$$

where ω_k is the occurrence probability of class C_k defined as:

$$\omega_k = \sum_{X_i \in C_k} \omega_{X_i}, \quad (9)$$

μ_k is the mean intensity of class C_k defined as:

$$\mu_k = \sum_{X_i \in C_k} \omega_{X_i} \mu_{X_i}, \quad (10)$$

and μ_T is the total mean intensity of C_0 and C_1 , defined as:

$$\mu_T = \sum_{X_i \in C_{0,1}} \omega_{X_i} \mu_{X_i}. \quad (11)$$

In practice, we arrange μ_{X_i} in ascending order and separate those regions into two classes, i.e., $C_0 = \{X_i \mid \mu_{X_i} \leq \tau\}$ and $C_1 = \{X_i \mid \mu_{X_i} > \tau\}$ using a threshold τ which gives the greatest σ_B^2 . The darker class C_0 is the lesion region.

D. Multi-Scale Segmentation Mechanism

Due to the complex condition of different dermoscopic images, mis-segmentation may occur in SE-guided segmentation. We develop a multi-scale superpixel-based segmentation mechanism to improve the segmentation accuracy. In fact, we observed features of pixels in healthy skin are consistent. Thus, we view superpixels in healthy skin as normal, while those in the lesion region are outliers. Hence, we can distinguish healthy and lesion regions by the outlier detection method. Intuitively, a higher outlier score of a superpixel reflects a higher possibility to be a lesion region.

Outlier Detection by Isolation Forest. Isolation Forest (*iForest*) [31] detects outliers by building an ensemble of binary trees that separate training data points called *iTrees*. The susceptibility of data points to being outliers is measured by the average traversal path length on *iTrees*. The average traversal path length-based outlier scores of *iForest* are well-graded. These graded scores help mis-segmented superpixels to be reclassified correctly in the following binary segmentation procedure by thresholding.

Given a dermoscopic image segmentation with lesion region and healthy skin, we train an *iForest* model containing a collection of *iTrees* using superpixels $\{s_i, i = 1, \dots, K\}$ in the healthy skin whose attributes are the average RGB colors. With this ensemble of *iTrees*, the average path lengths $h(s_i)$ of all superpixels $\{s_i, i = 1, \dots, N\}$ are counted, and the outlier score o of an superpixel s_i is calculated as:

$$o(v_i, \psi) = 2^{-\frac{E(h(s_i))}{c(\psi)}}, \quad (12)$$

where $E(h(s_i))$ is the average of $h(s_i)$ from the collection of *iTrees*, ψ is the number of superpixels in healthy skin, and $c(\psi)$ is the normalization term. The outlier scores of all

superpixels are obtained from the t Trees, forming a score map O at the size of the image.

Multi-Scale Integration. We integrate the outlier scores from different superpixel scales and form the multi-scale score map. The weighted score of pixel j being an outlier is defined as:

$$O(j) = \frac{\sum_{\epsilon \in \gamma} (w^\epsilon O^\epsilon(j))}{\sum_{\epsilon \in \gamma} (w^\epsilon)}, \quad (13)$$

where $O^\epsilon(j)$ is the score of pixel j at scale ϵ , γ is the number of different scales, and w^ϵ is the weight of scale ϵ . We use the σ_B^2 in Eq. (8) to indicate the confidence of single-scale segmentation where larger σ_B^2 should be associated with larger weights. Specifically, the weight of a scale ϵ is defined as:

$$w^\epsilon = \exp\left\{\frac{\sigma_B^2(\epsilon) - \min_{\epsilon \in \gamma} \sigma_B^2(\epsilon)}{\min_{\epsilon \in \gamma} \sigma_B^2(\epsilon)}\right\}, \quad (14)$$

where $\sigma_B^2(\epsilon)$ is the between-class variance of scale ϵ .

The binary segmentation result is obtained by applying GHT thresholding [32] on the multi-scale score map. We also perform hole filling to avoid small holes in the lesion part. Following [9], we compute the region score of every connected component which increase with region size and proximity to the image center. This is achieved by filtering each connected component with a two-dimensional Gaussian filter. The connected component with the largest region score is selected as the final lesion region.

IV. EXPERIMENTS AND RESULTS

In this section, we first describe our experimental setup, including datasets, evaluation metrics, baselines, and implementation details of SLED. Next, we quantitatively evaluate SLED on four datasets to verify the effectiveness of SLED. Besides, we perform ablation studies and case studies to analyze SLED in detail. At last, we evaluate the efficiency of SLED. All experiments are conducted to answer the following questions:

- **Q1:** Does SLED outperform state-of-the-art baselines regarding skin lesion segmentation?
- **Q2:** Dose our outlier detection-based multi-scale segmentation mechanism effectively utilize the consistent healthy skin prior?
- **Q3:** Is SLED sensitive to major parameters?
- **Q4:** Is SLED efficient enough for skin lesion segmentation compared to baselines?

A. Experimental Setup

Datasets. We evaluate SLED on four public benchmark datasets: ISIC 2016 [33], ISIC 2017 [34], ISIC 2018 [35], and PH2 [6]. The first three datasets are provided by the International Skin Imaging Collaboration (ISIC) archive from the ‘‘Skin Lesion Analysis toward Melanoma Detection’’ challenge hosted by the International Symposium on Biomedical Imaging (ISBI) in 2016, 2017, and 2018 respectively. We evaluate the performance of different methods on the test sets, which contain 379, 600, and 1000 RGB dermoscopic images respectively at the resolution ranging from 1022×767 to

4288×2848 , along with their corresponding ground truth. The PH2 dataset is another frequently used benchmark, especially for unsupervised skin lesion segmentation. It contains a total of 200 RGB dermoscopic images at the resolution of 768×560 pixels, along with their pixel-level lesion ground truth annotated by expert dermatologists.

Evaluation Metrics and Baselines. We adopt five metrics used in ISIC challenges for evaluating all compared methods, which are pixel-level accuracy (AC), pixel-level sensitivity (SE), pixel-level specificity (SP), Dice Coefficient (DI), and Jaccard Index (JA), as defined in [33]. We compare SLED with a variety of baseline methods including unsupervised skin lesion segmentation methods, an unsupervised foreground extraction method, unsupervised salient object detection methods, and several clustering methods. For unsupervised skin lesion segmentation methods, we consider superpixel merging (Sp. Merging [3]), saliency map thresholding (Saliency-CCE), and deep learning-based clustering (SGSCN [5]). For the unsupervised foreground extraction method, we consider Deep Region Competition (DRC [19]), where skin lesions are taken as foreground. For unsupervised salient object detection methods, we consider Unsupervised Domain Adaptive Salient Object Detection (UDASOD [17]) and texture-guided saliency distilling (A2S-v2 [18]), where skin lesions are taken as salient objects. For clustering methods, we consider normalized cut (NCut [15]), K -means, and hierarchical clustering (SpecWRSC [36]). The number of segments of K -means, NCut, and SpecWRSC is set to be three, which has been reported to perform well for skin lesion segmentation [5]. To achieve a fair comparison, we perform the same preprocessing, homogeneous region bisection, and postprocessing method for clustering-based methods as SLED. The details of important methods are as follows:

- **Sp. Merging [3]** segments skin lesions by greedily merging superpixels using the distance of the mean color of each superpixel as the criterion.
- **Saliency-CCE [4]** utilizes a hand-crafted color feature extractor called color channel volume to obtain the saliency map of skin lesions and binarize this map through adaptive thresholding to obtain lesion masks.
- **SGSCN [5]** is a spatial guided self-supervised clustering network that groups pixels that are spatially close and have consistent features.
- **DRC [19]** is an unsupervised foreground extraction approach by reconciling energy-based prior with generative image modeling in the form of Mixture of Experts.
- **UDASOD [17]** is an unsupervised domain adaptive salient object detection method which learns saliency from synthetic but clean labels.
- **A2S-v2 [18]** is an unsupervised salient object detection method with a confidence-aware saliency distilling strategy and a boundary-aware texture matching strategy.
- **SpecWRSC [36]** is an efficient hierarchical clustering algorithm running in nearly-linear time in the input size of the input graph. We choose the largest K modules from the hierarchical clustering tree to obtain K clusters.

TABLE II
COMPARISON OF UNSUPERVISED SKIN LESION SEGMENTATION METHODS. **BOLD**: THE BEST PERFORMANCE ON EACH METRIC, UNDERLINE: THE SECOND BEST PERFORMANCE.

Method%	ISIC 2016					ISIC 2017					ISIC 2018				
	AC↑	SE↑	SP↑	DI↑	JA↑	AC↑	SE↑	SP↑	DI↑	JA↑	AC↑	SE↑	SP↑	DI↑	JA↑
UDASOD	71.15	45.44	76.57	34.50	27.96	59.07	60.07	55.99	31.19	23.70	67.87	35.92	79.60	24.51	18.86
Sp. Merging	86.67	67.13	95.39	69.97	61.06	79.89	59.16	88.72	54.66	46.02	84.53	69.82	92.79	70.11	60.89
DRC	83.78	68.51	97.11	66.84	53.32	83.77	70.35	95.58	59.11	45.40	83.85	70.00	<u>97.00</u>	68.71	56.05
Saliency-CCE	85.91	74.72	95.70	72.18	60.64	83.87	74.07	92.98	61.77	49.53	85.51	77.44	94.34	72.85	61.91
A2S-v2	87.51	82.64	93.85	75.52	65.67	82.85	68.65	92.80	61.35	51.10	<u>86.22</u>	72.13	97.35	75.01	65.94
SpecWRSC	84.83	65.95	92.69	68.76	58.05	83.03	68.21	89.96	61.01	50.52	81.20	69.39	86.34	68.97	58.41
NCut	85.24	64.86	93.54	68.78	58.14	83.79	67.12	90.90	62.13	51.84	82.48	68.12	88.31	69.11	58.78
K -means	89.24	69.88	95.76	76.13	66.37	84.90	70.77	90.64	67.78	58.11	83.70	71.73	88.09	71.46	61.57
SGSCN	86.61	63.36	96.59	71.08	60.24	85.13	54.98	<u>95.56</u>	59.95	50.04	82.30	71.17	87.36	70.97	61.81
SLED _{SS}	<u>90.69</u>	77.85	<u>97.23</u>	<u>81.61</u>	<u>72.21</u>	<u>86.96</u>	<u>75.98</u>	92.98	<u>70.62</u>	<u>60.56</u>	<u>86.22</u>	<u>79.77</u>	90.52	<u>76.81</u>	<u>67.98</u>
SLED _{MS}	91.82	<u>80.83</u>	97.72	84.33	76.02	88.81	77.96	94.61	73.90	64.45	86.93	80.12	91.84	77.68	69.35
Improvement	4.31	-	0.61	8.81	10.35	3.68	3.89	-	12.13	13.35	0.71	2.68	-	2.67	3.41

Implementation Details. For all datasets, images are resized into 768×560 pixels, artifacts in dermoscopic images are removed using existing methods, including hairs [37], dark corners [38], and color charts [13]. Color constancy [39] is also performed on images to cope with illumination problems. We set the parameters of superpixel graph construction empirically, with the spatial distance threshold r of 0.3 times image height and width, the local scaling parameter σ of 30, and retained edge number K of 50. To evaluate the effectiveness of the multi-scale mechanism in SLED framework, we report both the results of single-scale SLED (SLED_{SS}) and multi-scale SLED (SLED_{MS}), corresponding to SLED without and with the multi-scale mechanism. In the reported results, we empirically set the number of superpixels of SLED_{SS} to be 400. The segmentation results of SLED_{MS} integrate the results of SLED_{SS} with superpixel numbers from 200 to 700 at increments of 50. All the experiments are conducted on a server with two Intel(R) 2.30 GHz CPUs and 500 GB RAM.

B. Quantitative Results (Q1)

Table II shows the results of unsupervised skin lesion segmentation methods on three ISIC datasets. Compared to state-of-the-art methods, SLED_{MS} and SLED_{SS} achieve the best and second-best performance on three metrics including AC, DI, and JA on both three datasets. SLED_{MS} witnesses improvements from 0.61% to 13.35% on these three metrics, as shown in the last row of Table II. Since SE and SP are a pair of metrics to measure how well methods can identify true positives and true negatives respectively, SLED_{MS} failed to achieve the best performance on both metrics. However, SLED_{MS} achieves the best performance on at least one metric on both three datasets and achieves quite well performance on the other metric, demonstrating the superiority of SLED_{MS} on this pair of metrics. Both SLED_{SS} and SLED_{MS} achieve better performance than all other clustering-based methods, which thanks to their ability to adaptively determine the number of segments of SE. We can also see that SLED_{MS} achieves better performance than SLED_{SS} on all metrics,

TABLE III
COMPARISON OF UNSUPERVISED SKIN LESION SEGMENTATION METHODS ON PH2 DATASET.

Method%	AC↑	SE↑	SP↑	DI↑	JA↑
UDASOD	63.18	48.22	68.03	31.56	23.68
Sp. Merging	89.10	79.63	96.00	82.83	73.97
DRC	82.63	69.18	97.65	72.41	59.76
Saliency-CCE	84.62	78.90	93.77	76.79	65.62
A2S-v2	85.66	87.56	91.37	78.21	67.15
SpecWRSC	85.96	79.08	89.74	78.12	68.54
NCut	88.15	76.16	94.94	80.17	70.51
K -means	91.64	83.82	95.03	86.14	77.78
SGSCN	91.80	84.26	93.82	87.89	<u>80.15</u>
SLED _{SS}	<u>92.00</u>	<u>89.35</u>	94.76	<u>88.02</u>	80.11
SLED _{MS}	93.00	89.97	<u>96.37</u>	90.34	83.50
Improvement	1.20	2.41	-	2.45	3.35

TABLE IV
PERFORMANCE OF SLED ON THE ISIC 2016 DATASET USING DIFFERENT OUTLIER DETECTION METHODS.

Method%	AC↑	SE↑	SP↑	DI↑	JA↑
SLED _{Ecod}	75.58	24.51	<u>99.51</u>	33.36	23.77
SLED _{K-NN}	84.80	47.94	99.78	60.07	47.72
SLED _{OCSVM}	<u>91.34</u>	<u>79.52</u>	97.48	<u>82.59</u>	<u>74.13</u>
SLED _{iForest}	91.82	80.83	97.72	84.33	76.02

which proves the effectiveness of our outlier detection-based multi-scale mechanism.

We also evaluate SLED on the popular PH2 dataset, as shown in Table III. SLED_{MS} and SLED_{SS} achieve the best and second-best performance on four metrics and achieve quite high SP scores comparable to baseline methods. Improvements of SLED_{MS} on this dataset range from 1.20% to 3.35% on four metrics, as shown in the last row of Table III. Through quantitative comparison with nine baselines on four datasets, SLED is proven to achieve new state-of-the-art performance among unsupervised skin lesion segmentation methods.

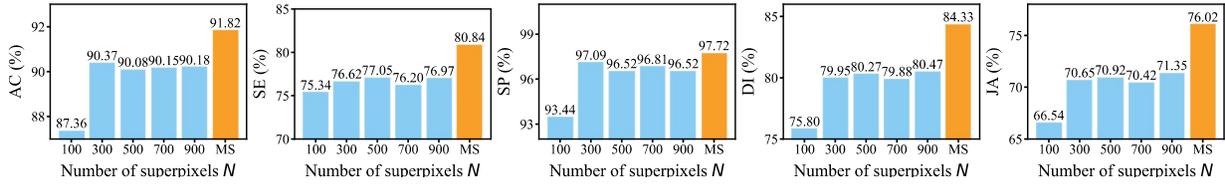


Fig. 4. Performance of SLED_{SS} with different number of superpixels (blue) and SLED_{MS} (orange) on the ISIC 2016 dataset.

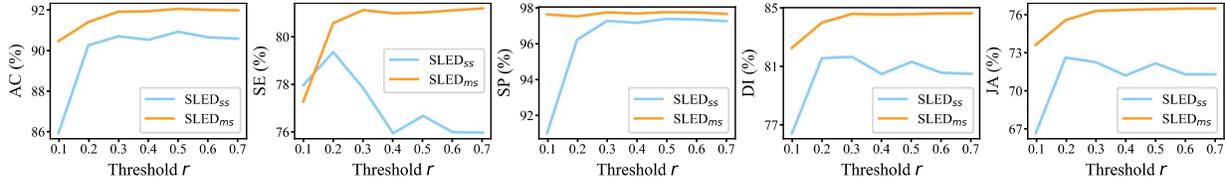


Fig. 5. Parameter sensitivity experiments for threshold r on the ISIC 2016 dataset.

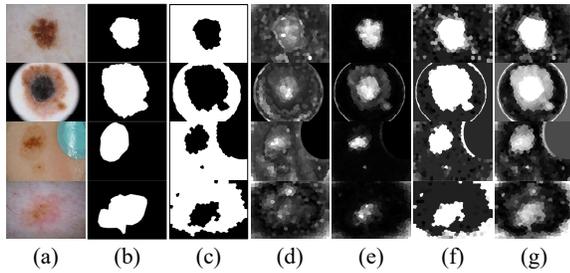


Fig. 6. Visual comparison of outlier score maps from different outlier detection methods. (a) Dermoscopic images; (b) Ground truth; (c) Detected healthy skin by SLED_{SS}; (d)-(g) Outlier score maps from healthy skin by (d) Ecod [40], (e) K -NN [41], (f) OCSVM [42], and (g) i Forest [31] respectively.

C. Ablation Study (Q2, Q3)

Sensitivity Analysis. We analyze the sensitivity of parameters involved in SLED. One important parameter is the superpixel number N . A larger value of N reduces the risk of overmerge but impeded the efficiency of SLED. We explore the performance of SLED_{SS} with different values of N as shown in Figure 4. The performance of SLED_{SS} is slightly fluctuating but generally stable when $N > 100$, indicating that SLED_{SS} adapts well among a wide range value of N . SLED_{MS} outperforms any SLED_{SS} results in four out of five metrics by integrating segmentation of SLED_{SS} at different superpixel scales, demonstrating the effectiveness of the multi-scale segmentation mechanism.

Another important parameter is the spatial distance threshold r , which is used to balance the importance of color features and the spatial position of superpixels in the graph construction. A larger value of r means greater importance of the color feature. Figure 5 shows the sensitivity of r to SLED. It can be observed that the performance of SLED is poor when $r = 0.1$ and gets stable when r is larger. SLED_{SS} witnesses a small drop in performance when r is larger than 0.3, but this drop can be eliminated by the multi-scale segmentation mechanism of SLED_{MS}.

Outlier Detection Methods. The proposed multi-scale seg-

mentation mechanism is a general approach, which can be implemented by many unsupervised outlier detection methods. To find the method that best models healthy skin, we utilize different outlier detection methods to implement several variants of SLED, including SLED_{Ecod} (Ecod [40]), SLED _{K -NN} (K -Nearest Neighbors [41]), SLED_{OCSVM} (OCSVM [42]), and SLED _{i Forest} (Isolation Forest [31]). Table IV presents the performance of these variants. SLED _{i Forest} achieves best performance in all metrics, which indicates that i Forest models healthy skin better. SLED_{OCSVM} ranks second with comparable performance.

Figure 6 illustrates examples of outlier score maps using different outlier detection methods. Both Ecod and K -NN fail to distinguish the lesion region and healthy skin. OCSVM distinguishes the lesion region but fails to reflect the diverse pixel feature in the lesion region, as shown in the second and third rows. Visually the outlier score maps of i Forest better reflect the features of the lesion region by giving different superpixels graded scores. When the detected healthy skin by SLED_{SS} is not accurate, as shown by the last row, all methods fail to give a good score map. However, the score map of i Forest still reflects the lesion region. In all, i Forest best models healthy skin, and best fits our framework.

D. Case Study

Qualitative Comparison. Figure 7 gives a qualitative comparison of different segmentation methods. Variations of lesions in color, texture, shape, size, and location impede lesion segmentation accuracy. Low contrast between lesions and healthy skin (shown by 2nd and 3rd rows) and changing illumination (shown by 4th row) are the other two challenges. Furthermore, many lesions show diverse features and can be divided into several sub-regions, misleading some methods to take less prominent parts of lesions as healthy skin. Both K -means, NCut, and SpecWRSC suffer from the problem of fixed segments number, leading to poor segmentation results in some cases. Compared to other methods including SLED_{SS}, SLED_{MS} gives more accurate lesion boundaries.

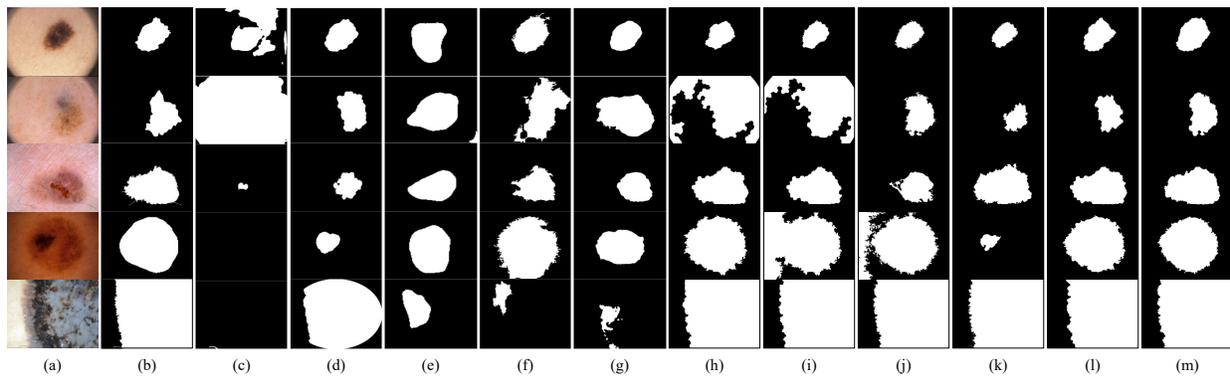


Fig. 7. Comparison of segmentation results. (a) Dermoscopic images; (b) Ground truth; (c) UDASOD (d) Sp. Merging; (e) DRC; (f) Saliency-CCE; (g) A2S-v2; (h) SpecWRSC; (i) NCut; (j) K -means; (k) SGSCN; (l) $SLED_{SS}$; (m) $SLED_{MS}$.

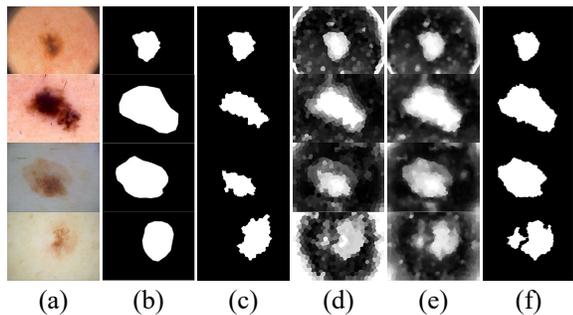


Fig. 8. Visualization of outlier score maps. (a) Dermoscopic images; (b) Ground truth; (c) Segmentation results of $SLED_{SS}$; (d) Single-scale outlier score maps from (c); (e) Multi-scale outlier score maps; (f) Segmentation results of $SLED_{MS}$ from (e).

TABLE V
TIME USAGE OF METHODS ON PH2 DATASET.

Method	UDASOD	Sp. Merging	DRC	Saliency-CCE	A2S-v2	SpecWRSC	NCut	K -means	SGSCN	$SLED_{SS}$	$SLED_{MS}$
Time (min)	1	60	292	18	1	25	24	22	396	25	51

Examples of Outlier Score Maps. Figure 8 shows several examples of outlier score maps. The multi-scale mechanism helps reduce the mis-segmentation of $SLED_{SS}$, as shown in the second and third rows. In these two rows, the segmented lesion regions by $SLED_{SS}$ are smaller than the ground truths, leading to inaccurate single-scale score maps. Multi-scale score maps however better distinguish lesion regions by integrating different single-scale score maps, leading to more accurate segmentation results of $SLED_{MS}$. It should also be noted that when the features of pixels in healthy skin are not consistent, the proposed multi-scale mechanism induces noises. For example, the image in the last row has inconsistent backgrounds due to the influence of light illumination, and the segmentation result of $SLED_{MS}$ is worse than $SLED_{SS}$.

E. Efficiency (Q4)

We test the efficiency of different methods on the PH2 dataset as shown in Table V. The running time of $SLED_{SS}$ is comparable to Saliency-CCE, NCut, and K -means. By calculating the segmentation of $SLED_{SS}$ with different scales in parallel, the running time of $SLED_{MS}$ is comparable to Sp. Merging, and less than DRC and SGSCN. Although UDASOD and A2S-v2 consume the least running time, they both require tremendous model training time. In all, SLED is quite efficient.

V. CONCLUSION

In this paper, we have presented SLED, a novel unsupervised skin lesion segmentation framework. To address the challenges of diverse pixel features within the lesion region and the consistency of pixel features in healthy skin, we introduce two key components in our framework: SE guided segmentation and a multi-scale mechanism utilizing isolation forest outlier detection. Our extensive experimental evaluations on four widely used skin lesion segmentation benchmarks confirm the superiority of SLED over existing methods in terms of effectiveness and efficiency. We believe that SLED holds great potential for improving dermatological diagnosis and aiding in early disease detection.

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