Enhancing pixel-by-pixel discriminative MELANOMA image segmentation through the utilization of convolution neural networks

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Abstract

Skin Cancer or melanoma is a cause of major concern in recent years, with rising numbers of patients suffering from the disease. Using proper diagnosis procedures, the cancerous region can be identified and localized. Machine learning methods have been traditionally used for identifying and localizing the unwanted growth of skin lesions. The challenges in using the Machine learning methods is to identify the similarity of skin lesions in terms of both texture and color. It is observed from the literature, that the application of Deep Convolutional Neural Networks gave better performance in the segmentation of skin cancer images. This paper proposes an automated method for the segmentation lesion boundaries by using U-Net which effectively captures the context feature and the semantic feature information to enhance the pixel-level discriminative representation capability of Fully Convolutional Networks.

Keywords:

Melanoma, Deep Learning, Convolutional Neural Networks

I. Introduction

Skin Cancer Segmentation is the process of identifying and isolating regions of skin that are affected by cancerous growth. This segmentation is essential for accurate diagnosis and treatment planning of skin cancer, particularly melanoma, which is the deadliest form of skin cancer. Convolutional neural networks (CNNs) have been shown to be effective in performing image segmentation tasks, including skin cancer segmentation. In this research paper, we will explore the use of CNNs for skin cancer segmentation, with a focus on melanoma.

The paper will begin by providing an overview of skin cancer, including its causes, symptoms, and treatment options. We will then discuss the importance of accurate skin cancer segmentation, particularly for melanoma, and the challenges associated with this task.

In section-II, the literature review in regard of the applications of Deep learning for Skin Cancer Segmentation are discussed. In Section –III, the proposed methodology using U-NET Architecture is discussed. Results of the proposed algorithm are discussed in Section – IV followed by References in Section –V.

Overall, this research paper will provide valuable insights into the use of CNNs for skin cancer segmentation, particularly for melanoma, and will contribute to the ongoing effort to improve the accuracy and efficiency of skin cancer diagnosis and treatment.

II. Literature

Skin Cancer (Melanoma) Segmentation is a critical task in dermatology that requires accurate and efficient segmentation algorithms to aid in the diagnosis and treatment of skin cancer. Convolutional Neural Networks (CNN) and U-Net are popular deep learning models used for skin cancer segmentation tasks. In this literature survey, we will compare the performance of U-Net with other related models for skin Cancer (Melanoma) Segmentation using CNN and Python.

Some basic machine learning algorithms such as SVM[1] and Random Forest[2], were made use of before the advent of deep learning , for image classification and segmentation, U-Net[3] was introduced in In 2015, and evaluated in a medical image segmentation task and proved to be efficient. Since 2015, when vanilla U-Net was introduced, U-Net and U-Net-based architectures have been widely used for segmentation tasks (e.g., skin lesion segmentation). Other robust models like ISIC [4] also have been introduced recently and tested on medical segmentation.

Among these, Mask R-CNN[5] and DeepLab[6] are also promising methods in the area of Deep Learning. Bagheri et al. 2018[7] deployed Mask-RCNN and DeepLab methods on the ISBI 2017

dataset and attained a Jaccard value of 79%. , Zahangir Alom et al.[8] exploited Recurrent Residual Convolutional Neural Networks (RRCNN) on U-Net-based models and proposed R2U-Net

Gu et al. [13] used comprehensive attention-based convolutional neural networks (CA-Net) in medical tasks to reach better accuracy. CA-Net improved the Dice Coefficient from 87% to 92% on the ISIC 2018 dataset

R2U-Net achieved a Dice Coefficient of 0.86 on the ISIC 2017 dataset. Zafar et al. 2020[9] made use of the ResNet50[10] architecture as the backbone of U-Net to reach a Jaccard index of 77% on the ISIC 2017 dataset.

Jha et al. [11] introduced Double-U-Net combining two U-Net stacks on top of each other. The Double U-Net model gained a Dice Score of 0.8962 on the ISIC 2017 dataset.

Kaul et al. [12] presented FocusNet, an attention-based CNN proposed especially for medical segmentation. It, FocusNet, achieved a Dice Score of 0.83 on the ISIC 2017 dataset.

III.   Proposed Methodology

Segmentation of skin cancer (Melanoma) using convolutional neural networks (CNNs) and the U-Net architecture is a popular approach in medical image analysis. The following is a high-level methodology for implementing this technique in Python:
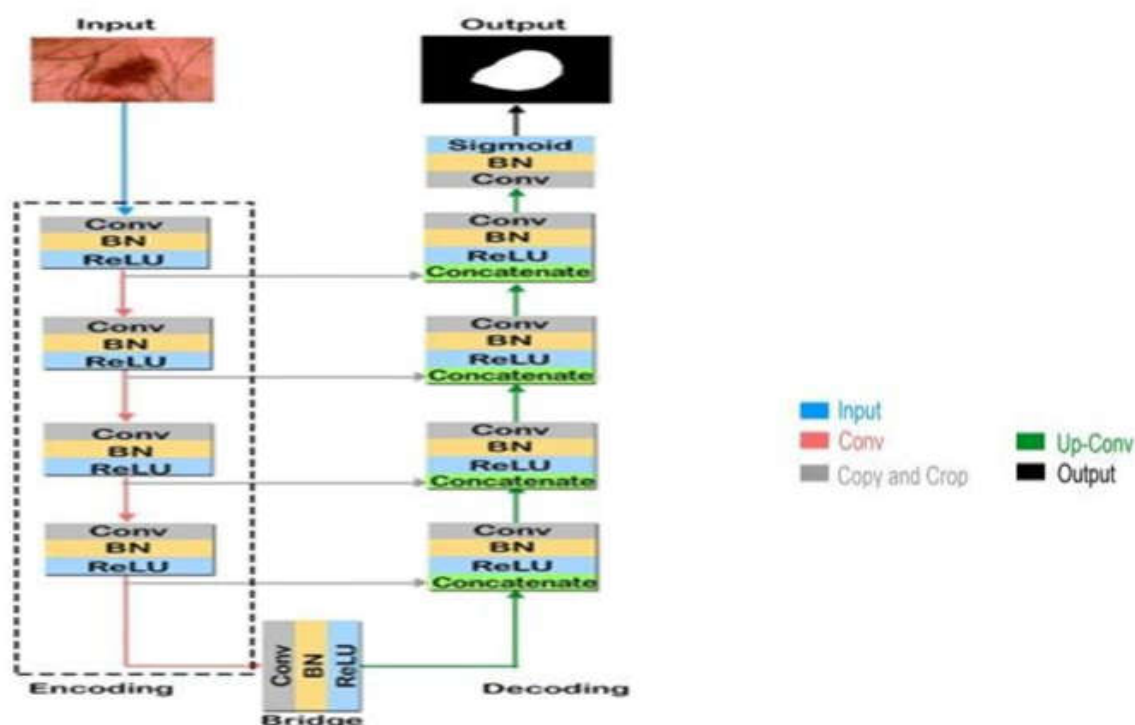
Figure 1: Flow Chart of Proposed Work

Data Collection: Collect a large dataset of skin lesion images, which includes melanoma and non-melanoma images. You can use public datasets like ISIC, HAM10000, or Dermofit Image Library. Data Preprocessing: Preprocess the data to ensure that the images are normalized and resized to a fixed size. Also, augment the data by applying random rotations, flips, and zooms to increase the size of the dataset.

Training, validation, and testing data split: Split the dataset into training, validation, and testing sets in the ratio of 60%, 20%, and 20%, respectively.

U-Net Architecture: Implement the U-Net architecture in Python, which consists of a contracting path and an expansive path. The contracting path captures the context and features of the input image, while the expansive path reconstructs the image from the extracted features. The architecture is well- suited for medical image segmentation tasks, as it has skip connections that help to preserve spatial information

Testing: Evaluate the trained model on the testing dataset to determine its accuracy in segmenting melanoma from non- melanoma images. You can use metrics like Dice Coefficient, Jaccard Index, and Intersection over Union to measure the accuracy.

It is a part of a deep learning model architecture. The architecture consists of several convolutional layers with batch normalization and activation functions. There are also skip connections using the

add operator to pass activations from the input layer to the output of some convolutional layers. The architecture shown below is a U-Net architecture commonly used for image segmentation tasks.

Table 1: Layers of UNET

| Layer (type)	Output Shape	Param #	Connected to
input_1 (Input Layer)	[(None, 256, 256, 3)]	0	[]
conv2d (Conv2D)	(None, 256, 256, 64)	1792	['input_1[0][0]']
batch normalization (Batch Norm alization)	(None, 256, 256, 64)	256	['conv2d[0][0]']
activation (Activation)	(None, 256, 256, 64)	0	['batch_normali zation[0][0]']
conv2d_1 (Conv2D)	(None, 256, 256, 64)	36928	['activation [0][0]']
conv2d_2 (Conv2D)	(None, 256, 256, 64)	256	['input_1[0][0]']
tf.operators.add (TFOpLambda)	(None, 256, 256, 64)	0	['conv2d_1[0][0]','conv2d_2[0][0] ']
batch_normalization_1 (BatchNo rmalization)	(None, 256, 256, 64)	256	['tf.operators.ad d[0][0]']
activation_1 (Activation)	(None, 256, 256, 64)	0	['batch_normali zation_1[0][0]']
conv2d_3 (Conv2D)	(None, 128, 128, 128)	73856	['activation_1[0][0]']
batch_normalization_2 (BatchNo rmalization)	(None, 128, 128, 128)	512	['conv2d_3[0][0]']
activation_2 (Activation)	(None, 128, 128, 128)	0	['batch_normali zation_2[0][0]']
conv2d_4 (Conv2D)	(None, 128,	147584	['activation_2[0

	128, 128)		][0]']
conv2d_5 (Conv2D)	(None, 128, 128, 128)	8320	['tf.operators.ad d[0][0]']
tf.operators.add_1 (TFOpLa mbda)	(None, 128, 128, 128)	0	['conv2d_4[0][0]', 'conv2d_5[0][0] ']
batch_normalization_3 (BatchNo rmalization)	(None, 128, 128, 128)	512	['tf.operators.ad d_1[0][0]']
activation_3 (Activation)	(None, 128, 128, 128)	0	['batch_normali zation_3[0][0]']
conv2d_6 (Conv2D)	(None, 64, 64, 256)	295168	['activation_3[0][0]']
batch_normalization_4 (BatchNo rmalization)	(None, 64, 64, 256)	1024	['conv2d_6[0][0]']
activation_4 (Activation)	(None, 64, 64, 256)	0	['batch_normali zation_4[0][0]']
conv2d_7 (Conv2D)	(None, 64, 64, 256)	590080	['activation_4[0][0]']
conv2d_8 (Conv2D)	(None, 64, 64, 256)	33024	['tf.operators.ad d_1[0][0]']
tf.operators.add_2 (TFOpLambda)	(None, 64, 64, 256)	0	['conv2d_7[0][0]', 'conv2d_8[0][0] ']
batch_normalization_5 (BatchNo rmalization)	(None, 64, 64, 256)	1024	['tf.operators.ad d_2[0][0]']
activation_5 (Activation)	(None, 64, 64, 256)	0	['batch_normali zation_5[0][0]']
conv2d_9 (Conv2D)	(None, 32, 32, 512)	118016 0	['activation_5[0][0]']
batch_normalization_6 (BatchNo rmalization)	(None, 32, 32, 512)	2048	['conv2d_9[0][0]']
activation_6 (Activation)	(None, 32, 32, 512)	0	['batch_normali zation_6[0][0]']
conv2d_10 (Conv2D)	(None, 32, 32, 512)	235980 8	['activation_6[0][0]']
conv2d_11 (Conv2D)	(None, 32, 32, 512)	131584	['tf.operators.ad d_2[0][0]']
tf.operators.add_3 (TFOpLa mbda)	(None, 32, 32, 512)	0	['conv2d_10[0][0]', 'conv2d_11[0][0]']
up_sampling2d (UpSampling2D)	(None, 64, 64, 512)	0	['tf.operators.ad d_3[0][0]']
concatenate (Concatenate)	(None, 64, 64, 768)	0	['up_sampling2 d[0][0]', 'tf.operators.add _2[0][0]']

batch_normalization_7 (BatchNormalization)	(None, 64, 64, 768)	3072	['concatenate[0] [0]']
activation_7 (Activation)	(None, 64, 64, 768)	0	['batch_normali zation_7[0][0]']
conv2d_12 (Conv2D)	(None, 64, 64, 256)	1769728	['activation_7[0][0]']
batch_normalization_8 (BatchNormalization)	(None, 64, 64, 256)	1024	['conv2d_12[0][0]']
activation_8 (Activation)	(None, 64, 64, 256)	0	['batch_normali zation_8[0][0]']
conv2d_13 (Conv2D)	(None, 64, 64, 256)	590080	['activation_8[0][0]']
conv2d_14 (Conv2D)	(None, 64, 64, 256)	196864	['concatenate[0] [0]']
tf.operators.add_4 (TFOpLa mbda)	(None, 64, 64, 256)	0	['conv2d_13[0][0]', 'conv2d_14[0][0]']
up_sampling2d_1 (UpSampling2D)	(None, 128, 128, 256)	0	['tf.operators.ad d_4[0][0]']
concatenate_1 (Concatenate)	(None, 128, 128, 384)	0	['up_sampling2 d_1[0][0]', 'tf.operators.ad d_1[0][0]']
batch_normalization_9 (BatchNormalization)	(None, 128, 128, 384)	1536	['concatenate_1 [0][0]']
activation_9 (Activation)	(None, 128, 128, 384)	0	['batch_normali zation_9[0][0]']
conv2d_15 (Conv2D)	(None, 128, 128, 128)	442496	['activation_9[0][0]']
batch_normalization_10 (BatchNormalization)	(None, 128, 128, 128)	512	['conv2d_15[0][0]']
activation_10 (Activation)	(None, 128, 128, 128)	0	['batch_normali zation_10[0][0]]
conv2d_16 (Conv2D)	(None, 128, 128, 128)	147584	['activation_10[0][0]']
conv2d_17 (Conv2D)	(None, 128, 128, 128)	49280	['concatenate_1 [0][0]']
tf.operators.add_5 (TFOpLa mbda)	(None, 128, 128, 128)	0	['conv2d_16[0][0]', 'conv2d_17[0][0]']
up_sampling2d_2 (UpSampling2D)	(None, 256, 256, 128)	0	['tf.operators.ad d_5[0][0]']
concatenate_2 (Concatenate)	(None, 256, 256, 192)	0	['up_sampling2 d_2[0][0]', 'tf.operators.add [0][0]']
batch_normalization_11 (BatchNormalization)	(None, 256, 256, 192)	768	['concatenate_2 [0][0]']
activation_11 (Activation)	(None, 256, 256, 192)	0	['batch_normali zation_11[0][0]]

conv2d_18 (Conv2D)	(None, 256, 256, 64)	110656	['activation_11[0][0]']
batch_normalization_12 (BatchN ormalization)	(None, 256, 256, 64)	256	['conv2d_18[0][0]']
activation_12 (Activation)	(None, 256, 256, 64)	0	['batch_normali zation_12[0][0]']
conv2d_19 (Conv2D)	(None, 256, 256, 64)	36928	['activation_12[0][0]']

IV.   Results & Discussion

In conclusion, skin cancer (Melanoma) segmentation using Convolutional Neural Network (CNN) and U-Net in Python has proven to be a promising approach for accurate and efficient segmentation of melanoma in dermoscopic images. The use of deep learning techniques, particularly CNN and U-Net architectures, has shown significant improvements in the accuracy of melanoma segmentation compared to traditional segmentation method.
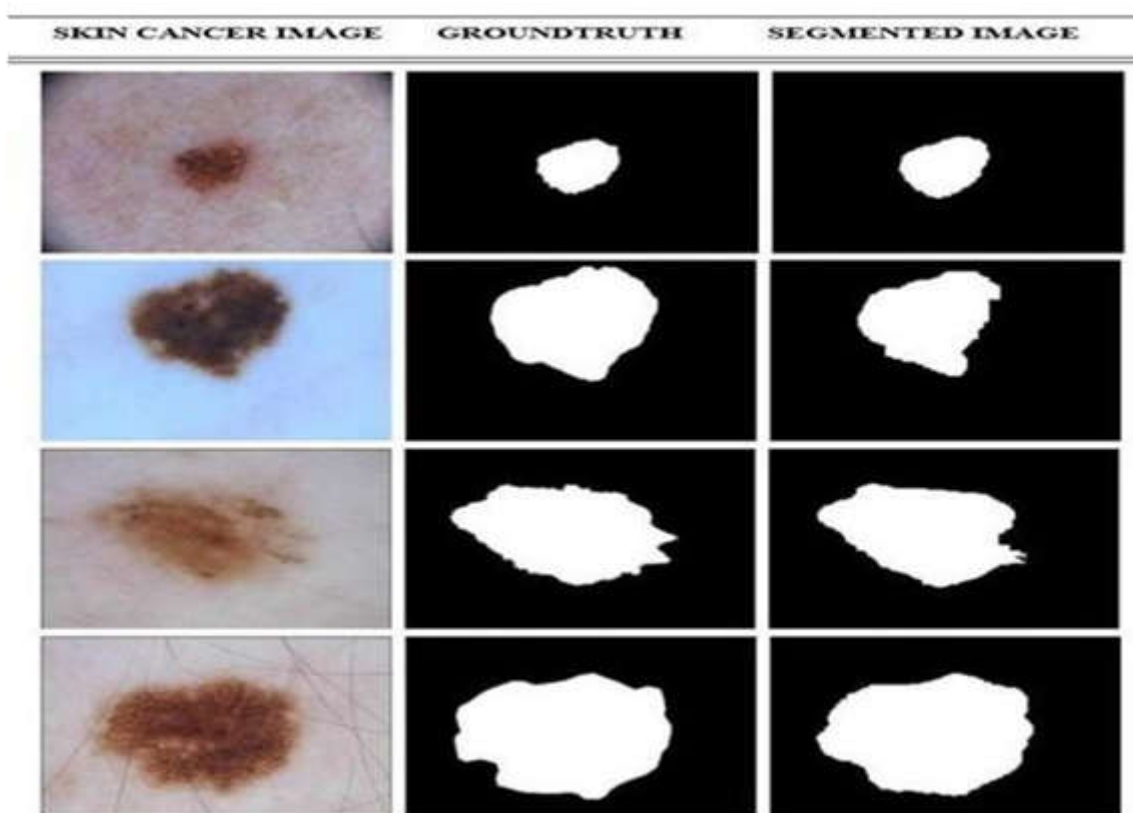
Figure 2: Original, Ground Truth & Segmented Images

The proposed method involves training a CNN model using dermoscopic images and their corresponding ground truth masks for melanoma segmentation. The trained model is then used to segment melanoma in new dermoscopic images. The U-Net architecture has been shown to be particularly effective due to its ability to preserve spatial information and to capture contextual information from multiple scales.

The evaluation of the proposed method has shown that it achieves high accuracy, IOU, and dice coefficient scores. These results demonstrate the potential of using CNN and U- Net architectures for skin cancer (Melanoma) segmentation and suggest that this method could be useful in clinical practice for aiding dermatologists in the early detection and diagnosis of skin cancer.

Future work could involve further improving the accuracy of the model by incorporating more advanced techniques such as transfer learning or data augmentation. Additionally, the method could be extended to other types of skin lesions for more comprehensive skin cancer diagnosis.

Image	Accuracy	F1 Measure	Jaccard	Recall	Precision
A	0.939682	0.523103	0.35419	1	0.35419
B	0.688004	0.714368	0.555655	0.555655	1
C	0.953369	0.525466	0.356361	0.356361	1
D	0.988602	0.915774	0.844634	0.870152	0.966445

Table 2: Performance Metrics Values

Accuracy	F1 Measure	Jaccard	Recall	Precision
0.90911	0.75319	0.65541	0.73356	0.87777

Table 3: Mean metrics values of all the images

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