Performance Analysis of EfficientNet Based Segmentation Models for Automatic Detection of Malaria Disease

Araştırma Makalesi/Research Article

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(Geliş/Received:13.03.2023; Kabul/Accepted:22.05.2023)
DOI: 10.17671/gazibtd.1264480

Abstract— Malaria is a disease caused by the Plasmodium parasite, which is common in the tropics. The traditional methods commonly used to diagnose malaria, one of the world's deadliest diseases, are microscopic diagnostic methods in which blood samples taken from suspected individuals are manually examined, or rapid diagnostic tests that are sensitive to human errors. These processes are inexpensive but experienced and qualified clinicians are needed. Due to this shortcoming, modern diagnostic tools are crucial in the struggle against the disease. In this study, an approach based on deep learning (DL) methods was used, which offers beneficial solutions in the diagnosis of disease from medical images. In the proposed approach, U-Net, Pyramid Scene Parsing Network (PSPNet), LinkNet, and Feature Pyramid Network (FPN) segmentation methods were modified with 8 different pre-trained variants of the EfficientNet deep learning model to obtain improved models. In the malaria segmentation performed with these models, the highest Dice score of 91.50% was achieved in the use of the U-Net model with EfficientNetB6. This model offers a faster and more robust solution to detecting parasites compared to traditional methods. Moreover, it can serve as an effective expert system for assisting field experts since it can achieve high Dice scores in identifying parasites on the images.

Keywords— malaria detection, deep learning, segmentation, efficientNet

Sıtma Hastalığının Otomatik Tespiti için EfficientNet Tabanlı Segmentasyon Modellerinin Performans Analizi

Özet— Sıtma, tropik bölgelerde yaygın olan Plasmodium parazitinin neden olduğu bir hastalıktır. Dünyanın en ölümcül hastalıklarından biri olan sıtmanın teşhisinde yaygın olarak kullanılan geleneksel yöntemler, şüpheli kişilerden alınan kan örneklerinin manuel olarak incelendiği mikroskobik teşhis yöntemleri veya insan hatalarına duyarlı hızlı teşhis testleridir. Bu işlemler ucuzdur, ancak deneyimli ve nitelikli klinisyenlere ihtiyaç vardır. Bu eksiklik nedeniyle, modern teşhis araçları hastalıkla mücadelede çok önemlidir. Bu çalışmada tıbbi görüntülerden hastalık teşhisinde faydalı çözümler sunan derin öğrenme yöntemlerine dayalı bir yaklaşım kullanılmıştır. Önerilen yaklaşımda, U-Net, Pyramid Scene Parsing Network (PSPNet), LinkNet ve Feature Pyramid Network (FPN) segmentasyon yöntemleri, EfficientNet derin öğrenme modelinin 8 farklı önceden eğitilmiş varyantı ile modifiye edilerek gelişmiş modeller elde edilmiştir. Bu modeller ile yapılan sıtma segmentasyonunda %91,50 ile en yüksek Dice skoru EfficientNetB6 ile U-Net modelinin kullanımında elde edilmiştir. Bu model, geleneksel yöntemlere kıyasla parazitleri tespit etmek için daha hızlı ve daha sağlam bir çözüm sunar. Ayrıca, görüntüler üzerinden parazitleri tespit etmede yüksek Dice skorları elde edebildiğinden, alan uzmanlarını desteklemek için etkili bir uzman sistem olarak hizmet edebilir.

Anahtar Kelimeler— sıtma tespiti, derin öğrenme, segmentasyon, efficientNet

1. INTRODUCTION

Malaria is a very common contagious disease, especially in Asia and Africa and it can result in death if left untreated. According to the report published by the World Health Organization (WHO) in 2021, there were 241 million malaria cases with approximately 627000 deaths worldwide in 2020 [1]. Some clinical methods such as thick-thin blood smear examinations, polymerase chain reaction (PCR), and rapid diagnostic tests (RDT) are used for the diagnosis of malaria [2, 3]. However, these manual methods require expertise and take a lot of time. For instance, the results of blood tests used to diagnose malaria are usually available within 24 hours, depending on the laboratory's intensity. RDT, which is used for rapid malaria diagnosis, shows results within 15-20 minutes. The Giemsa staining test, which is performed by examining the blood smear under the microscope, gives results in a longer time. This test diagnoses malaria parasites by imaging them directly on blood cells, and results are usually available within 24 hours. Furthermore, it is important to note that the cost of these tests should not be overlooked or underestimated [4–6]. Moreover, this process could potentially result in the misdiagnosis of patients due to the high workload of medical personnel [7]. For this reason, using computer-aided diagnosis and detection processes that can rapidly analyse large amounts of data and provide results instead of relying on manual processes can yield accurate results while also being cost-effective.

In recent years, scientists have been concentrating on identifying malaria using artificial intelligence techniques, which have a crucial role in medical diagnosis and treatment procedures [8]. Liang et al. proposed a 16-layer convolutional neural network (CNN) for malaria detection and they used single-cell images. They stated that the proposed model obtained 97.37% accuracy as a result of the 10-fold cross-validation technique [9]. Rajaraman et al. proposed a customized CNN model for the detection of Malaria-infected cells. Then, the performance of the model, which achieved 94% accuracy, was compared with pre-trained deep learning (DL) models such as AlexNet, VGG-16, Xception, ResNet-50, and DenseNet-121 [10]. In another study, Bibin et al. achieved 96.20% accuracy with their model based on deep belief networks [11]. Sriporn et al. used AlexNet, VGG-16, NasNetMobile, ResNet-50, Inception-V3, and Xception DL models to detect malaria. In the study, they evaluated the performance of different activation functions and optimizer combinations of the models and they reported that they reached an overall accuracy level of 98.86% [12]. Umer et al. utilized stacked CNN architecture in their study where they performed 5-fold cross-validation on images for malaria detection. They reported that the model performed quite well compared to the state-of-the-art models with 99.98% accuracy [13]. Abubakar, Ajuji, and Yahya first performed feature extraction through six different DL models and then detected malaria using Decision Tree (DT), Support Vector Machine (SVM), Naive Bayes (NB), and K-Nearest Neighbor (KNN) classifiers. In the study, the SVM classifier showed the best performance with an accuracy value of over 94% [14]. Rahman et al. evaluated the effect of conditional image synthesis on malaria detection by comparing the performance of several state-of-the-art DL models on a fairly large image dataset [15]. Islam et al. proposed an attention-based transformer model for diagnosing the malaria parasite. In order to obtain optimum results, hyperparameters were fine-tuned and as a result of the tests performed on the original and modified dataset, an accuracy value of over 99% was obtained [16].

Some researchers have tried to detect malaria parasites through segmentation methods based on image processing [17–19]. On the other hand, deep learning techniques also achieve useful results in image segmentation. For the segmentation of the malaria parasite, Hung et al fine-tuned the pre-trained Faster Region-based Convolutional Neural Network (Faster R-CNN) method on ImageNet and reported that the method performed well [20]. In another study, Davidson et al. used a model based on the Faster R-CNN method, providing high performance [21]. Loh et al. utilized the Mask R-CNN DL method for malaria segmentation and counting in images. According to the conducted tests, the utilized approach provided reports 15 times more quickly than manual counting [22]. Yang et al. used a modified U-Net model for malaria diagnosis and tested this new model on six different malaria image datasets [23].

Although there has been previous research in the literature demonstrating the automatic diagnosis of malaria parasites, it has been recognized that there seems to be still a need for breakthroughs in deep learning-based image segmentation approaches. Therefore, this study presents new and more powerful segmentation architectures for malaria segmentation, in which eight different pre-trained variants of the EfficientNet deep learning model are used as backbones. The main contributions of this paper lie in the following.

- The performance of four different state-of-the-art segmentation architectures was evaluated.
- The performances of the segmentation architectures were tested on a relatively large dataset compared to previous studies.
- For the first time, EfficientNet deep learning model was used as the backbone of segmentation architectures for the detection of malaria disease.
- The U-Net segmentation model with EfficientNetB6 achieved promising Dice score results in the detection of parasites.

The remainder of the article is organized as follows. In Section 2, the data set used in the study and the models used in the proposed approach is presented in detail. In Section 3, implementation details and evaluation metrics are described. In Section 4, the results and discussion obtained by the experimental tests are presented. Finally, the article is concluded in Section 5.

2. METHODOLOGY

2.1. Data Description

Images collected from different sources and presented on a public platform by Abbas and Dijkstra [17] were used in the study [24]. This dataset contains 883 Giemsa stained RGB images and 883 binary ground truth images with 1382 × 1030 pixels. In Giemsa stained images, malaria parasites are seen as dark purple and red blood cells as light pink. Figure 1 displays some instances from the dataset.

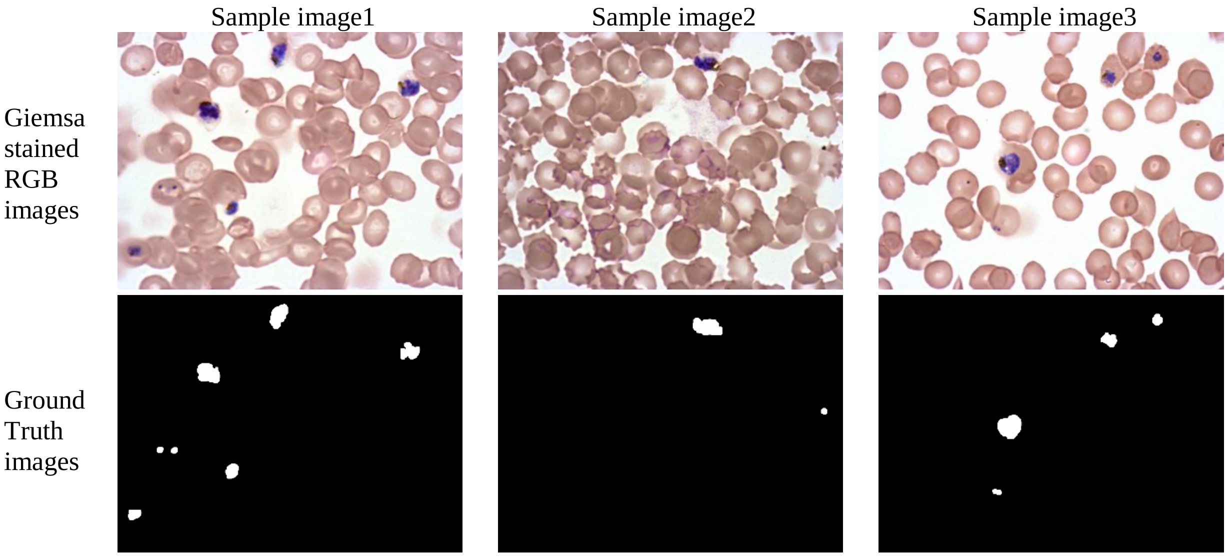


Figure 1. Samples of Giemsa stained RGB images and ground truth images

2.2. Proposed Method

In this study, rapid and efficient detection of malaria parasites was aimed using Giemsa-stained RGB images. For this purpose, an approach was proposed based on U-Net [25], Pyramid Scene Parsing Network [26, 27], LinkNet [28], and Feature Pyramid Network [29] segmentation methods, which are widely used in the literature. In the study, these models were selected based on their exceptional qualities in performing segmentation tasks. While the U-Net model was preferred due to its high sensitivity and ability to produce detailed segmentation results, PSPNet was preferred due to its ability to obtain more precise segmentation results using multi-scale feature maps [25–27]. LinkNet is chosen for its ability to deliver high performance with low computational cost, thanks to its speed and lightweight nature. On the other hand, FPN was preferred due to its efficiency in pixel-level classification tasks and the utilization of features across various scales [28, 29]. In the proposed approach, eight different variants of the EfficientNet model were used one by one as the backbone of each segmentation method. Thus, by utilizing the expertise of a previously trained network with a lot of visual input, the training process was sped up and time was saved. Moreover, thanks to the composite scaling feature, which involves proportionately scaling the depth, width, and resolution dimensions of the model, these 3 dimensions were balanced, and more efficient performance was achieved. On the other hand, this feature effectively reduced the size of the model, enabling faster execution and higher overall performance [30]. The schematic diagram of the proposed approach in the study was illustrated in Figure 2.

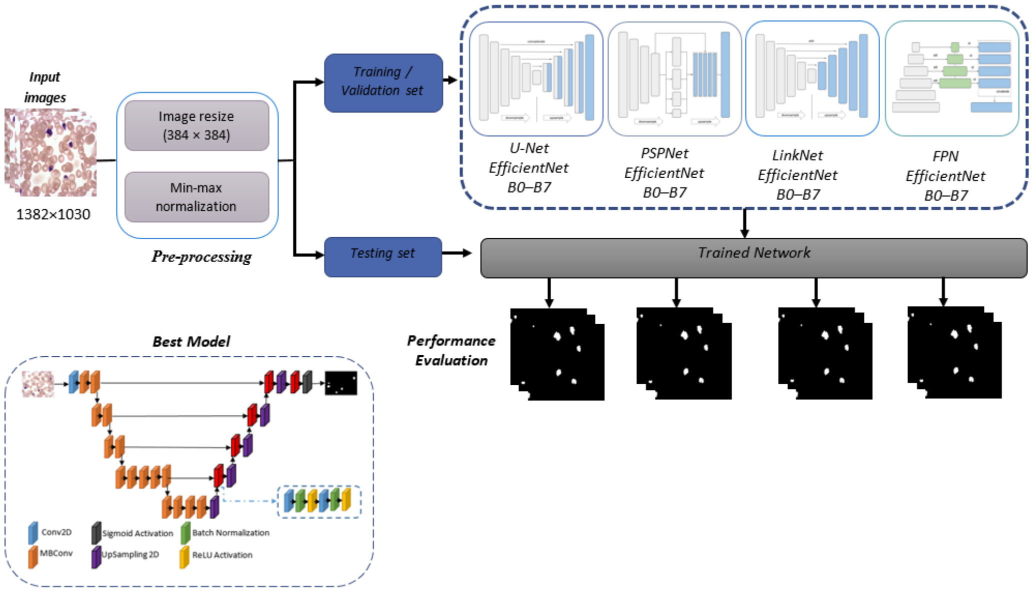


Figure 2. Schematic diagram of the proposed approach

2.2.1. U-Net

The U-Net architecture proposed by Ronneberger et al. in 2015 has reached fairly successful results in terms of image segmentation. U-net is a symmetrical model with one contracting path (encoder) and one expansion path (decoder) parts. It is a traditional convolutional network whose encoder part consists of a 3x3 convolution operation repeated twice. The ReLU activation function and a 2x2 max-pooling layer come after this convolution. The purpose of the encoder is to extract the feature map of the input image and pass it to the decoder. The decoder, on the other hand, aims to increase the decreasing size of the encoder. For this purpose, 2x2 upward convolution is applied on the expansion path and the number of filters is halved. Afterward, the clipped feature map from the encoder part is copied, the output obtained in the decoder is combined, and convolution is applied [25].

2.2.2. Pyramid Scene Parsing Network (PSPNet)

The main architecture of PSPNet [26], proposed by Zhao et al. in 2017, is based on the Fully Convolutional Network (FCN) architecture proposed by Long et al. in 2015 [27]. While FCN can successfully label each pixel, it is not able to accurately identify the relationship between pixels. Developed to overcome this challenge, PSPNet first extracts the feature map from the input image using ResNet and sends it to the pyramid pooling layer to perform the segmentation. This layer then convolves the feature maps into different sizes and creates a final feature map. Lastly, it creates the segmentation map using the final convolutions [26].

2.2.3. LinkNet

The LinkNet segmentation architecture, proposed by Chaurasia and Culurciello in 2017, is designed as a DL network that can learn without causing a significant increase in parameters. The same as other segmentation networks, it consists of an encoder on the left and a decoder on the right. While the encoder encodes the information in the resource space, the decoder maps this data into spatial categorization to carry out the segmentation [28].

2.2.4. Feature Pyramid Network (FPN)

Feature Pyramid Network, proposed by Lin et al. in 2017, has an architecture consisting of bottom-up, top-down pathways, and lateral connections [29]. In this model, a feature pyramid with strong semantics is created by utilizing the pyramid shape of the convolutional feature hierarchy. The top-down pathway and lateral link combine low-resolution and semantically powerful features with high-resolution and semantically weak features.

2.3. Training Loss Function

The suggested model learns parameters from images by minimizing the loss function. The data were unbalanced, as red blood cells uninfected with the malaria parasite took up more space in the images used in the study. Due to this situation, a loss function was chosen that combined the Focal Loss and Dice loss functions, which are frequently applied to unbalanced data sets. The calculations of the loss function were presented in Equation 1.

$$T_L = F_L + D_L \tag{1}$$

Here, the total loss function (T_L) is produced by summing the focal loss(F_L) and Dice Loss(D_L) functions. $F_L$function lessens the influence of easy-to-learn instances and concentrates on cases that are challenging to train by adding α and γ parameters to the Cross-Entropy loss function [31]. Equation 2 illustrates the calculation of the F_L function.

$$F_L(p_t) = -\alpha_t \, (1-p_t)^{\gamma} \log(p_t) \qquad (2)$$

Here, α is intended to avoid class imbalance, while $\gamma \geq 0$ is the focusing parameter that adjusts concentrating on challenging instances and is typically used as 2.

D_L is a function that assists in resolving issues with unbalanced training data and performs well in binary segmentation tasks. To calculate D_L function, the formula shown in Equation 3 is utilized [32].

$$D_L = \frac{2\sum_i^N p_i g_i}{\sum_i^N p_i^2 + \sum_i^N g_i^2} \qquad (3)$$

Here, p_i and g_i, stand for pairs of pixel values that, respectively, represent the prediction and the ground truth.

3. EXPERIMENTS

3.1. Experimental Setup

All experiments were conducted on a 64-bit Ubuntu operating system machine equipped with an Intel (R) Xeon (R) 2.20 GHz CPU, 25.5 GB RAM, and NVIDIA Tesla P100 GPU in the Google Cloud environment. The proposed model was implemented using the segmentation models library which is built on the Keras API and TensorFlow platform with Python programming language [33]. The initial weights of the suggested model were chosen using the transfer learning method [34]. All images utilized in the study were initially resized at 384 × 384 pixels and normalized using the min-max method. The reason for resizing the images as 384 × 384 was the necessity of dividing the width and height values of the input layer of the PSPNet model by 6 times the number selected for the downsample factor parameter. In this study, the downsample factor value was determined as 8. The images in the dataset were first divided into two parts. 20% of the data was allocated for testing and 80% for training and then 10% of the data that was reserved for training was utilized for validation. As a result, 635 images were used in the training, 184 images in the test, and 70 images in the validation stages. In the study, the best hyperparameters were determined using a trial-and-error approach. Initially, the hyperparameters that have a significant impact on the models' performance were identified. Subsequently, numerous training processes were conducted for all possible combinations of these hyperparameters. Eventually, the hyperparameters that yielded the highest performance were selected. In Table 1, the hyperparameters of each segmentation model are presented in detail. As can be seen from Table 1, min-max normalization was used for the normalization of the images in the study, and the learning rate was set as 0.0001. Adam was used for optimization. The batch-size value is selected as 2 for EfficientNetB7 and 5 for all other EfficientNet variants. To avoid overfitting during the training stage, an early stopping approach was utilized, and the value of early stop was set to 10. Accordingly, during training, the validation accuracy value was calculated for each epoch, and training was terminated when the validation accuracy did not rise during the course of the next 10 epochs.

Table 1. Hyperparameters of image segmentation models used in the study

	U-Net	**PSPNet**	**LinkNet**	**FPN**
Image size	384x384	384x384	384x384	384x384
Normalization technique	Min–max	Min–max	Min–max	Min–max
Learning rate	0.0001	0.0001	0.0001	0.0001
Batch size (EfficientNet B0-B6)	5	5	5	5
Batch size (EfficientNetB7)	2	2	2	2
Beta_1	0.9	0.9	0.9	0.9
Beta_2	0.999	0.999	0.999	0.999
Upsampling layers (number)	5	5	5	5
Activation function	ReLU-Sigmoid	ReLU - Sigmoid	ReLU - Sigmoid	ReLU-Sigmoid
Padding	Same	Same	Same	Same
Filter Size (Decoder)	256, 128, 64, 32, 16	512, 512, 512, 512, 512	256, 128, 64, 32, 16	128, 128, 128, 128, 128
Pyramid Filters				256
Downsample factor		8		
Kernel initializer	he_ normal	he_ normal	he_ normal	he_ normal

3.2. Evaluation Metrics

The effectiveness of the malaria segmentation model suggested in the paper was assessed using the Dice Coefficient, Specificity, and Sensitivity metrics, which are extensively employed in the literature. Dice is computed using Equation 4 and is utilized to assess how well estimation results match the ground truth.

$$Dice = \frac{2TP}{2TP + FP + FN} \qquad (4)$$

The formula given in Equation 5 is used to determine sensitivity, which evaluates the success rate of positive sample predictions. Here, TP stands for "true positives", while FN stands for "false negatives".

$$Sensitivity = \frac{TP}{TP+FN} \qquad (5)$$

Equation 6's formula calculates specificity, which is a measure of the percentage of correctly detected negative samples. Here, FP stands for the number of false positives and TN stands for the number of true negatives.

$$Specificity = \frac{TN}{TN+FP} \qquad (6)$$

4. RESULTS AND DISCUSSION

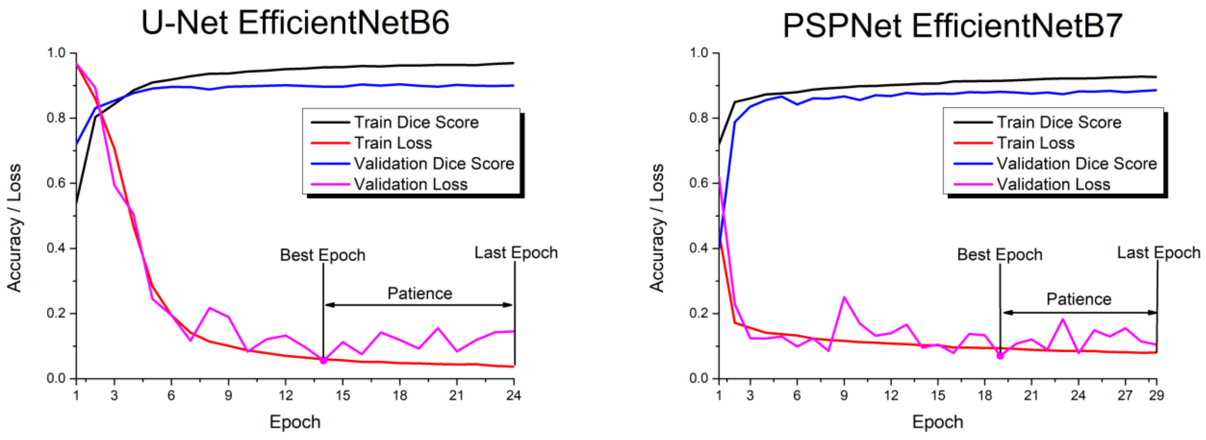
Many experiments were conducted to evaluate the malaria segmentation performance and robustness of improved segmentation models proposed in the study. Table 2 displays the best Dice, Sensitivity, and Specificity values obtained for each model as a consequence of the experiments. When the results of each segmentation model with the EfficientNet variations are compared, the U-Net EfficientNetB6 model outperformed all others with a Dice score of 91.50% and a sensitivity value of 91.43%. In terms of Dice score and sensitivity, the best model was followed by FPN_ EfficientNetB6, LinkNet_EfficientNetB5, and PSPNet_EfficientNetB7, respectively. On the other hand, the greatest Specificity value acquired in the study was 99.96%, obtained by the FPN_ EfficientNetB2 model.

Table 2. Malaria segmentation results of proposed models

Model		Dice Score (%)	Sensitivity (%)	Specificity (%)
U-Net	EfficientNetB0	91.19	89.24	99.93
	EfficientNetB1	90.76	88.20	99.94
	EfficientNetB2	91.23	89.52	99.93
	EfficientNetB3	90.36	88.65	99.92
	EfficientNetB4	91.10	89.92	99.92
	EfficientNetB5	91.12	87.86	99.95
	EfficientNetB6	**91.50**	91.43	99.91
	EfficientNetB7	90.45	87.31	99.94
PSPNet	EfficientNetB0	85.69	80.23	99.93
	EfficientNetB1	86.20	82.09	99.91
	EfficientNetB2	87.58	83.56	99.93
	EfficientNetB3	86.70	84.92	99.89
	EfficientNetB4	87.19	85.30	99.89
	EfficientNetB5	88.53	86.32	99.91
	EfficientNetB6	87.48	83.67	99.92
	EfficientNetB7	**89.12**	88.89	99.89
LinkNet	EfficientNetB0	90.49	88.67	99.92
	EfficientNetB1	90.36	88.66	99.92
	EfficientNetB2	89.73	85.63	99.95
	EfficientNetB3	90.71	88.11	99.94
	EfficientNetB4	90.72	90.81	99.90
	EfficientNetB5	**91.10**	91.00	99.91
	EfficientNetB6	90.62	88.67	99.93
	EfficientNetB7	90.08	87.58	99.93
FPN	EfficientNetB0	90.88	89.46	99.92
	EfficientNetB1	89.94	85.68	99.95
	EfficientNetB2	90.44	86.04	99.96
	EfficientNetB3	90.75	87.94	99.94
	EfficientNetB4	90.11	86.09	99.95
	EfficientNetB5	91.12	88.63	99.94
	EfficientNetB6	**91.28**	90.21	99.92
	EfficientNetB7	91.21	90.72	99.92

Additionally, as can be seen from the table, the results of the PSPNet model with different EfficientNet variants were quite low in comparison to other segmentation models. It was seen that even the lowest Dice Score of the U-Net model, 90.36%, was greater than 89.12%, the highest score of the PSPNet model. Except for the PSPNet model, there were no significant differences observed when utilizing variations of the EfficientNet DL model in the other segmentation models.

The Dice score and loss function curves of the best segmentation models obtained during training were given in Figure 3. The proposed model in the study has the advantage of providing rapid convergence to an optimal solution. The results show that modified segmentation methods with a pre-trained EfficientNet model benefit from the transfer learning strategy.



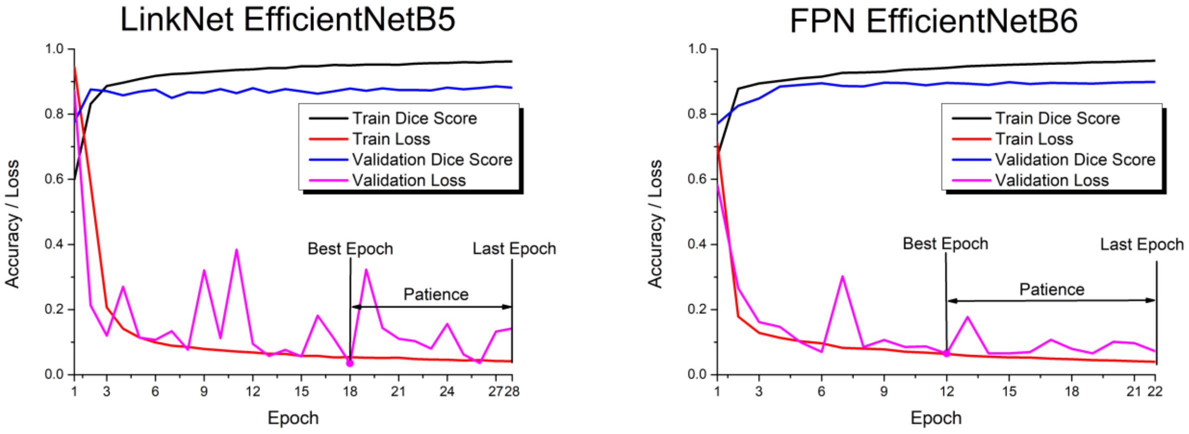
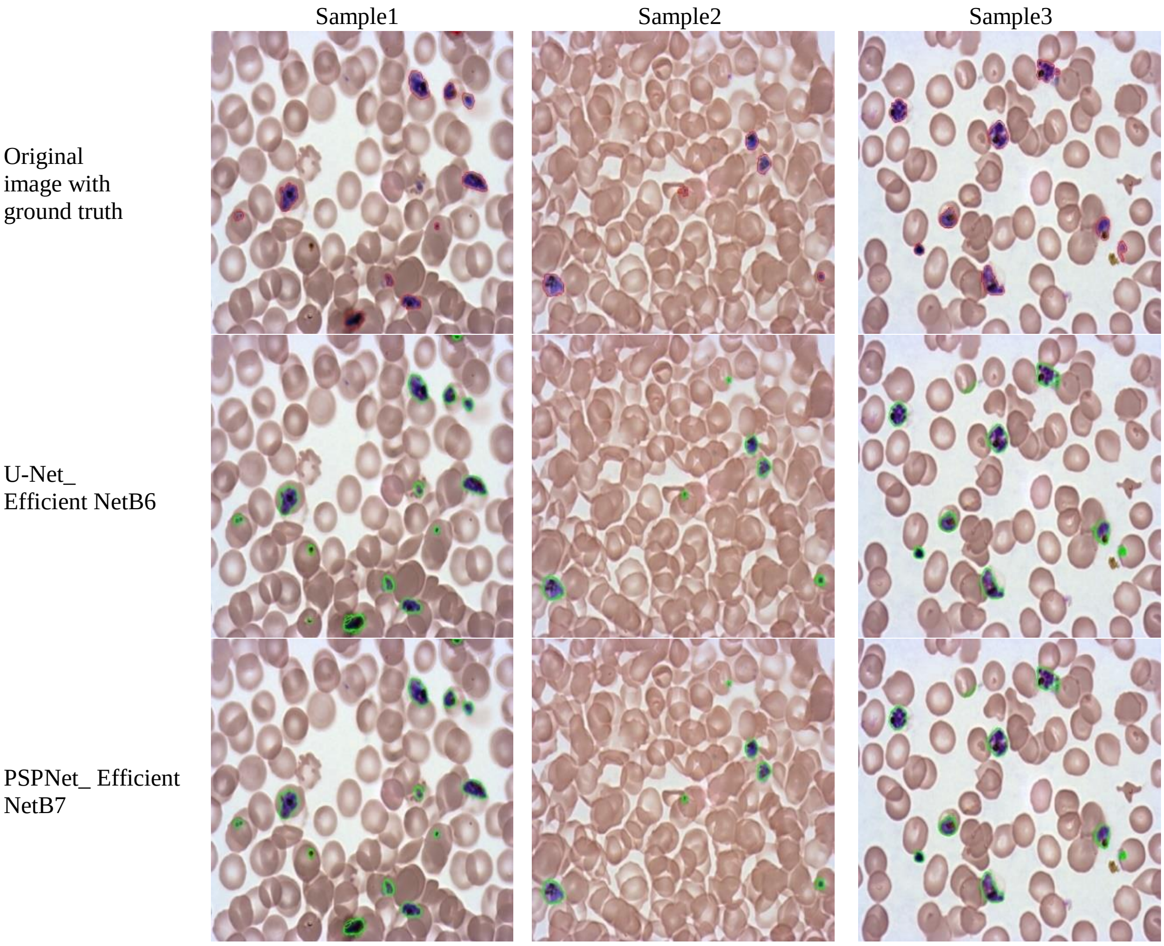


Figure 3. Training and validation accuracy/loss curves of the segmentation models

To visually demonstrate the segmentation effectiveness of the suggested model, three random samples from the malaria dataset were chosen, and the results are shown in Figure 4. Examining Figure 4, it can be seen that the segmentation models suggested in the study produced excellent outcomes when segmenting small parasite sections. The results showed that the use of rich features learned with the EfficientNet model, which was previously trained on the ImageNet dataset, can improve segmentation performance.



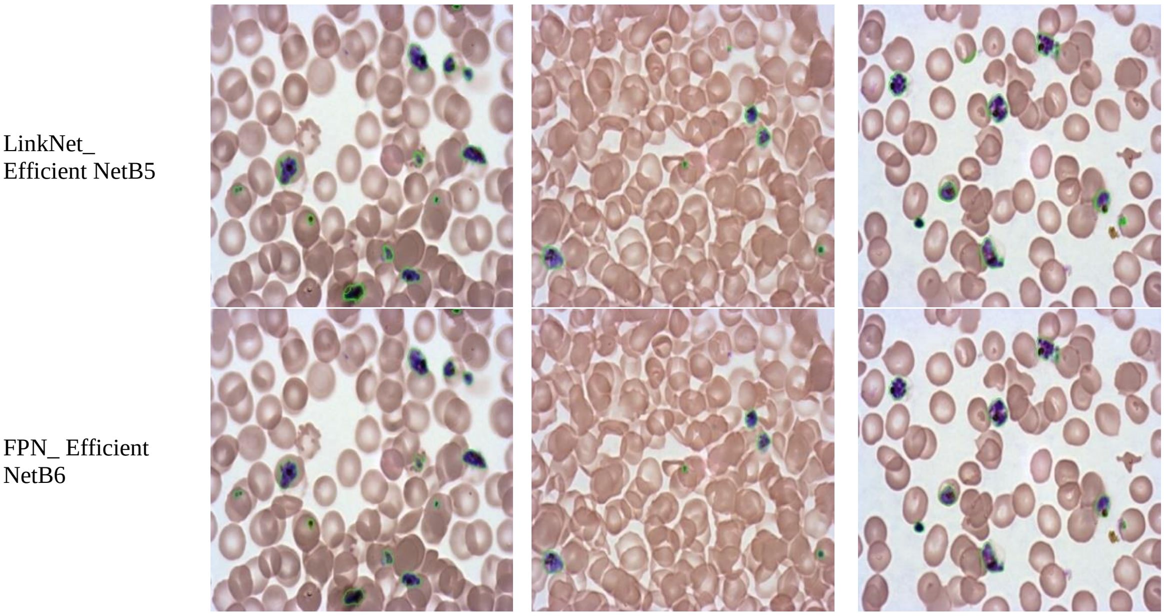


Figure 4. Segmentation results of models on random samples from the dataset.

Since malaria is a deadly disease that affects hundreds of millions of people around the world each year, it is necessary to develop some tools to accurately diagnose malaria cases automatically and quickly. Recently, deep learning-based methods have shown promising performance. For this purpose, in this study customized models based on deep learning architecture were introduced for malaria segmentation. In the proposed approach, the EfficientNet DL model is integrated into U-Net, PSPNet, LinkNet, and FPN segmentation methods. Since the datasets used in previous studies for malaria parasite segmentation in the literature mentioned in the study are varied, the success of the proposed approach was only compared with Abbas and Dijkstra [17] so as to have a fair comparison. Abbas and Dijkstra [17] developed a new two-stage Otsu method for malaria segmentation owing to the fact that they achieved more successful results compared to a simple Otsu segmentation. In their method, they detected the background and red blood cells and parasites in the first stage. In the second step, they reversed the detected background density and segmented the parasites by applying three-level segmentation to this image. With this method, they obtained the highest Dice score of 82.3%. In this study, the highest Dice score value of 91.50% was obtained with the U-Net_EfficientNetB6 segmentation model. This high performance obtained in the study shows that the proposed DL approach can be used effectively to detect parasites.

5. CONCLUSION

In this paper, a novel method based on DL architectures is proposed to assist in the rapid and accurate detection of malaria infection. In the proposed method, four different segmentation models were used to segment the Plasmodium parasite in Giemsa-stained RGB images. In this context, four different deep architectures were designed by using the U-Net, PSPNet, LinkNet, and FPN segmentation models together with 8 different variants of the EfficientNet DL model. The customized models were trained and tested on a relatively large dataset containing 883 images collected from different sources by Abbas and Dijkstra [17]. The U-Net_EfficientNetB6 segmentation model achieved 91.50% diagnosis accuracy on the test set images, showing promising results in the detection of parasites. The proposed approach is believed to serve as a rapid and efficient expert system to assist field clinicians in the early diagnosis of malaria. However, the limited availability of publicly accessible datasets, particularly for segmentation tasks related to malaria diagnosis, presents a constraint on the broad implementation of the deep learning approach proposed in this study. Consequently, the study's limitations encompass the utilization of a solitary dataset for conducting the proposed approach.

In future research, it is planned to develop an architecture with attention blocks that are used for pixel-based prediction in semantic segmentation tasks [35]. In addition, a multi-class segmentation application is aimed to detect the types of Plasmodium parasites in images.

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