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RESEARCH ARTICLE

CLASSIFICATION of CELLS INFECTED with the MALARIA PARASITE with RESNET ARCHITECTURES

İsmail AKGÜL[1,*], Volkan KAYA[2]

[1]Erzincan Binali Yıldırım University, Faculty of Engineering and Architecture, Department of Computer Engineering, iakgul@erzincan.edu.tr, ORCID: 0000-0003-2689-8675
[2]Erzincan Binali Yıldırım University, Faculty of Engineering and Architecture, Department of Computer Engineering, vkaya@erzincan.edu.tr, ORCID: 0000-0001-6940-3260

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ABSTRACT

Malaria is a disease that causes a parasite called plasmodium to be transmitted to humans as a result of the bite of female anopheles' mosquitoes. Malaria is detected by examining the blood sample taken from the patient as a result of a microbiological examination under a microscope by specialist physicians. Although microscopy is widely used, its efficiency is low because it is time-consuming and depends on the interpretation of the specialist physician. In recent years, deep learning methods used in the field of computer vision increase the efficiency of specialist physicians by making a significant contribution to the decision-making process in solving real-life problems. In this study, ResNet architectures were preferred to quickly classify the malaria parasite using deep learning methods. For the training and testing of ResNet architectures, a dataset consisting of a total of 27558 red blood cell images containing 13779 parasitized and 13779 uninfected were used. Using this dataset, ResNet architectures were compared. As a result of the comparison, the best success accuracy (94.09%) was obtained with the ResNet-50 v2 model.

Keywords: *Deep learning, Convolutional neural network, ResNet, Malaria parasite classification*

1. INTRODUCTION

Malaria is a serious health problem that affects many people around the world. Malaria is a disease that causes a parasite called plasmodium to be transmitted to humans as a result of the bite of female anopheles mosquitoes [1,2]. People infected with the malaria parasite have a high fever, chills, headache, nausea and vomiting, cough, muscle pain and fatigue, sweating, chest and abdominal pain. While malaria is rare in temperate climates, it is common in tropical and subtropical climates [3,4]. Many drugs are used to treat malaria. However, the malaria parasite is highly resistant to these drugs. In long-term malaria cases, jaundice, anemia, respiratory complaints, and pneumonia may develop. Diagnosis of malaria may be difficult due to clinical deficiencies, long incubation period, or acquired immunity. Clinical diagnosis, microscopic diagnosis, molecular diagnosis, serology, antigen test, drug resistance test methods are used in the diagnosis of malaria [5]. The most widely used method among these methods is the microscopic diagnosis method [6,7]. In the microscopic diagnosis method, the only way to diagnose malaria in a person who has malaria is to have the patient's blood tests done [8].

Therefore, Malaria is detected by examining the blood sample taken from the patient under a microscope by specialist physicians as a result of a microbiological examination [9,10]. Although the microscopic diagnosis method is widely used, its efficiency is low because it takes more time and depends on the interpretation of the specialist physician. [11]. Deep learning algorithms, which have been used in the field of computer vision recently, increase the efficiency of specialist physicians by making a significant contribution to the decision-making process in solving real-life problems. [12,13].

Many deep learning-based methods have been used in the literature on the detection and classification of the malaria parasite. In the study of detecting the malaria parasite using microscopic images, a new deep neural network model has been proposed to detect the malaria parasite falciparum. In this proposed model, the VGG model network and the support vector machine (SVM) were combined using transfer learning and a success accuracy of 93.13% was obtained [1].

In a deep learning-based automated malaria parasite detection study, a new model for diagnosing malaria using microscopic smear images is proposed. The proposed model detected the malaria parasite with an accuracy of 99.23%. In addition, both web-based and mobile-based applications have been developed to validate the model efficiency [14]. In the study of Masud et al., the performance of a special convolutional neural network model was evaluated using a cyclic stochastic gradient descent with an automatic learning rate finder to detect malaria. As a result of the evaluation, 97.30% accuracy was obtained from the best performing model [15].

In the study of Pattanaik et al., a computer aided diagnosis (CAD) system is recommended to identify the malaria parasite. The proposed CAD system was evaluated using the malaria parasite dataset and achieved 89.10% detection accuracy. In addition, 93.90% sensitivity and 83.10% specificity rates were obtained with this system [16]. Sriporn et al., used the Xception deep learning model to analyze malaria. Comparing this model with ResNet-50, Inception-V3, VGG-16, NasNetMobile and AlexNet models, 98.86% success accuracy was achieved [17].

In a different study, an image classification model using convolutional neural networks was developed to detect malaria parasites and an accuracy of 95% was achieved [18]. In another study detecting malaria parasite, the performances of single shot multiple box detector (SSD), faster regional convolutional neural network (Faster R-CNN) and RetinaNet models were evaluated and compared. As a result of the comparison, it was observed that the Faster R-CNN model achieved the best success accuracy, despite the longer training time compared to other models [19].

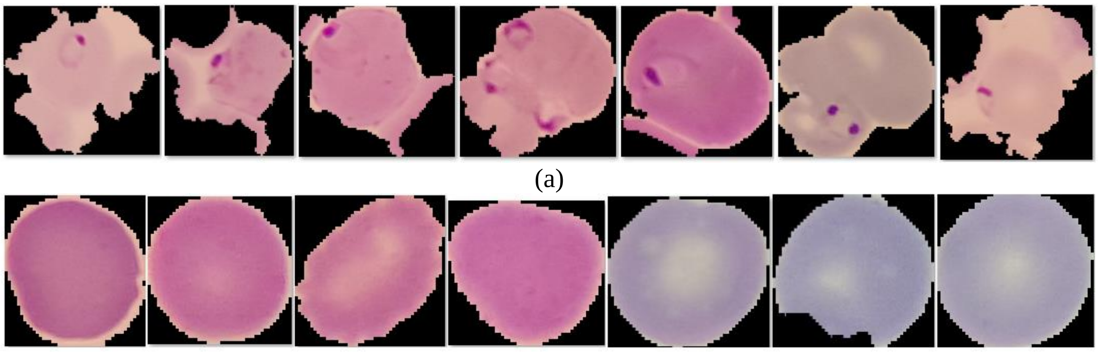
Sinha et al., a convolutional neural network model was proposed to reduce the time complexity in describing malaria. Sequential and ResNet deep learning algorithms are compared in this study, which uses the same data set as the proposed model. As a result of the comparison, the Sequential model achieved 98% success accuracy using training data, 96% success accuracy using validation data, and 96% success accuracy using test data. The ResNet model, on the other hand, achieved success accuracy of 96.50% using training data, 96.78% using validation data, and 97% using test data [20].

In this study, ResNet architectures were compared using a dataset with a total of 27558 red blood cell images from the National Library of Medicine [21] containing 13799 parasitized and 13799 uninfected to quickly classify the malaria parasite. As a result of the comparison, the best classification accuracy was obtained with ResNet-50 v2. The use of ResNet models with this data set and especially the comparison of the ResNet model versions by applying them together makes an important contribution to the literature.

2. MATERIALS AND METHODS

2.1. Dataset and Preprocessing

In this study, a dataset with a total of 27558 red blood cell images containing 13779 parasitized and 13779 uninfected from the National Library of Medicine was used to classify the malaria parasite [21]. All images in the data set were re-labeled in the same class after they were converted to 96×96 pixels in gray color format. 90% of the total number of images in the data set was used for training and testing the models and 10% for validation. Of the total 24802 images allocated for training and testing the models, 80% were reserved for training and 20% for testing. The images of malaria parasitized and uninfected data in the data set are shown in Figure 1.



(a)

(b)

Figure 1. Dataset images (a) parasitized (b) uninfected.

2.2. ResNet Neural Network Models

ResNet is a classic neural network model introduced in 2015 to facilitate the training of deeper networks [22]. In the ResNet architecture, there are different model structures and versions. In this study, malaria parasite classification was performed using two different versions of the ResNet-50, ResNet-101, and ResNet-152 model structures. The diagram of ResNet models used in the classification of the malaria parasite is given in Figure 2. In addition, the traditional block structures used in the ResNet-50, ResNet-101, and ResNet-152 model structures are given in Table 1.

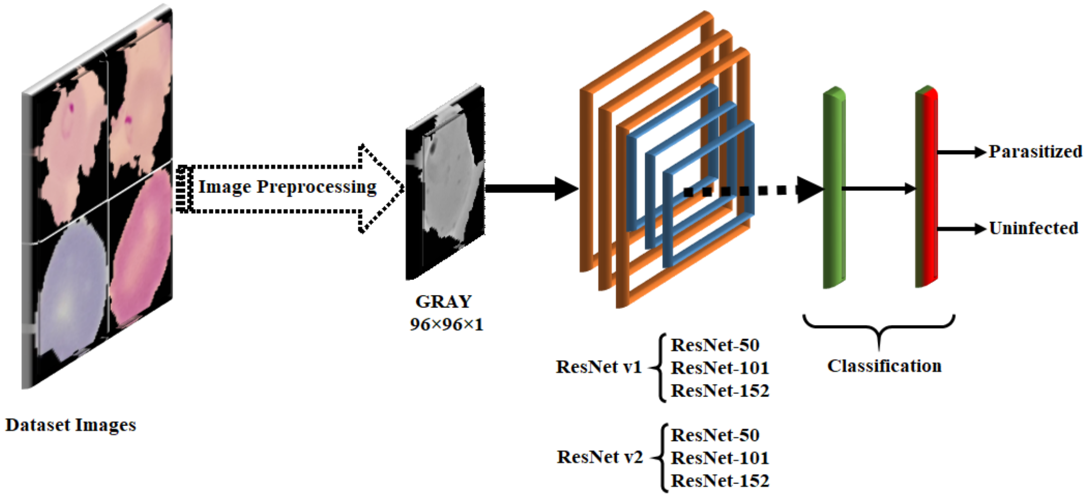


Figure 2. Model diagram used in the classification of malaria parasite.

Table 1. Traditional block structures used in ResNet model structures.

Layer Name	**Output Size**	**ResNet-50**	**ResNet-101**	**ResNet-152**
Conv1	96×96	7×7, 64, stride 2		
		3×3 max pool, stride 2		
Conv2	48×48	$\begin{bmatrix}1\times1,64\\3\times3,64\\1\times1,256\end{bmatrix}\times 3$	$\begin{bmatrix}1\times1,64\\3\times3,64\\1\times1,256\end{bmatrix}\times 3$	$\begin{bmatrix}1\times1,64\\3\times3,64\\1\times1,256\end{bmatrix}\times 3$
Conv3	24×24	$\begin{bmatrix}1\times1,128\\3\times3,128\\1\times1,512\end{bmatrix}\times 4$	$\begin{bmatrix}1\times1,128\\3\times3,128\\1\times1,512\end{bmatrix}\times 4$	$\begin{bmatrix}1\times1,128\\3\times3,128\\1\times1,512\end{bmatrix}\times 8$
Conv4	12×12	$\begin{bmatrix}1\times1,256\\3\times3,256\\1\times1,1024\end{bmatrix}\times 6$	$\begin{bmatrix}1\times1,256\\3\times3,256\\1\times1,1024\end{bmatrix}\times 23$	$\begin{bmatrix}1\times1,256\\3\times3,256\\1\times1,1024\end{bmatrix}\times 36$
Conv5	6×6	$\begin{bmatrix}1\times1,512\\3\times3,512\\1\times1,2048\end{bmatrix}\times 3$	$\begin{bmatrix}1\times1,512\\3\times3,512\\1\times1,2048\end{bmatrix}\times 3$	$\begin{bmatrix}1\times1,512\\3\times3,512\\1\times1,2048\end{bmatrix}\times 3$
	1×1	average pool, 2-d fc, sigmoid		

Except for Conv1 convolution block used in ResNet-50, ResNet-101 and ResNet-152 models, other convolution blocks consist of building blocks with 3 convolution layers as shown in Eq. 1.

$$\begin{bmatrix} 1\times 1, 64 \\ 3\times 3, 64 \\ 1\times 1, 256 \end{bmatrix} \tag{1}$$

Therefore, the building block given in Eq. 2 is,

$$\begin{bmatrix} 1\times 1, 64 \\ 3\times 3, 64 \\ 1\times 1, 256 \end{bmatrix} \times 3 \tag{2}$$

It consists of 3×3=9 convolution layers. Similarly, other convolution building blocks also include this convolution model [23].

ResNet architectures used in malaria parasite classification take the input image in gray color format and 96×96 pixels, and then a convolution layer with 64 2-step 7×7 filters is applied in the first convolution block (Conv1), which contains only one convolution layer. Then, a maximum pooling layer is applied with a 2-step and 3×3 pixel size filter and given as input to the second convolution block (Conv2), and it is followed by the third convolution block (Conv3), the fourth convolution block (Conv4), and the fifth convolution block (Conv5), respectively. Then, malaria parasite classification accuracy is obtained by using the sigmoid classification layer, which classifies as much as the number of classes specified in the data set from the features obtained from the average pooling and fully connected layer.

2.3. Model Training and Testing

5 K-Fold cross-validation was used to train the ResNet model structures used in the study. 19842 images are used for model training and 4960 images are used for model testing. In addition, after the training of the models, the model was validated with 2756 images separated from the data set to test the performance of the model structures. It is a difficult problem to process all the datasets to be used in training ResNet model structures at the same time. Therefore, the data set is divided into smaller groups using the Mini Batch Size parameter and the model networks are trained. However, during the training of the model networks, the epoch parameter is used to return all the data to the neural network. Adamax optimization algorithm is used to minimize the error of the model networks and increase their performance. Binary crossentropy loss function is used to determine the performance and error rates of the models. In addition, the sigmoid activation function is used to estimate the output from the model networks. The parameters and values used for training ResNet model structures are given in Table 2.

Table 2. Parameters used in ResNet model structures.

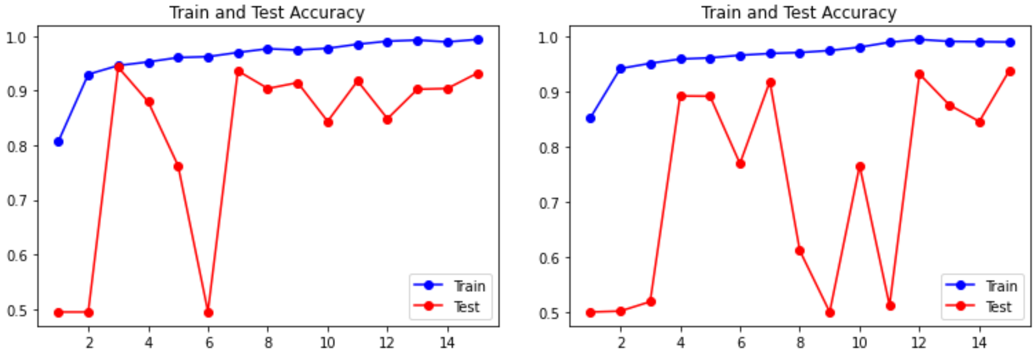
Parameters	**Values**
K-Fold	5
Mini Batch Size	64
Epoch	15
Optimizer	Adamax
Loss Function	Binary Crossentropy
Classifier Activation	Sigmoid

3. RESULTS AND DISCUSSION

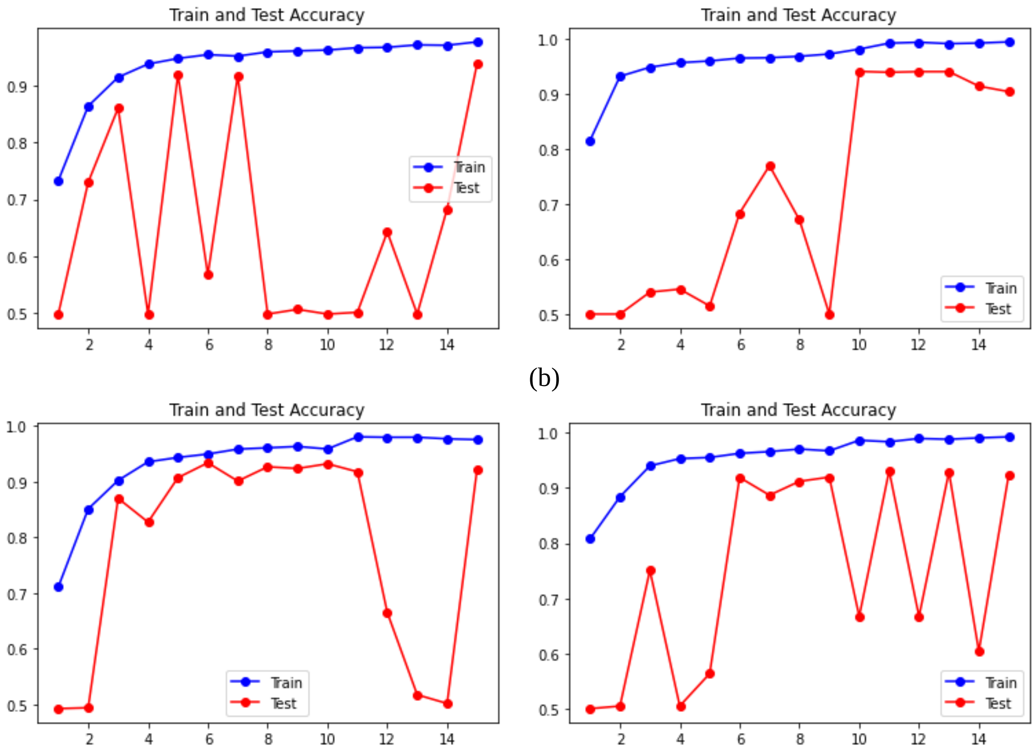
In the study, malaria parasite was classified using versions of traditional ResNet models (ResNet-50 v1, ResNet-101 v1, ResNet-152 v1, ResNet-50 v2, ResNet-101 v2 and ResNet-152 v2). 5 K-Fold cross-validation was used to determine the validity and performance of model structures in malaria parasite classification. In Table 3, the loss values and accuracy rates obtained as a result of 5 K-Fold cross-validations of the models are given. In addition, the training-test accuracy graphs obtained as a result of training the ResNet models with the best performance are given in Figure 3 and the loss graphs are given in Figure 4.

Table 3. Loss values and accuracy rates obtained as a result of 5 K-Fold cross-validations of ResNet models.

Version	Models	Loss/Acc	Model 1	Model 2	Model 3	Model 4	Model 5
v1	ResNet-50	Loss	1.7374	2.2477	0.6678	5.6796	**0.2476**
		Acc (%)	56.42	53.22	78.41	50.00	**93.19**
	ResNet-101	Loss	**0.2004**	0.6429	0.2499	5.5997	1.6313
		Acc (%)	**93.73**	87.28	91.87	50.02	64.31
	ResNet-152	Loss	0.2755	0.7025	0.5807	0.2881	**0.2301**
		Acc (%)	90.04	74.66	79.70	91.23	**91.79**
v2	ResNet-50	Loss	1.2799	0.2701	**0.2623**	0.4078	0.3315
		Acc (%)	65.87	93.89	**93.23**	94.03	94.13
	ResNet-101	Loss	1.8249	0.3592	**0.3199**	1.1886	3.2701
		Acc (%)	65.77	92.40	**90.38**	73.45	54.03
	ResNet-152	Loss	0.3638	3.7516	**0.3132**	1.7687	0.5809
		Acc (%)	86.47	50.45	**92.40**	62.90	77.92



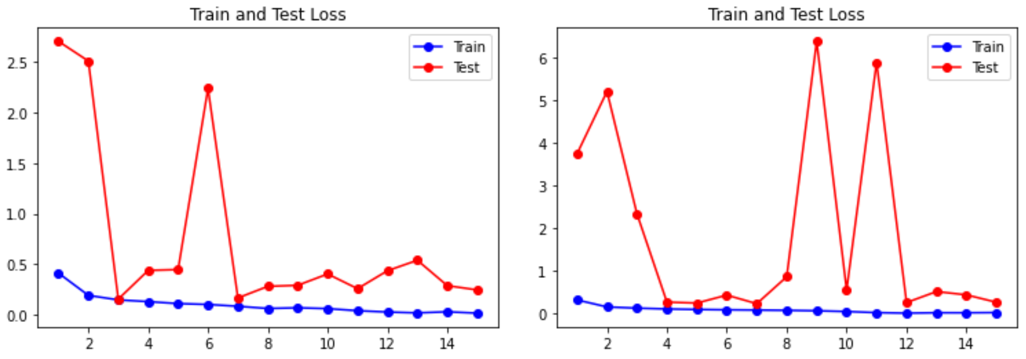
(a)



(b)

(c)

Figure 3. Training-test accuracy graphs of ResNet model structures (a) ResNet-50 v1 (left) – ResNet-50 v2 (right), (b) ResNet-101 v1 (left) – ResNet-101 v2 (right), (c) ResNet-152 v1 (left) – ResNet-152 v2 (right).



(a)

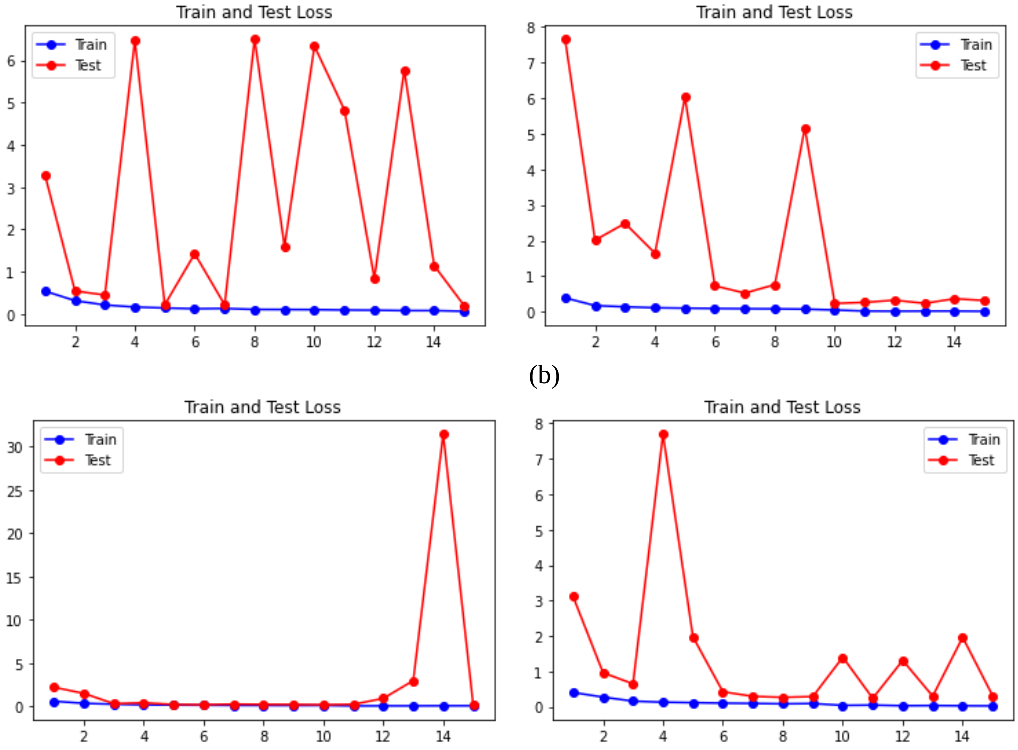


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Figure 4. Training-test loss graphs of ResNet model structures (a) ResNet-50 v1 (left) – ResNet-50 v2 (right), (b) ResNet-101 v1 (left) – ResNet-101 v2 (right), (c) ResNet-152 v1 (left) – ResNet-152 v2 (right).

When Table 3, Figure 3, and Figure 4 were examined, it was seen that ResNet-101 v1 and ResNet-50 v2 were the models with the best training-test success in classifying the malaria parasite in ResNet model structures. The model with the worst training-test success was found to be ResNet-101 v2 and ResNet-152 v1.

Considering the rates in Table 3, the performance of the models was tested by choosing the best models with the lowest loss value as a result of the training of the models, and the results are given in Table 4.

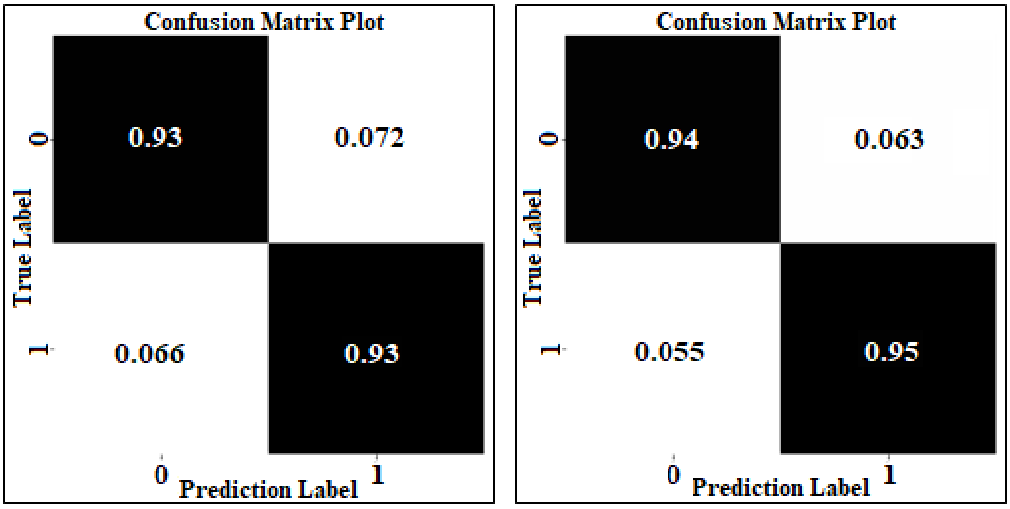
To test the validity of the ResNet models that showed the best success as a result of the 5-K Fold, the model was validated using 2756 images separated in the dataset. The final test accuracy rates and loss values obtained for these models are given in Table 5 and the confusion matrix graphics are given in Figure 5.

Table 4. Performance measures of the models with the lowest loss value obtained as a result of 5 K-Fold cross-validations of ResNet models.

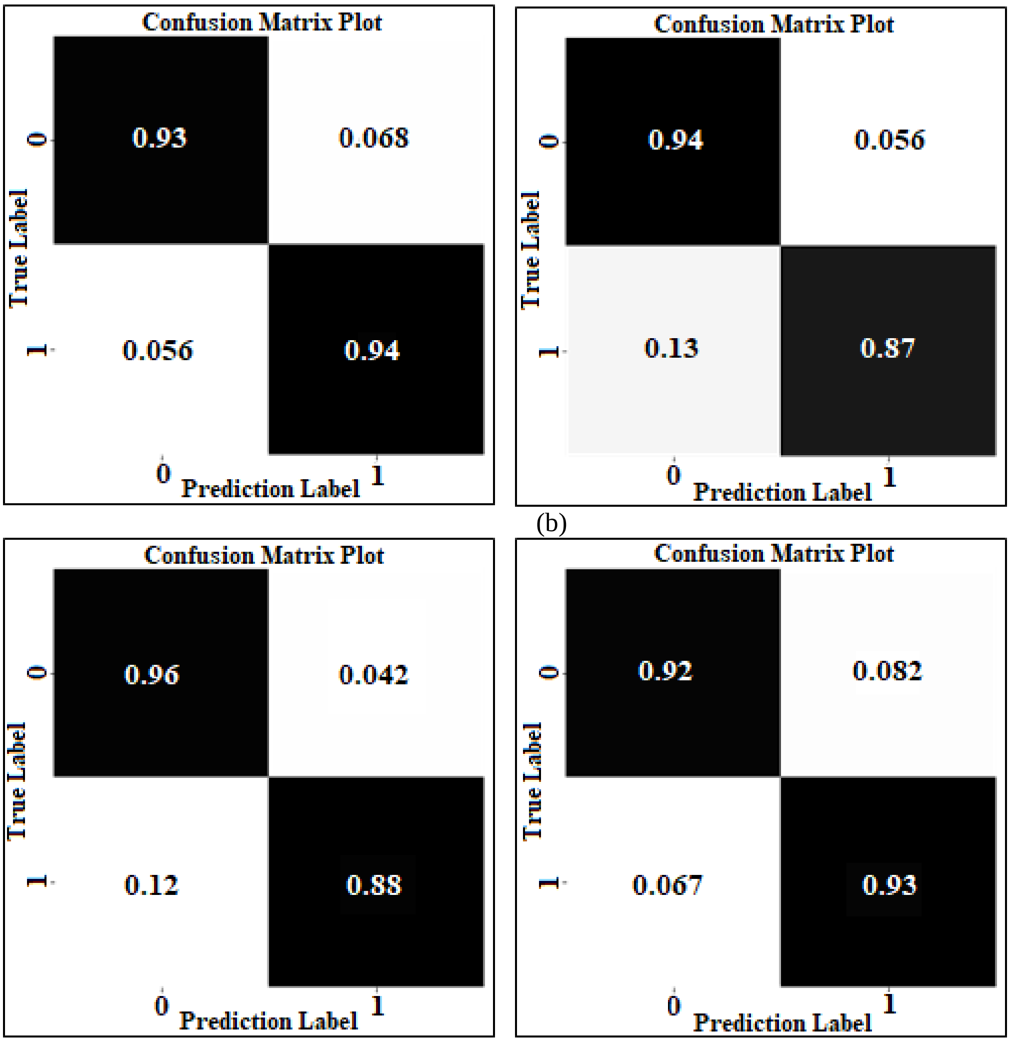
Version	Models	Class	Precision	Recall	F1-Score	Support
v1	ResNet-50	Parasitized	0.94	0.93	0.93	1407
		Uninfected	0.93	0.93	0.93	1349
	ResNet-101	Parasitized	0.95	0.93	0.94	1407
		Uninfected	0.93	0.94	0.94	1349
	ResNet-152	Parasitized	0.89	0.96	0.92	1407
		Uninfected	0.95	0.88	0.91	1349
v2	ResNet-50	Parasitized	0.95	0.94	0.94	1407
		Uninfected	0.93	0.95	0.94	1349
	ResNet-101	Parasitized	0.88	0.94	0.91	1407
		Uninfected	0.94	0.87	0.90	1349
	ResNet-152	Parasitized	0.93	0.92	0.93	1407
		Uninfected	0.92	0.93	0.92	1349

Table 5. The accuracy rates and loss values obtained using the validation dataset in the best.

Version	Models	Accuracy (%)	Loss
v1	ResNet-50	93.07	0.2568
	ResNet-101	93.83	0.2001
	ResNet-152	91.91	0.2338
v2	ResNet-50	94.09	0.2333
	ResNet-101	90.75	0.2999
	ResNet-152	92.53	0.2915



(a)



(b)

(c)

Figure 5. Confusion matrix obtained using the validation dataset in the best model (a) ResNet-50 v1 (left) – ResNet-50 v2 (right), (b) ResNet-101 v1 (left) – ResNet-101 v2 (right), (c) ResNet-152 v1 (left) – ResNet-152 v2 (right) (0: Parasitized, 1: Uninfected).

When Table 4, Table 5 and Figure 5 are examined, ResNet-50 v1 showed 93.07%, ResNet-101 v1 93.83%, ResNet-152 v1 91.91%, ResNet-50 v2 94.09%, ResNet-101 v2 90.75%, and ResNet-152 v2 92.53% success in classification of malaria parasite using the validation dataset. It was observed that the ResNet-50 v2 model with the least number of parameters reached the best success accuracy (94.09%).

4. CONCLUSIONS

In this study, ResNet-50 v1, ResNet-101 v1, ResNet-152 v1, ResNet-50 v2, ResNet-101 v2 and ResNet-152 v2 models from ResNet architectural structures were compared in classification of malaria parasite. The National Library of Medicine dataset consisting of 27558 red blood cell images was used to compare the models. 90% of the total number of images in the data set was used for training and testing the models and 10% for validation. The images separated for training and testing were trained separately using the 5 K-Fold cross-validation method.

The models were trained using the 5 K-Fold cross-validation method with the data in the training test dataset. The final test was conducted using the validation dataset on the best performing models from the trained models. It was seen that the best success accuracy among the models discussed in the study was obtained with the ResNet-50 v2 model with 94.09%. In conclusion, the results obtained with ResNet architectures are promising for the classification of malaria parasites in the field of medical imaging. In future studies, it is planned to carry out studies using different datasets and different model architectures in the field of health.

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REFERENCES

[1] Vijayalakshmi, A. And Rajesh, K.B., (2020), Deep learning approach to detect malaria from microscopic images, Multimedia Tools and Applications, 79(21), 15297-15317.

[2] Yang, F., Poostchi, M., Yu, H., Zhou, Z., Silamut, K., Yu, J., Maude, R.J., Jaeger, S. and Antani, S., (2019), Deep learning for smartphone-based malaria parasite detection in thick blood smears, IEEE journal of biomedical and health informatics, 24(5), 1427-1438.

[3] Diker, A.D., (2020), Sıtma Hastalığının Sınıflandırılmasında Evrişimsel Sinir Ağlarının Performanslarının Karşılaştırılması, Bitlis Eren Üniversitesi Fen Bilimleri Dergisi, 9(4), 1825-1835.

[4] Li, S., Du, Z., Meng, X. and Zhang, Y., (2021), Multi-stage malaria parasite recognition by deep learning, GigaScience, 10(6), giab040.

[5] Akılotu, B.N., Kadiroğlu, Z., Şengür, A. and Kayaoğlu, M., Evrişimsel Sinir Ağları ve Transfer Öğrenme Yöntemi Kullanılarak Sıtma Tespiti.

[6] Rahman, A., Zunair, H., Reme, T.R., Rahman, M.S. and Mahdy, M.R.C., (2021), A comparative analysis of deep learning architectures on high variation malaria parasite classification dataset, Tissue and Cell, 69, 101473.

[7] Chakradeo, K., Delves, M. and Titarenko, S., (2021), Malaria Parasite Detection Using Deep Learning Methods, International Journal of Computer and Information Engineering, 15(2), 175-182.

[8] Swastika, W., Widodo, R.B., Balqis, G.A. and Sitepu, R., (2021), The Effect of Regularization on Deep Learning Methods For Detection of Malaria Infection, In 2021 International Conference on Converging Technology in Electrical and Information Engineering (ICCTEIE), Bandar Lampung, 87-90.

[9] Yang, Z., Benhabiles, H., Hammoudi, K., Windal, F., He, R. and Collard, D., (2021), A generalized deep learning-based framework for assistance to the human malaria diagnosis from microscopic images, Neural Computing and Applications, 1-16.

[10] Swastika, W., Kristianti, G.M. and Widodo, R.B., (2021), Effective preprocessed thin blood smear images to improve malaria parasite detection using deep learning, In Journal of Physics: Conference Series, Malang, 1869(1), 012092.

[11] Imran, T., Sharif, M., Tariq, U., Zhang, Y.D., Nam, Y., Nam, Y. and Kang, B.G., (2021), Malaria Blood Smear Classification Using Deep Learning and Best Features Selection, Comput. Mater. Contin, 71, 1-15.

[12] Raj, M., Sharma, R. and Sain, D., (2021), A Deep Convolutional Neural Network for Detection of Malaria Parasite in Thin Blood Smear Images, In 2021 10th IEEE International Conference on Communication Systems and Network Technologies (CSNT), Bhopal, 510-514.

[13] Montalbo, F.J.P. and Alon, A.S., (2021), Empirical Analysis of a Fine-Tuned Deep Convolutional Model in Classifying and Detecting Malaria Parasites from Blood Smears, KSII Transactions on Internet and Information Systems (TIIS), 15(1), 147-165.

[14] Fuhad, K.M., Tuba, J.F., Sarker, M., Ali, R., Momen, S., Mohammed, N. and Rahman, T., (2020), Deep learning based automatic malaria parasite detection from blood smear and its smartphone based application, Diagnostics, 10(5), 329.

[15] Masud, M., Alhumyani, H., Alshamrani, S.S., Cheikhrouhou, O., Ibrahim, S., Muhammad, G., Hossain, M.S. and Shorfuzzaman, M., (2020) Leveraging deep learning techniques for malaria parasite detection using mobile application, Wireless Communications and Mobile Computing, 2020, 1-15.

[16] Pattanaik, P.A., Mittal, M. and Khan, M.Z., (2020), Unsupervised deep learning cad scheme for the detection of malaria in blood smear microscopic images, IEEE, 8, 94936-94946.

[17] Sriporn, K., Tsai, C.F., Tsai, C.E. and Wang, P., (2020), Analyzing Malaria Disease Using Effective Deep Learning Approach, Diagnostics, 10(10), 744.

[18] Shah, D., Kawale, K., Shah, M., Randive, S. and Mapari, R., (2020), Malaria Parasite Detection Using Deep Learning:(Beneficial to humankind), In 2020 4th International Conference on Intelligent Computing and Control Systems (ICICCS), Madurai, 984-988.

[19] Nakasi, R., Mwebaze, E., Zawedde, A., Tusubira, J., Akera, B. and Maiga, G., (2020), A new approach for microscopic diagnosis of malaria parasites in thick blood smears using pre-trained deep learning models, SN Applied Sciences, 2(7), 1-7.

[20] Sinha, S., Srivastava, U., Dhiman, V., Akhilan, P.S. and Mishra, S., (2021), Performance assessment of Deep Learning procedures on Malaria dataset, Journal of Robotics and Control (JRC), 2(1), 12-18.

[21] https://lhncbc.nlm.nih.gov/LHC-downloads/downloads.html#malaria-datasets

[22] He, K., Zhang, X., Ren, S. and Sun, J., (2016), Deep residual learning for image recognition. Proceedings of the IEEE Computer Society Conference on Computer Vision and Pattern Recognition, 2016-December, 770–778. https://doi.org/10.1109/CVPR.2016.90.

[23] Wu, H., Xin, M., Fang, W., Hu, H.M. and Hu, Z., (2019), Multi-level feature network with multi-loss for person re-identification, IEEE, 7, 91052-91062.