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Detection of Malaria Diseases with Residual Attention Network

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Abstract: To describe a model using classic machine learning techniques for creating machine learning systems, a person who specializes in this technique needs to extract feature vectors. This period also breaks into expert time. Also, these methods could not process raw data without preprocessing and expert assistance. Deep learning has made great progress in solving problems at this point, and machine learning research has continued for many years. Unlike traditional machine learning and image processing techniques, deep networks enable learning processes using raw data. In this study, a deep learning approach for the classification and diagnosis of malaria is developed. For this purpose, Residual Attention Network (RAN) a deep learning Convolutional Neural Network (CNN) technique was used with previously classified datasets. The goal is to design computer-aided software for classifying blood cell images (blood samples) as "parasitized" or "uninfected". In the program, a decision support system was implemented by a deep learning approach. As a result, the RAN model achieved the best ability to produce better results in processing and classification images compared to other algorithm types. RAN model's training simulation results showed a 95.79% classification accuracy rate. Using the Support Vector Machine (SVM) obtained only 83.30% classification accuracy rate. Besides, it is evaluated that for the classification of blood cell images and diagnosis of malaria using deep learning methods can be used successfully. In addition, deep learning methods have the advantage of automatically learning features from input data and require minimal input by specialists in automated malaria diagnosis.

Keywords: *Deep Learning, Residual Attention Network, Support Vector Machine, Malaria Disease*

1. Introduction

Rapid changes in technology have had an important impact on human life. These developments make technology and physical computer systems indispensable in human life. Computers, hardware, software and supported devices support humanity for almost a lifetime. In short, you can see the use of technology in every field of life. Two of these areas are the health and medicine sectors. Such systems are commonly used in disease diagnosis, classification and treatment stages (for decision support purposes). The use of computer systems in medicine has become necessary due to the high number of diseases, requirement of significant amount of data for diagnosis and treatment, and the additional cost of collecting and processing these data. Early diagnosis is very important for medical scientists in the treatment of many diseases. The research aimed at early diagnosis is in a privileged position. In parallel, scientists working on the development of various functions and libraries to overcome the challenges of data collection and image processing especially deep learning algorithms. In this way, computer systems can be used for decision support purposes that allow medical scientists to make more accurate and quick decisions [1].

Malaria is a mosquito-borne disease that affects humans and animals. Fever, fatigue, vomiting and headache are typical symptoms of malaria. Severe malaria cases result in yellow skin, seizures and serious consequences. Such symptoms generally begin about 10-15 days after being bitten by a mosquito that carries malaria. If the disease is not properly treated, the infection can reoccur. A person who recovers from infection is not adequately disinfected; milder symptoms may reoccur. In 2016, there were 216 million malaria cases worldwide, resulting in thousands of deaths. Depending on the disease, there may be an increase in health care costs, a decrease in the workforce and adverse impacts on the tourism and trade sectors due to the disease's infectivity. The type of malaria found in Turkey is mildly advanced and does not result in direct death. These situations can lead to neglected illnesses. However, malaria disease seen in Turkey does not result in direct death but is fatal in a very important amount by leading to spontaneous abortion, stillbirth, low birth weight and maternal death. Classification with deep learning of these critically affecting diseases is very important in facilitating patient procedures and supporting medicine [2].

Today, deep learning algorithms are commonly used in the medical field. Similarly, artificial intelligence has a high accuracy share and its prediction is excellent. One more additional a role in disease prevention activities is the fact that it reduces health care costs. Some of positive effects in the health and medical fields are diagnostic programs, treatment protocol development, drug development, customized medicine, patient follow-up and care. In this context, one of the paper's objectives is to study the expectation that labor costs and medical costs needed to diagnose malaria disease can be reduced, shortly, cost-effective diagnosis. Such positive results may indicate the importance of research [3, 9, 30].

Another contribution of the deep learning approach is that it has a positive impact on the treatment process by noticing small details that may not be noticed in the patient's symptoms and illness. For these conditions, the process of diagnosing and treating malaria is important, by using artificial learning algorithm both measures prove faster and more economical. In this way, the use of computer-aided algorithms and approaches that support the procedures performed by the physician in the diagnosis and

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treatment process lead to a rapid decision-making process in this area reveals the purpose and importance of the study in a clear manner [4].

As a result of the literature review, it has been determined that there are many studies on the examination of medical images with advanced methods such as artificial intelligence, machine learning and deep learning. In this way, it is considered that computer science has made a great contribution to the field of medicine. In particular, the rapid examination of blood samples facilitating the detection and diagnosis of diseases increases the importance of the studies in this field. In this study, the kind of researches conducted on CNN, Machine Learning and Image Processing related to malaria has been determined. As a result, the algorithms used were revealed that CNN's RAN model was not used and this model was preferred in our study Algorithms such as Thresholding (IM), KNN, BN, Decision tree, Convolutional Neural Network (CNN) were used in these processes, also a new method has been established to identify the presence of malaria parasites image processing techniques and Support Vector Machine (SVM) and using (ANN) algorithms were used to classification malaria diseases moreover, VGG16-SVM outperforms existing CNN models in all performance indicators such as accuracy, precision, specificity and precision. As a result, the algorithms used were revealed that CNN's RAN model was not used and this model was preferred in our study [5-10, 29-30]. However, to the best of our knowledge, no attention mechanisms have been applied to building feed forward networks to achieve the most advanced results in image classification tasks. Recent advances in image classification have focused on the training of feed forward convolutional neural networks using "very deep" structures [11-17].

This study will develop a deep learning approach for the classification and diagnosis of malaria. For this purpose, a Residual Attention Network (RAN) model that is a deep learning Convolutional Neural Network (CNN), was used with previously classified datasets. The goal is to design computer-aided software for classifying blood cell images (blood samples) as “parasitized” or “uninfected”. In this study, it was implemented by a deep learning approach using the RAN model. RAN model was used because it can produce better results in image processing and classification compared to other algorithm types. At the end of the study, whether the examined image is infected with a parasite or not.

2. Convolution Neural Network

Convolutional Neural Networks (CNNs) are the most frequently used models in image processing and computer vision systems. They are designed to mimic the structure of the animal's visual cortex. Specifically, CNN has neurons arranged in three dimensions: width, height, and depth. A particular layer of neurons is connected only to a small area of the previous layer. Figure 1, shows the layer structure of the CNN architecture [18].

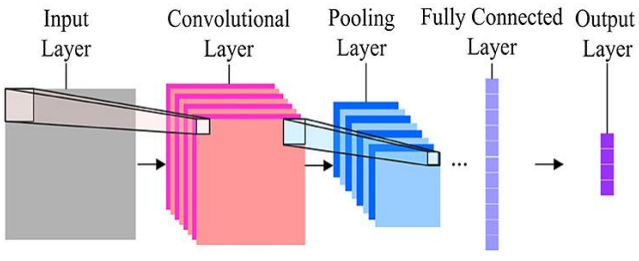

Figure 1. Convolutional Neural Networks (CNN) layer structure

2.1. Residual Attention Network

Residual Attention Network (RAN) is built by stacking multiple attention modules. Each attention module is divided into two branches: the mask branch and the trunk branch. The trunk branch performs functional processing that is adaptable to the most advanced network structures. Given an input x trunk branch output T (x). The mask branch uses the same size T (x) mask M as the bottom-up top-down structure [19-22] and softens the output feature T Weight Learn (x). The bottom-up top-down structure mimics the fast feedforward and feedback attention process. The output mask is used as a control gate for stem-branching neurons as in the Highway Network [23]. The output of attention module H is as follows (Eq. 1).

$$H_{j,c}(x) = M_{j,c}(x) + T_{j,c}(x) \quad (1)$$

Where, j spans all spatial locations and c∈ {1, ..., C} is the channel index. You can train the entire structure end-to-end. In the attention module, the attention mask serves not only as a function selector during forward inference, but also as a gradient update filter during back propagation. In the soft mask branch, the gradient of the input feature's mask is (Eq. 2).

$$\frac{\partial M(x,\theta)T(x,\phi)}{\partial \phi} = M(x,0)\frac{\partial T(x,\phi)}{\partial \phi} \quad (2)$$

Where, θ is the mask branch parameter and φ is the trunk branch parameter. This property makes the attention module robust against noisy labels. Mask branches can prevent false gradients (from noisy labels) and update trunk parameters [23].

2.1.1. Attention Residual Learning

Simply stacking the attention module will reduce performance. First, as the dot generation with the mask range of 0 to 1 is repeated, the value of the deep portfolio decreases. Second, soft masks can destroy the superior properties of trunk branches, such as just the same mapping of residual units. To alleviate the problems above, we propose attention residual learning. Similar to the idea of residual learning, if a soft mask unit can be constructed as the same mapping, performance will not be worse than the corresponding one without care. Therefore, change the output H of the attention module as follows (Eq. 3).

$$H_{j,c}(x) = M_{j,c}(x) + T_{j,c}(x) \quad (3)$$

The range of M(x) is [0,1], M(x) approximates 0 and H(x) approximates the original feature F (x). This method is called “attention residual learning”. Cumulative attention residual learning is different from residual learning. In origin ResNet, residual learning is formulated as Hi, c(x) = x + Fi, c(x). Fi and c(x) approximates the residual function. Officially, Fi, c(x) indicates features generated by deep convolutional networks. The key is in mask branch M(x). These function as a function selector that enhances superior functions and suppresses noise from the trunk function. Also, stacking attention modules back up attention residual learning due to its progressive nature. Attention residual learning can maintain the good characteristics of the original function, but also provides the ability to bypass the soft mask Branch to the top layer and weaken the mask branch function selection function. Stacked attention modules can gradually improve the function map. The activity becomes clearer as the depth increases as shown in Figure 2. By using attention residual learning, you can systematically improve performance by increasing the depth of the suggest residual attention network [22].

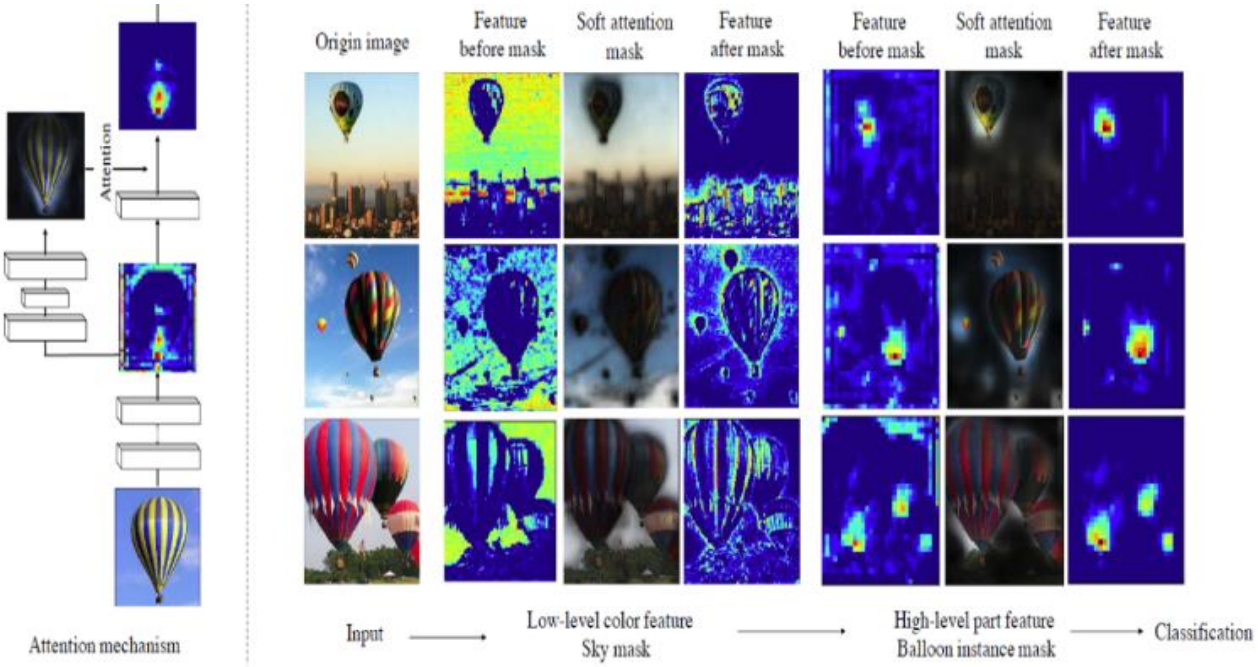

Figure 2. Example of hot air balloon images created using the attention network model [10]

2.1.2. Soft Mask Branch

According to the attention mechanism idea, the mask branch includes a fast feed forward sweep and a top-down feedback step [22]. The former operation quickly collects global information for the entire image, while the latter operation combines global information with the original function map. In a convolutional neural network, two steps are extended to a bottom-up top-down fully convolutional structure. From the input, maximum pooling is performed several times and after a few fields remain, the receptive field increases rapidly. After reaching the lowest resolution, the global information is expanded by asymmetric top-down architecture to guide the input features at each location. Linear interpolation samples the output after several residual units. The number of bilinear interpolations is the same as the maximum pooling to keep the output size the same as the input feature map. The soft mask layer used in attention network model is shown in Figure 3 [23].

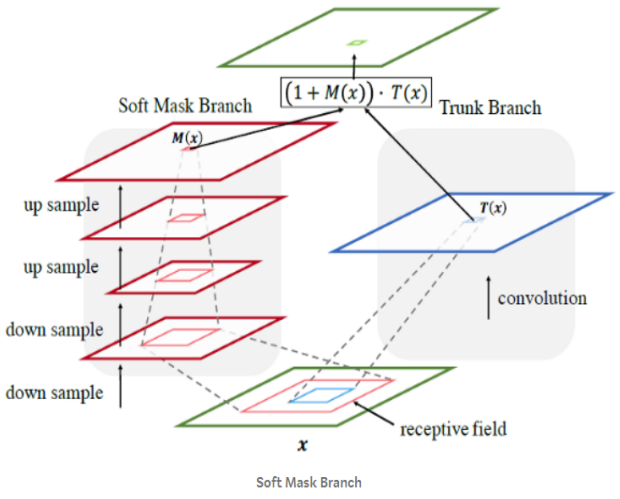

Figure 3. Soft mask layer used in attention network model [10]

Lastly, the sigmoid layer normalizes the output range to [0,1] after two consecutive 1x1 convolutional layers. We also added a skip connection among the bottom-up and top-down parts to capture information from the different calibrated system.

3. Material and Method

In this study, primarily a ready data set is used for the deep learning algorithms. The dataset has consisted of infectious and healthy images taken from the blood cell samples by using a microscope. The images dataset obtained from Malaria Cell Images Dataset [24] and also it was benefited the internet address of Lister Hill National Center for Biomedical Communications (LHNCBC) that is a part of the National Library of Medicine (NLM) [2]. With these image data, a deep learning approach has performed the diagnosis and classification of malaria disease.

This study mainly classifies images of healthy individuals and infected individuals. In order to detect features for classification, Residence Attention Network (RAN) model was used which is a Convolutional Neural Network (CNN) that uses an attention mechanism coupled with an advanced feed network architecture with state-of-the-art technology in the form of end-to-end training. Figure 4 shows the RAN-based deep learning architecture developed within the scope of the study.

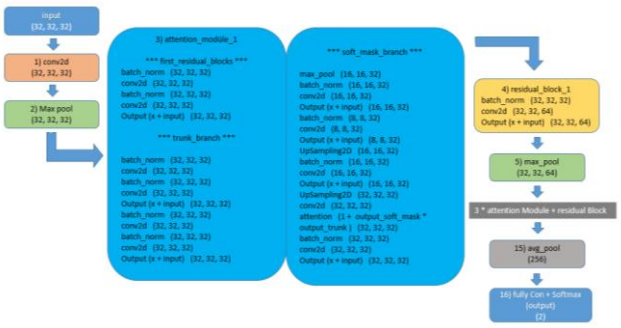

Figure 4. RAN model developed for image classification

Also, the results were compared statistically by using different classification algorithms like Support Vector Machine (SVM). The

difference between the techniques of deep learning (RAN model) and machine learning field are determined. One of the difference is determined by comparing the obtained classification accuracy rate results. Also in this study, other different deep learning CNN model algorithms like pre-trained models VGG16, ResNet50, MobileNetV2 and AlexNet were used and compared with RAN.

In this study, the software was developed for examination and classification of SMEAR images belonging to the Malaria disease written by using Python programming language. For this purpose, the program was utilized with TensorFlow, Keras and scikit-learn libraries prepared with machine learning and deep learning algorithms.

Within this scope;

- Keras library is included within TensorFlow library for the classification of SMEAR images with the Convolutional Neural Network (CNN).
- Support Vector Classification (SVC) algorithm within scikit-learn library was used for the classification of SMEAR images with the technique of Support Vector Machine (SVM).

In the study process, a high-specification computer, appropriate programs, and libraries are required to facilitate and accelerate deep learning procedures. Due to the size of the image data, a computer with special hardware Intel i7-6700HQ, NVIDIA GeForce GTX 970M 4GB, 16GB RAM. In this way, it can analyze and process many data (images). And achieve fast and accurate results.

3.1. Examination of SMEAR Images of Blood Samples Infected and Not Infected with Malaria Parasites

The samples of blood cell images used in this study which are infected or not with malaria parasites were supplied from the Malaria Cell Images Dataset [24] and it was utilized National Library of Medicine [2]. The dataset contains a total of 27.558 cell images containing equal instances of infected and uninfected cell images.

SMEAR images are divided into two classes as parasitic and non-parasitic (parasitized and uninfected). Images' dimensions were resized for CNN models' input layer as 32x32 for the purpose of providing the standardization.

Sample SMEAR pictures carrying malaria parasite are shown in Figure 5 and sample SMEAR pictures of not carrying malaria parasite are shown in Figure 6.

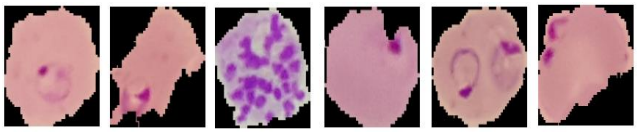

Figure 5. SMEAR blood sample images carrying Malaria parasite [2, 24]

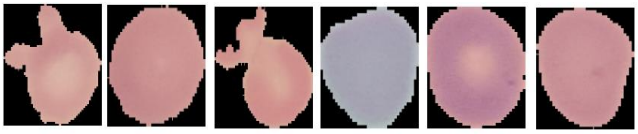

Figure 6. SMEAR blood sample images not carrying Malaria parasite [2, 24]

Sample SMEAR images are grouped by the software as 20.658 images for deep learning training and the 6.900 images for deep learning test.

4. Performance Measurement

Creation of new models are required for advance classification abilities or using an existing model to achieve more success, different models used and compared the accuracy result rates. For this aim, the confusion matrix was used to explain the predictive evaluation of classification. The confusion matrix is provided an actual information estimated accuracy rate for classification during test procedures. A confusion matrix and parameters used to calculate the models' classification results using accuracy rate are shown in Table 1 [25-27].

Table 1. The Confusion matrix parameters

		Predicted +	Predicted -
Actual	+	TP	FP
	-	FN	TN

*TP = True positive, FP = False Positive, FN = False Negative, TN = True Negative

Successful for 2-class classification performance measurement accuracy, sensitivity, specificity, accuracy, etc. results are very important. So, the accuracy score, negative predictive value, false-positive rate, false discovery rates, and false-negative rates are calculated using the calculation formulas shown in Table 2.

Table 2. Performance measurements and formulas for the two-class classification

Performance Measure	Formula
Sensitivity	$\frac{TP}{TP+FN}$
Specificity	$\frac{TN}{TN+FP}$
Precision	$\frac{TP}{TP+FP}$
Negative Predictive Value	$\frac{TN}{TN+FN}$
Accuracy	$\frac{TP+TN}{TP+TN+FP+FN}$

5. Experiments and Results

The following information about data availability was obtained from the Cell Images for Detecting Malaria (kaggle) and it was utilized NLM [2, 24].

The dataset contains a total 27.558 cell images containing equal instances of infected and uninfected cell images. Sample of malaria-infected and uninfected images are shown in Figure 7.

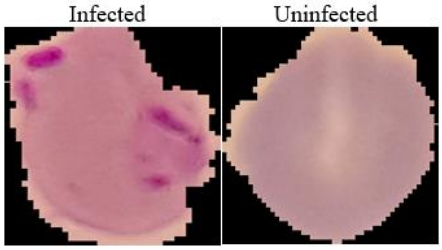

Figure 7. The images of blood sample show the difference between infected and uninfected cells [2. 24]

First, a dataset of malaria was classified as an infected and

uninfected image folder. Then the folder was divided into two groups as 20.658 images for training and 6.900 images for the test. In this study, Python programming language was used for examining the SMEAR images of malaria. For this purpose, it was utilized f0r "Machine Learning" and "Deep Learning" algorithms with TensorFlow, Keras and Scikit-learn python libraries.

As a result, for image classification by the Residual Attention Network (RAN) that is a Convolutional Neural Network (CNN) model, 95.79% training accuracy score (Figure 8) and 95.51% test accuracy score (Figure 9) were obtained by using the developed program.

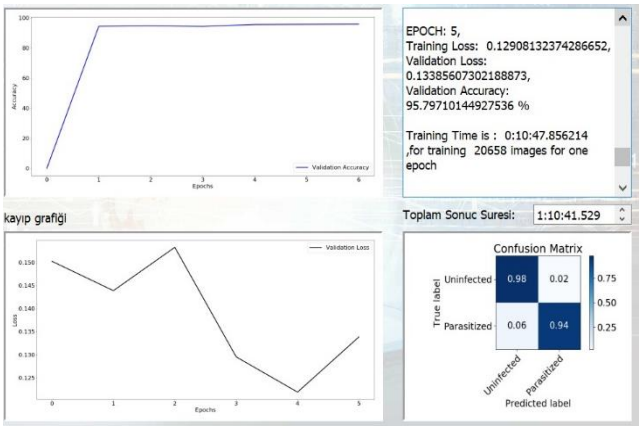

Figure 8. The result screen of Residual Attention Network (RAN) models training

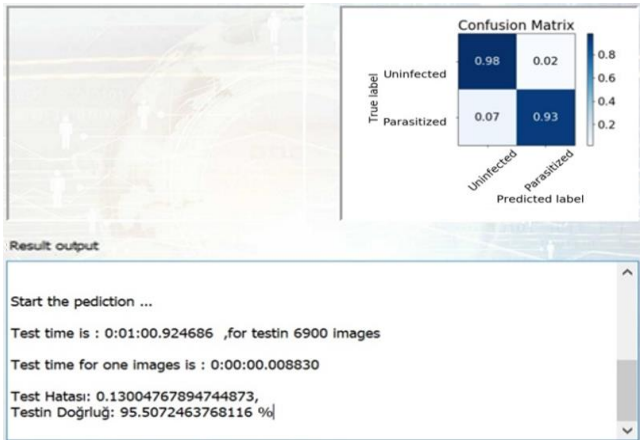

Figure 9. The result screen of Residual Attention Network (RAN) model testing

Also, images were classified with the Support Vector Machine (SVM) which is a Machine Learning model and 83.33% accuracy score was obtained (Figure 10).

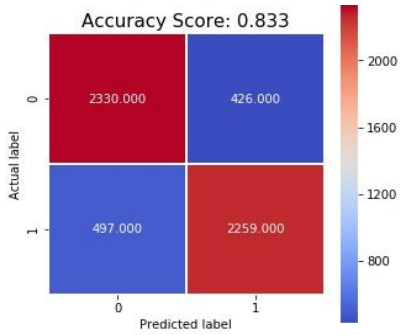

Figure 10. Classfied Support Vector Machine (SVM)

The SVM kernel functions (Eq. 4) in the scikit-learn library developed for the use of SVM algorithms used in machine learning in python applications are linear, radial basis function (RBF) [28].

$$K(xn, xi) = \exp(-\gamma \,||\, xn - xi \,||^2 + C) \quad (4)$$

Optimization Parameter C, γ

γ (Gamma), Core coefficient. The gamma value describes how effective a single training instance is. As the gamma value increases, other sample values are affected.

C, editing parameter. The strength of the arrangement is inversely proportional to C. This value should be positive. C implies the misclassification of educational examples against the simplicity of the decision surface. A low C flattened the decision surface and a high C aims to accurately classify all training samples. In addition, large C values may sometimes require up to 10 times longer training time.

6. Conclusion

Today, information systems are effectively used in many scientific studies. Particularly, Convolutional Neural Network (CNN) and Support Vector Machine (SVM) are distinguished with the advantages for image classification. They are provided by artificial intelligence and deep learning algorithms. Within this scope, different methods have been developed for increasing the efficiency of the CNN methods for increasing the accuracy rate in the estimation process. The most common of these methods is Residual Attention Network (RAN).

In this study, the diagnosis of the malaria disease by using deep learning image classification techniques was investigated. The study is based on CNN methods. In this context, the following points were investigated by this study;

- The usability of SVM method for deep learning techniques. Its advantages and disadvantages are compared with CNN methods.
- The usability of RAN methods for CNN deep learning techniques.
- The usability of layer models such as Transfer Learning, VGG16, Resnet50 and MobilenetV2 known as the pre-trained models and commonly used in the scientific research. Their advantages and disadvantages are compared with each other.
- The usability of SVM and CNN methods together.

At the end of the study conducted; the estimation processes performed by using Residual Attention Network (RAN) deep learning model yielded 95.79% accuracy rate for image classification. The accuracy rate of the estimation processes performed by Support Vector Machine (SVM) model yielded 83.33%. Accordingly, it is considered that the use of Residual Attention Network (RAN) model in the diagnosis of malaria with deep learning methods yielded more effective results. The preference of this model in the studies conducted in this context would be proper.

Within the scope of the study, it was concluded that VGG16, MobilenetV2, Resnet50 and AlexNet models that are the pre-trained CNN methods have advantages and disadvantages compared to each other. As a result, the point of this aim; VGG16 achieved 95.04%, ResNet50 achieved 94.37%, MobileNetV2 achieved 93.69% and AlexNet achieved 92.64% training accuracy rate. Data pertaining to these models are shown in Table 3.

Table 3. Comparison of CNN models training results

Model Type	Epoch Number	Model Accuracy	Model Loss
AlexNet	6	92.64%	0.2289
RAN	6	95.79%	0.1308
VGG16	6	95.04%	0.1756
MobileNetV2	6	93.69%	0.2925
ResNet50	6	94.37%	0.1860

Examined Table 4, it is seen that; the RAN model achieved the highest test accuracy rate of 95.51% in all models in the test stage with a total of 6.900 pictures. RAN model was followed by VGG16 with 94.94%, AlexNet with 93.55% and ResNet50 with 78.16%. The MobileNetV2 model has produced unstable results and has been able to accurately estimate only the parasitized pictures and achieve a 50% accuracy. The SVM model has achieved an accuracy of 83.30% and lagged behind the CNN models.

Table 4. Comparison of the models test results

Test Results	RAN	VGG16	Mobile NetV2	ResNet 50	AlexNet	SVM
Accuracy	95.51%	94.94%	50.00%	78.16%	93.55%	83.30%
Sensitivity	95.11%	95.40%	00.00%	94.83%	89.82%	82.42%
Specificity	96.95%	94.49%	50.00%	70.53%	98.05%	84.13%
Precision	97.01%	94.43%	00.00%	59.57%	98.23%	84.54%
Negative predictive value	93.00%	95.45%	100%	96.75%	88.87%	81.96%
F1-Score	96.05%	94.92%	00.00%	73.17%	93.84%	83.47%

One more result of the study showed that CNN and SVM methods can be combined through proper methods. Too many calculations are needed in respect of the dimensions of SMEAR images for making the required calculations in SVM model. Also, due to the variable dimensions of images, a previous image sizing process is needed. In this context, it was determined that features belonging to SMEAR images to be used as input data in SVM model could be obtained by CNN method for combining the CNN and SVM models. Thus, the process may be performed in a shorter period and a higher estimation accuracy rate obtained.

In conclusion, improving the result of the deep learning model training has great importance in terms of affecting the training data of the system developed. The deep learning model established has a position of a specialist determining whether the collected data are adequate for the training data or not.

At the end of the study, it has been determined that deep learning methods have the advantage of automatic learning with high accuracy. It is evaluated that deep learning methods can provide faster and more effective results with less expertise and fewer resources in the diagnosis of malaria. Also, interdisciplinary academic studies should be established in order to combine the knowledge and experience of medical professionals with deep learning-based systems, and model effectiveness and diversity should be increased.

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