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## Deep Learning-Based Image Analysis towards Improved Malaria Cell Detection

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#### Abstract

Malaria is a disease that happens by biting a female anopheles mosquito. All over the world, it was marked as an endemic. Nowadays, malaria disease diagnosis by using computer-assisted will empower the exact detection and hence gives the guarantee that delivers reliable medical services to accept rare regions. In this study, we target assembling а powerful, limited dependence of people, the sensitive model for robotized investigation of Malaria. When curing and eradicating malaria diagnosis. the exactness, high-performance quality, speed, and complexity of the techniques used for malaria sickness assessment are critical facts. This system would classify red blood cell images if they were parasitized cells or normal by using a Deep Learning model that based on CNN called Resnet50. Our performance outcomes of the investigation show how this model is very effective in feature extraction and how well it detects malaria cell images.

Keywords: Computer-AssistedDiagnosis, Feature Extraction, Image Analysis, Malaria Cell Image, ResNet

#### **1. Introduction**

Malaria, a mosquito-borne life-threatening disease, causes fever, vomiting, headaches and fatigue; in severe cases, it can cause coma or even death [1]. In the early days, a thing to handle malaria detection is by examining the Nan Yu Hlaing Myanmar Institute of Information Technology, Mandalay nan\_yu\_hlaing@miit.edu.mm

microscopic slide manually. Unfortunately, such work is very difficult in malaria predominance and resource-limited areas. The size of microscopic whole slide images is large, and it requires a long scanning.

An automated diagnosis process can handle the problem of manual detection. The automated distinguishing procedure will ensure the right finding of jungle fever illness and subsequently can promise to convey precise health insurance to scarce regions. To detect malaria disease using automated techniques, it still needs to adapt the methods, expertise, practices, and knowledge of conventional microscopy to a computer-assisted diagnosis [2]. Malaria-cells automated detection became an attractive subject to researchers in the last decade.

Previous researches have shown that the degree of satisfaction for detection in the pictures of the cell is very low. Hence, deep learning researches have been a rising, trendy subject with the routine methods on images and videos as a decision support system that can be paramount to faster and reliable diagnosis. In this article, we use Resnet50, a type of CNN architecture like a feature extractor for categorizing cells if they were malaria-infected or normal in a much more improved way. To prove the robustness and invariance in different test sets, this system performs k-different cross-validation and tests the model over different test sets where the value of k is 1 to 5. The model best performs than other popular CNN networks.

#### 2. Related Works

In recent years, researchers observed to handle the challenge of computer-assisted malaria cell diagnosis in red blood cells by applying the traditional machine learning and information-driven deep learning. Bipin, Nair, and Punita studied the foremost application [3] that applied Deep Belief Network (DBN) to classify human peripheral blood cells for malaria disease diagnosis. Their proposed model got the Accuracy score of 0.963.

In [4], scientists proposed the utilization of Artificial Neural Networks (ANN) for the diagnosis of the disease in the red platelet. They refined the results more by increasing the number of parameters and the sample size of the data provided. The techniques for the malaria diagnosis infected RBCs done using ANN gives results almost from 90-100%.

The authors wrote the survey paper on image processing and ML methodologies. They tended to develop on the latest trends in computerassisted malaria detection [5]. However, their observation was appearing as an advanced way that is nothing discovering because of the appearance of new deep learning approaches. Therefore, that simple recorded review illustrated the state-of-the-art before the advent of deep learning.

Zhaohui Liang discovered a robust machinelearning model. That model based on a convolutional neural network. To detect cell images that effect malaria disease, the authors applied 10-fold cross-validation [6]. He concluded that his proposed newly designed deep network model is a responsible application for blood smear classification compared to transfer learning and other similar studies.

In paper [7]. they applied image segmentation methods for red blood cells. They tended to decrease the overfitting problem attaching with training deep networks and to increase the size of the cell image database. Because of these factors, they used data augmentation methods. Their Lenet-5 architecture, a CNN-based approach could automatically have detected malaria disease and approved better classification accuracy by combining numerous datasets.

According to literature knowledge, although microscopic diagnosis is widely used, it has many drawbacks as follows. As malaria is generally associated with poverty and occurs mostly in the low economy and developing countries [8], most laboratories or diagnostic facilities are not equipped with standard testing facilities. In addition to these points, the disease detection needs one who has the expertise to examine the blood film and the stage of disease present in blood cells.

Additionally, the monotonic of the assessment immensely influences the quality of examination. The global shortage of pathologists and reliable diagnostic facilities have a serious impact on malaria disease treatment, unfortunately of developing countries and the case of malaria is no exception.

As another choice, a procedure for computerassisted malaria diagnosis within the blood cells by using cell images is described. Using an effectively efficient device, e.g., a smartphone can easily obtain those cell images.

#### **3.** Classification using Deep Learning

Deep learning is a piece of a more extensive group of machine learning (ML) algorithms dependent on ANN with representation learning. Learning can be supervised, semi-supervised or unsupervised. The word deep in DL refers to the number of layers through which it transforms the data. The evolution of advancements in deep networks can help automatic disease detection. They can also give human-level precision. One obvious thing is the capacity that can perform in either semi-supervised or unsupervised learning over huge databases.

Calculating deep learning algorithms are using many thousands of parameters. Therefore, it needs a tremendous dataset for training the network. Unfortunately, those huge datasets cannot be available readily. Therefore, if we were using small databases, it will not suffice to coach a deep learning model for fine-tuning. Although the dataset is not enough to learn, can encounter one of the main challenges of training a convolutional neural network. It is an issue of overfitting [9].

For handling the computer vision problem, CNN based pre-trained models extract features by learning. Visualizing these features supports a better knowledge of learning operation and allows rising performance accuracy with that customized model.

#### 3.1. Convolutional Neural Network

Convolution Neural Network (CNN) is a type of deep learning model and solve the classification problem by using the standard neural network. However, it uses another layer to describe information and certain features. Yann LeCun first implemented CNN in 1990 and became famous after 2012. The several challenges of increasing the number of hidden layers overcome in CNN. Its main components are convolutional layer, pooling scheme, normalization scheme, and fully connected layers.

The evolution of CNN networks is the ability to learn automatically a variety of filters in parallel specific to a training dataset under the constraints of a specific predictive modeling problem, such as image classification. It applies the resulted features to categorize input images. There are many pre-trained models for CNN. Figure 1 shows an example of the layer hierarchy and ordering in any CNN network.



Figure 1. CNN network architecture

#### 4. System Architecture

Figure 2 illustrates the design of the proposed architecture.



# Figure 2. Flow diagram of the proposed framework for malaria cell detection

#### 4.1. Data Acquisition

For the investigation of the proposed network, we use the dataset from the Lister Hill National Center for Biomedical Communications. It would consist of blood smear pictures for the experimentation of malaria diseases if they were fit-healthy or malariainfected. Figure 3 shows an example of a cell image within the dataset.

This dataset includes 27,558-segmented images. Among them, half of them (13779 RBC Images) are parasite images and the rest half

(13779 RBC images) are non- parasite images [10]. The ratio of the two class's samples is 1:1.



#### Figure 3. Red blood sample images (a) Parasitized cells (b) Uninfected cells

#### 4.2. Data Preprocessing

Preprocessing is a common name for operations with images to improve the level of abstraction before doing the classification. It suppresses unwanted distortions or enhances some image features important for further processing. In this work, to achieve categorical classification, change all labels into two classes by utilizing Keras utils bundle. The following facts are the methods that exist in our preprocessing steps:

- 1. Perform randomization to get good redistribution of the pictures.
- 2. Rotate the image randomly by 50 degrees.
- Flip the shape of images to get the arrays of 64 in each width and height, the channel into 3. Set this metric to all images to have the same dimensions.
- 4. Then, normalize all images with dividing by 255.

#### 4.3. Data Splitting

Divide the images into three parts to prevent from over fitting: a training, testing, and

validation set. We performed cross-validation through five different forms to avoid the challenges of the model biasing and ensure generalization errors. Each form of crossvalidation contains the following number of cells as in table 1.

K-Fold	Uninfected	Parasitized
1	2757	2756
2	2758	2758
3	2762	2776
4	2760	2832
5	2742	2657
Total	13779	13779

#### Table 1. Cell count for cross-validation

#### 4.4. Feature Extraction

Feature extraction learning in Deep non-handcrafted approaches performs on features, unlike the classical approaches. To get better results more correctly, chose certain promising features from cell images that help for the categorization task. The proposed architecture learns in its first convolution layer for detecting features like colors and edges, cell counting. This can carry out to differ between the normal and infected cells within the deeper layers.

#### 4.5. Classification with ResNet50

Scientists developed a deep residual model using over a million pictures from the popular ImageNet database called as ResNet-50, an acronym for Residual Network. This model is a kind of conventional CNN network. The 50 in its name represents the number of available layers. The network can learn from a giant representation of features for a rich of images. Before the evolution of ResNet, deep neural networks encountered a challenge in the vanishing gradient problem i.e. when the model begins to do backpropagation, the gradient starts getting littler and littler. ResNet consolidates identity shortcut connections, which essentially skirt the training at least one layer—a remarkable advantage.



Figure 4. The ResNet50 architecture

The ResNet-50 model has five steps, and each step consists of a convolution and Identity block. Unlike traditional neural networks, a network with Identity blocks layer feeds into the next layer about 2–3 hops away without feeding into the continuous next layer. This process is identity connections.

- 1. Zero padding pads the input image.
- 2. The convolution step is the first step before entering the common layer. It extracts features from input cell images. There are three

convolution layers in each convolution block and each identity block has three convolution layers.

- 3. BatchNorm adjusts the input layer to increase the performance of the network.
- 4. ReLU layer a piecewise linear function within the network. It is the activation function and enables to transform the addedweighted input from the node into the activation of the node or output for that input.
- 5. MaxPooling accumulates features from maps generated by convolving a filter over an image. Its function is to reduce the spatial size of the representation, to reduce the number of parameters and computation in the network.
- 6. An average-pooling layer performs downsampling. Flattening have not yet any hyperparameters or name.
- 7. The Fully Connected layer reduces its input to the number of classes using a softmax activation. It categorizes the input image using the capabilities from the previous layer output relied on the training data.

#### 5. Result and Discussions

The system builds a ResNet50 architecture using Keras 2.2.4 with Tensorflow 1.13.1 backend. The system in which the experiment was carried out runs on Windows 10 and has a RAM 8GB and no graphic processing unit (GPU) were used.

The task, which is at hand, is a binary classification of images. Therefore, this system uses the sigmoid activation other than softmax because sigmoid performs well with binary classification. The system uses the batch size 100. Dividing the total objects in training with batch size calculate steps per epoch for training.

After preprocessing, the model has to be compiled. Then, some parameters such as optimizer, loss function, and metrics are calculated. The optimizer is the key elements that enable the network to work on the data. The optimizer used for this model is Stochastic Gradient Descent (SGD). SGD optimizer performs better than other optimizers do. Selection of a loss function is a difficult task. This model uses Categorical-Cross Entropy to find the loss.

The metrics measured during the training of the dataset were Accuracy and Loss. Figure 5 describes how many loss measurements are achieved in the training and validation through various epochs.



**Figure 5.** Loss function Vs epochs

We represented the classified data with the confusion matrix. In the confusion matrix, it consists of True Positive (TP), True Negative (TN), False Positive (FP) and False Negative (FN). We also represented other different metrics in the classification report: accuracy, f1-score, and error rate for the classification problem. The ratio of calculation and correctness of the process is measured with the sensitivity and specificity metrics. Then, we compared the performance of the proposed system with two other popular deep learning models, GoogleNet and InceptionNet.



Figure 6. Accuracy metric

Figure 6 illustrates the accuracy curve of this system and Table 2 describes the performance score of the model.

**Table 2.Performance metric of models** 

Model	Res- Net50	Google- Net	Inception -Net
Accuracy= TP+TN / TP+TN+FP+ FN	94	90	87
Sensitivity= TP/TP+FN	0.96	0.9	0.88
Specificity= TN/TN+FP	0.92	0.87	0.83
F1-Score	0.94	0.9	0.85
Error Rate	0.06	0.1	0.17

#### 6. Conclusion

Of course, can use other popular pre-trained deep networks like those that AlexNet, GoogleNet, or InceptionNet for this system, but ResNet-50 can solve for excellent the generalization performance with fewer error rates on recognition tasks. Therefore, resNet-50 is a useful tool to know for computer-assisted malaria cell diagnosis. In previous researches before the evolution of ResNet, scientists presented а problem in training deep convolutional neural networks. When appearing ResNet, they overcome that issue. Besides, ResNet50 can skip at least one layer, unlike conventional networks.

In this work, we applied a data augmentation technique to the training set that shows promising results compared to other traditional machine learning techniques, which require rigorous feature engineering and complex data pipelines as seen in the literature. This work can be extended to analyze more forms of infection problems in the RBC. Using proper datasets consisting of sufficient data, it can also estimate the different stages of malarial infection. We can create more improved, which looking for infected cells by using self-contained hardware consisting of a digital microscope connected to a Raspberry Pi 3 and a blood sample-collecting device. Use a different version of this approach to find fractures and defects in bone structures from X-ray images.

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### An Effective Skin Diseases Detection Using Different Segmentation Methods

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#### Abstract

The skin is the outer surface of the human body and is the largest organ of integumentary. Skin pigmentation varies among different people and skin type can be either dry, oily or Melanocyte in human skin combination. produces melanin, which then absorbs harmful UV rays in the sun, causing skin damage and diseases. The some common diseases are namely that acne. eczema. melanoma. scabies. warts. cellulitis, etc. If the symptoms of the skin diseases are not treated at an early stage then it can cause many health problems and even death. Image segmentation plays an essential role to extract around infected skin disease region. In this paper, various segmentation methods like canny edge detection, adaptive threshold method and k-mean clustering have been used to detect the skin diseases namely that melanoma, scabies and cellulitis from the given image set. Depending on the segmentation methods is detected at the result output for a corresponding input skin disease image.

**Keywords:** *Edge detection; Adaptive threshold; K-mean clustering; Melanoma; Scabies; Cellulitis;* 

#### 1. Introduction

The skin is the largest organ of the body that covers and defends from outside attacker. Skin has three layers: the epidermis, dermis and hypodermis. The epidermis is the outermost layer of the skin that protects barrier over the body's surface and creates our skin tone. The dermis is below of the epidermis layer that involves connective tissue, hair follicle and sweet glands. Hypodermis is the deepest of the skin layer that function is to connect the skin to bone and muscle [5].

Skin diseases can be temporary or permanent, and may be painless or painful. Some have situational causes, while others may be genetic. Melanoma is the most dangerous type of skin disease. It is the less common although it is the most serious. Melanomas can growth anywhere on human body. The sign of melanoma are changing of existing mole and the development of a new pigmented or unusual growth of skin. Cellulitis is a skin disease that occurs when bacterial infection of the deeper layers of skin. Bacteria can enter human body through cuts and bites. Cellulitis can affects the skin of the lower legs and anywhere human body or face. The symptoms of cellulitis are redness, swelling, warmth, chills and fever. Scabies is propagating skin to skin touching and then sharing an infected person's clothes, towel or bedding. The main symptoms of scabies are intense itching and a rash in areas of the body. Scabies can affect wrist, elbow, armpit, waist, buttocks [8].

Automatic segmentation is aimed to benefit early detection of the skin disorder. Manual operation is depending on fixed visual quality inspection performed by human operators, which is time consuming, slow, inconsistent and costly. There are many benefits by using automatic detection system such as less labor, low cost, fast and reliable result for detection of diseases affection region [2]. In this paper, the acquired skin image is preprocessed by using histogram equalization and average filter method. After preprocessed, image segmented by canny edge detection, adaptive threshold and K-means clustering techniques are proposed to detect around the skin disease region.

This paper is created into five sections. Section 2 describes related work of this work. In section 3, we describe the proposed method of the system. Implementation result and analysis is described in Section 4 and conclusion is given in Section 5 of this paper.

#### 2. Related Works

In many different fields, there is a lot of research done on image segmentation using different methods. Also, there are different applications of the image segmentation. Some of the existing works are discussed in this section.

Sonali, Raju Shikha [1] proposed an efficient approach of image segmentation for skin cancer detection. First, they have done image acquisition and then convert RGB image to gray scale. After color conversion Otsu, K-mean and GVF methods are used for image segmentation. Next, features can be extracted by using Asymmetry Index, Border, Color Index and Diameter and then TDS are calculated. Lastly, TDS score determines the presence of Melanoma skin cancer by classifying it as a benign, suspicious or highly suspicious skin lesion.

A.Ranichitra, D.Seethalakshmi [2] proposed a comparative analysis of segmentation techniques to extract skin lesion regions. They used three segmentation techniques and compare performance of these techniques by statistical features mean, contrast, energy and standard deviation. Arneesh, Akhilesh [3] focused their research on skin diseases namely that eczema, chicken pox, psoriasis and ringworm. They used various segmentation methods of the image processing techniques.

The presented work of this system is intended at successfully detecting skin diseases namely melanoma, cellulitis and scabies using different segmentation methods. This paper will assist to find the most appropriate segmentation method for three skin diseases. Three segmentation methods are implemented on the images of each of the three skin diseases using open CV of python and the different results of each dataset are detected.

#### 3. Proposed Method

The proposed method consists of three basic shown in Figure1. Firstly. image steps acquisition of the system and then preprocessing is done by removing unwanted noise various of input image. Next. image segmentation methods are used likely canny edge detection, adaptive threshold method and k-mean clustering. Lastly segmented output result image is displayed.





#### 3.1. Image Acquisition

Image acquisition is an initial stage of the system because, without an image, no processing is possible. In this system, available images from the skin diseases patients or internet are also taken. Figure2 show the sample image data set for melanoma, scabies and cellulitis.







Figure 2. Sample data set image (a) melanoma (b) scabies (c) cellulitis

#### **3.2. Image Pre Processing**

Image pre-processing is to enhance image quality by eliminating unwanted data of input image [6]. In preprocessing steps involve resizing the image, RGB to gray scale reduction conversion. noise and image enhancement [9]. Firstly, input image is resized to adjust uniform  $300 \times 200$  sizes and then resized image converted RGB to gray scale format. The average filter method is used for image smoothing and noise reduction. The histogram equalization is applied on the image to enhance the brightness, sharpness and contrast.

#### **3.3. Segmentation Methods**

Image segmentation is a method that divides an image into disconnects places that are correlative in some features, such as intensity, color, or texture [1]. We implemented three segmentation methods in this proposed work.

- Canny edge detection
- Adaptive threshold method •
- K-mean clustering

#### **3.3.1. Canny Edge Detection**

Canny Edge Detection is a popular edge detection algorithm among user [7]. First step of this process, Gaussian filter is used to eliminate the unnecessary data in the image. Second is finding intensity gradient of the image. Then two threshold values, minimum and maximum are considered to decide all edges. If the intensity gradient magnitude is greater than maximum threshold value is denoted as the "edge". If the gradient magnitude is smaller than minimum threshold value is to be not edge, so discarded. Lastly canny edge detection is done.

#### 3.3.2. Adaptive Threshold Method

Adaptive threshold is the method where the threshold value is calculated for smaller regions. Therefore adaptive method is different threshold values for different regions [3].

In this segmentation process, two adaptive functions "ADAPTIVE THRESH MEAN" and "ADAPTIVE THRESH GAUSSIAN" functions are used to calculate the threshold value from the image which makes it easier to decide the neighborhood area. If the foreground is obtained not empty, then the process is repeated. If the foreground is empty, then the pixels at the background are denoted. Then, the adaptive threshold segmentation method is done.

#### 3.3.3. K-mean Clustering

K-mean clustering is a partitioning method of the image that collects of data into a k number of cluster [4]. It divides a given set of data into k number of discontinuous clusters. A set of data points and a set of centers are considered in the image [3]. Using three cluster points are randomly considered from the image in our experimental result. The segmentation process is completed by reducing the sum of squares of distances between the objects and the corresponding cluster or the center of mass of the object.

#### 4. Implementation Result and Analysis

The implementation tools of this system used are openCV, pycharm IDE and python. The implementation outcomes are shown in the following figures for the input and corresponding output images of the skin diseases- melanoma, scabies and cellulitis by using three segmentation methods.



#### Figure 3. (a) Input image for cellulitis (b) result for canny edge detection (c) result for adaptive threshold method (d) result for kmean clustering

The input image and corresponding output images of cellulitis diseases are shown in Figure3. Cellulitis is best detected by using canny edge detection method. In adaptive threshold method, the around disease area has not been properly identified and there are still noises. In k-mean clustering method, the features of the infected image are undetected according to the presence cluster.



Figure 4. (a) Input image for melanoma (b) result after canny edge detection (c) result after adaptive threshold method (d) result after k-mean clustering

In Figure4, input melanoma disease affected image is shown and different segmentation methods are applied. Figure4 (b), (c), (d) are showing the result of the segmented image after canny edge detection, adaptive threshold and kmean clustering. In our implementation result, kmean clustering is best segmented for melanoma skin diseases. In adaptive threshold method, the result output image consists of too many noises and canny edge detection to be losing information of image.



(9)

(c)

the signal-to-noise ratio can also be defined as the ratio of the RMS noise and net signal. A Root Mean Square Noise is described as the square root of the mean of variances from the background region. The below Table 1 is decided by SNR values of the results disease infected images using different segmentation methods to find the obvious results.

(")	(6)		
X			

(h)

(**d**)

#### Figure 5. (a) Input image for scabies (b) result after canny edge detection (c) result after adaptive threshold (d) result after k-mean clustering

The input scabies disease image and corresponding output images are shown in Figure5. Output result image for canny edge detection is shown in Figure5 (b). During the time of canny edge detection process some edges around the disease region are detected. But the disease region is not effectively entire segmented. Figure5 (c) is the output image using after adaptive threshold. In adaptive threshold method, specific information is distorted caused by the existing noises and the result output image is not clear. Figure5 (d) is shown the output for k-mean clustering method. K-mean clustering method is the best segmented for scabies skin diseases in our experimental results.

In general, signal-to-noise ratio (SNR) is the ratio between the average signal value and the standard deviation of the background. Especially,

Table 1. SNR v	alues for	<sup>•</sup> three	skin	diseases
using differen	t segmen	tation	metl	nods

Diseases	Segmentation Methods		
	Canny	Adatpive	K-mean
Melanoma	13.3715	10.9837	19.7523
Scabies	7.8643	10.2284	22.6643
Cellulitis	19.7594	14.5826	12.3279



#### Figure 6. Comparison of segmentation methods with SNR values for skin disease images

The precision of feature calculation assists to the result of image segmentation. determine Comparison of segmentation methods with SNR values are showed in figure6. The higher SNR more optimal values. the and accurate

segmentation method. Therefore, according to the segmentated result collected from the SNR values, it can be considered melanoma and scabies can be best detected by k-mean clustering. Canny edge detection is optimal segmentation method for cellulitis diseases.

#### **5.** Conclusion

In this paper, we implemented three segmentation methods on some skin diseases namely- melanoma, scabies and cellulitis. This system is intended to save time and money of the skin disease affected patients. The proposed method used openCV with the help of python to perform basic detection for improved image segmentation. From the observed result, k-mean clustering is best method for melanoma and scabies disease. The canny edge detection is best method for cellulitis skin disease. This system is designed to help and support for doctors in determology fields using image processing techniques. In future work, this methods can also be tested on a large dataset consisting of classification for many diseases.

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