# Predictive Modeling for Disease Diagnosis: Malarial Cell Detection

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Abstract— Disease diagnosis is a crucial medical research area, and in this study we put up an innovative model for predictive modeling, with the primary focus being on the diagnosis of malarial cells. Today Malaria hold one of the main positions on the list of public health problems worldwide, that's why the early and accurate diagnostics of this disease are vital to timely and qualitative treatment and control of it. We try to apply the Machine learning method, especially those deep learning algorithms, image processing schemes, to create a reliable model that can exactly foresee the malarial cell on microscopic images. Our main accomplishments are the development of our malaria cell image repository, design and train the deep leaning architecture to extract features and classify, and test our model and compare the frame with the latest benchmarks.

Keywords—CNN, Malaria, Transfer learning, Deep Learning

#### I. INTRODUCTION

Malaria being the serious global contagion of tropical origin is endangering 3.2 billion people, which is approximately 42% of the world's entire population. The World Malaria Report states that during 2015 almost 200 million new cases were recorded and malaria is approx 438 thousand deaths are associated.[1].The formal diagnosis of malaria requires inspecting of the slides prepared from the blood samples using a microscope, the procedure remains the best criterion even after the introduction of new methods.

Supposedly, manual microscopy is extremely efficient for diagnosis, it takes labor hours, though, to be mastered in this field one needs to be a trained expert. Nonetheless, in rural areas where malaria is prevalent and not everybody can adequately conduct microscopic examinations, there studies have shown it's main weaknesses.

Deep learning can improve the classification of cell images to lower misdiagnosis mainly based on inadequate data, and associated hurdle. Non-medical fields is where ML in the domain of Health can achieve tremendous and impressive progress. Nevertheless, as the medical field has been less frequent in applying this technology, the obstacle has been whether the experts could manage this territory and the privacy be maintained. [2]

Despite that a deep learning has not become a default tool in many fields it should be noted that this tool is now used more frequently in many disciplines. [3] An important achievement was the application of Convolutional Neural Networks (CNNs) in malaria diagnosis, as presented by Liang et al. it has been found that the computer-assisted classification of such images by CNN-based methods provides good classifying results in respect to medical imaging tasks.

By and large, each year, numerous blood films are scrouped over by the skillful professionals to find malaria, which include the manual counting of parasites and infected red cells of white blood cells. Consequently efficiency of the method highly depends of the microscopist's knowledge and skills. [4] In resource-censored environments with a lack of support systems for maintaining the quality of the skills, the diagnostic accuracy gets compromised, as decision-makers might land to incorrect diagnostics.

# II. LITERATURE REVIEW

This literature review will research the available studies on the utilization of deep learning in detecting malaria. [5] Fraction will focus on the papers that involved deep learning [algorithms] with special attention to Convolutional Neural Networks (CNN's) for the recognition of malaria-infected cells in microscopic images.

The model exemplifies itself as the best among previous studies with its capacity to detect malaria cells and the possibility to improve the diagnosis exactness. This also creates an increased scope for utilization of deep learning in healthcare, leading to evolution of artificial intelligence and machine learning algorithms. Even though including microscopy and RDTs has their limitations, deep learning still stands a more preferable option and more recently CNN plays a vital part in medical image classification. In this work, the purpose of the model is to supply the Inception-V3 network, which is considered to be effective due to its complexity and having reduced parameters. It is pre-trained from a greater dataset. [6]

There are models that explore in detail the role of CADx systems in the diagnosis of malaria including an in-depth discussion on the data transformation feature, performance of deep learning based models, independent testing for generality,

and the application of both conditional image synthesis and class imbalance for malaria diagnosis. It gives a summary of how that study has contributed to cancer diagnosis with the deep learning technology. [7]

Malaria detection is another difficult task, especially in rural areas, because manual detection method is labor intensive and its diagnostic accuracy is low. It is recommended to establish automated diagnosis systems to overcome shortcomings of manual microscopy. [8] It involves the segmentation of the red blood cells (RBC) and the feature extraction like thresholding, clustering, morphological operations and Hough transforms; while it will also deal with machine learning methods for the classification of malaria parasites. Thus the proposed model has RBC count using the starry skyline Hough transform and automated parasite stage classification governed by machine learning techniques such as MLP, LDA, SVM and WSELM.

Some study proposes a using of new image analysis approach for high content screening of drugs tolerant to malaria, it is able to separate the living and infected blood cells from the dead cells and such as trophozoite stages of malaria parasite. [9] The performance of the algorithm is validated by the total manual calculation amount of infected and non-infected red blood cells (RBCs) across many picture fields and the similarity of the parasitological effective concentration 50 (EC50) values for chloroquine and artemisinin with conventional methods.[10]

The model can be using the Inception-V3 architecture for malaria cell image classification, training it on a dataset of 27,558 images with three scenarios using different optimizers: SGD, RMSProp, and Adam. [11] The case of such RMSprop approach gives the results of the highest accuracy of 97% and the lowest value of loss. The study too end uses' data augmentation methods to improve model's operations and minimize overfitting in order to do so, they used such operations as rotation, flip, and zooming. [12]

Among the articles touches on the infinite danger of malaria in Africa, where it is associated with latent economic stability and infrastructural health systems. It therefore can serve to demonstrate deep learning models (CNNs) for malaria detection in terms with its architecture and low computational requirements. [13] The structure of this model aims to automate malaria detection along with high accuracy through leveraging CNN's image processing techniques well, even when image resolution is low and large volumes of images are needed for dataset discrimination. [14] Moreover, the technique can reach a high level of accuracy without the need for GPU processing and greatly reduce the evaluation time, therefore having a good potential for computationally efficient malaria diagnosis. [15]

One author presents a new image analysis algorithm based on model designed mainly for detecting and classifying the Plasmodium lifecycle stages and distinguishing between healthy or raised to death parasites in the drug-treated blood samples. The algorithm makes up the red cells counts and also flag parasitized erythrocyte based on specific dye staining. The investigation was authenticated with the measured parasite stage count via manual counting and quantitive analysis of clocks synchronized cultures. [16] In addition, the algorithm calculated the parasite concentration 50 effective concentration (EC50) values revealing that they are similar to the conventional

inhibitory concentrations dosages measured through standardized assays. [17]

However when compared with other proposed algorithms this one is highly accurate in the estimation of red cells counts as well as that of the parasitized ones from relatively stained erythrocytes in fluorescence images. Its performance was validated by the verification of the record using manual counting and analyzing the asexual parasite stages by syncopation cultures. [18] Moreover, the available algorithm provided the parasitological effective concentration 50 (EC50) value for chloroquine and artemisinin found to be identical to the known inhibitory concentrations determined through conventional assays. [19]

While one author serves as the pioneer of the newized Convolutional Neural Network (CNN) model which is referred to in the work as Malaria Convolutional Neural Network (MCNN) for the purpose of recognizing malaria pictures. The MCNN model strikes down the job of doing this manually work by itself and by way of its own, deep learning-powered approach of complicated image pattern recognition, the MCNN model can be used for medical analysis. [20] The model performed well with high specificity, sensitivity, and precision of 0.9929, 0.9848, and 0.9859, respectively and exceeding other researches in this direction. Transfer "learning" was implemented with pretrained models such as Inception V3, ResNet50, and VGG19 for efficiency. [21] The data preprocessing involved adding some padding and normalization for good model training and testing. The MCNN model drew attention for its efficiency and speed at malaria diagnosis, which suggested a lot of promise for the real-word medical practice. [22]

Study on Malaria Cell-Image Classification using Transfer Learning model including InceptionV3 for feature extraction and SVM (Support Vector Machines) for classifying, has an accuracy of 94.8%, overcoming the challenges of image classification. [23] The InceptionV3 is leveraged as a pretrained model to earlier the bottleneck layer, after which there is a custom fully connected dense layer, with an L2 regularized linear SVM classifier being used to classify. The dataset has data split into the training (20,000), validation (3,000) and test (3,560) sets, which are augmented. The model utilizes Google Colab as a platform to learn some parameters, the paper shows a way it almost classifies malaria infected cells with high accuracy which can be improved with further training and tuning of hyperparameters. [24]

While the former study outlines a computerized approach for classifying malaria cells via ResNet-50 CNN model, the latter focuses on building an Electron Microscopy tool for quick-response detection of bio-threat agents. [25] The automated system is created in such a manner to enhance the accuracy of diagnosis and decrease dependence of people on humankind by employing the transfer learning approach for feature extraction and classification of the blood cells as being parasitic or not. [26] The set of images consist of tags from Bangladesh, and preprocessing steps such as randomization, resizing, normalization and categorical classification are employed before implementing the algorithm. [27] The proposed computer system was able to identify blood smears with 95% accuracy on average, which is a perfect example of how

automated microscopy can be used as an inexpensive and solid malaria diagnostic tool for communities which are underserved in terms of resources. [28]

Papers that we covered included deep learning model based on light weight concept that is used for the detection of malaria parasites in blood smears images ought to have been referenced. [29] The model, a newly networks based on Convolutional Neural Network and transfer learning, has an amazing accuracy of 98.85 and sensitivity 98.79 and specificity 98.90 which get data fast and does not need much of input size. It employed a dataset of 27,558 RBC image segments randomly selected and mimicked from the National Library of Medicine repository. [30] The merit of the model is demonstrated through its high pace and accuracy, especially critical factor in areas with limited medical care. [31]

This first paper focuses on classifying images within JPEG composition in the context of detecting malaria infection using JPEG encoding domain. [32] This research investigates the possibility of sorting out pictures in the JPEG already compressed form itself, allowing sparing decompression and manipulating the process in such a way to make it more efficient. [33] The authors can estimate images by using an LSTM network to classify normal and malaria-infected red blood cells by means of different DCT coefficient and bitstream settings. The LSTM model obtained the classification accuracy using coded DC values (around 80%) but it also resulted in the classified accuracy exceeding 90% when using only coded DC values. [34] The study proves the possibility of processing images into identifiable categories even when they are in compressed state, which is highly effective in saving memory as well as computation time. Such approach could be used as a base for other deep-learning classification data analysis. [35]

This study presents a deep learning technique for malaria recognition from blood cell pictures that apply to a Convolutional Neural Network (CNN). The suggested CNN model applies a 5-fold cross validation technique which provide superb accuracy and better results than the existing ones in malaria detection. The provided model evaluates performance via, such scoring metrics like F1 Score, AUC Score, specificity or sensitivity.[36] The CNN architecture comprises three convolution layers, a couple of max pooling layers, ReLU activation functions, and at the output final batch, a sigmoid activation function. Combined with Adam optimizer and binary cross entropy loss function, the model applies to NIH Gov's Official Malaria dataset with resized 64x64x3 images, which generate high training and validation accuracies The model achieves a test accuracy of 99.44% which gives confidence in its robustness, and enables its use in a real-time deployment for medical diagnosis with high levels of precision. [37] This could be highly useful in malaria diagnosis where the availability of health professionals is limited or by providing time for the healthcare professionals to focus on other aspects of health care.

One used a well-designed propitious CNN model for classifying red blood cells of malaria- infection in the digital image and Malaria RBC dataset respectively CNN models comprised of distinct architectures were formulated, namely, Model A, Model B, and Model C, that were then trained using

these data set. It uses models that are efficient in classifying data, have limited model complexity, and it uses dropout regularization to prevent overfitting. Several augmentation methods were used to improve the learning process, whereas a median blur filter was applied especially for reducing noises in malaria images. The observed feasibility of the models was underpinned by the accuracy achieved. [39] These accuracy levels were high, with Model C reaching 99.22% on the original Malaria dataset. [40]

Another paper suggests a hybrid algorithm for image classification malaria which combines Convolutional Neural Network (CNN) for features extraction with K-Nearest Neighbor (KNN) for classification It aims at Plasmodium vivax and Plasmodium faliciparum parasites killing in different phases and finds optimal k-values for the KNN, which is able to achieve high accuracy. [41] The accuracy of the whole system constitutes 89.58% and exceeds other methods like SVMs and GLCM-KNN. [42] This determines that the hybrid model is better. The model architecture includes feature extraction with CNN in the first stage, then performing KNN classification. It is possible to know image data type and illumination effects on classification confidence are the critical. [43]

## III. METHODOLOGY

## A. DATASET

The database of 27,558 images of red blood cells (compared in the "parasite" and "non-parasite" group) forms the basis for training and evaluation of deep learning models for malaria diagnosis. The department dedicates 22,000 images to the learning model and retains 5,500 images for monitoring performance during training to reduce the risk of overfitting. [44]

# B. PROPOSED MODELS

#### 1) EfficientNetV2L:

This section will present the model and the EfficientNetV2 architecture is used and a basis for this research. The Oxford Institute laboratory personnel came up with an efficientnetv2L variant used in the training. The model architecture can be seen as the EfficientNetV2L with ImageNet weights and then being fine-tuned during the training. The input is the 224x224 x3 size images and the RGB colors, which are input in the input layer. Through the implementation of a systematic data augmentation scheme, our approach is founded on random flipping, rotation, zoom, contrast and Gaussian noise adding, thus enhancing model robustness. The architecture is mainly composed of 3x3 strided convolution layers, with max-pooling layers of size 2x2 apart, and global average pooling in shape at the end. In here the last dense layer comes with the SoftMax function for the purpose of binary classification. It is added up that the neural network incorporates around 160 million parameters in which, the fully connected layers, account for the majority of these. [45]

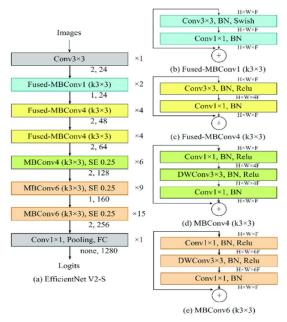


Fig. 1. EfficientNetV2L architecture

# 2) MobileNetV3Large:

The MobileNetV3Large model that is used here shows that it has outstanding performance in the computer vision task. MobileNetV3Large, which was developed by Google research, turned out to be a real breakthrough in its field: therefore, the model is the most efficient and at the same time it provides excellent accuracy in the processes of the conservation. It is right after that, the excellent outcome: this network becoming stateof-the-art in ImageNet localization and classification challenge. The mechanism consists of pre-trained lines and layers subsequently coded separately for each specific mission. Due to the input images sizing of 224x224 by 3 there are 2 training stages where the loss is applied in a stochastic gradient descent model. There, the second loss part is quadratic. The proper tuning of the learning rate schedule and model check-pointing mechanism are sure to conduct the experiment with more significant effectiveness. MobileNetV3Large, however, ensures efficiency and tackles parameter inefficiency in contrary to cropping-oriented models like VGG to a certain extent to bring some improvement in accuracy. [46]

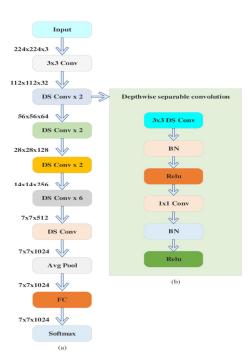


Fig. 2. MobileNetV3Large

# *3) InceptionResNetV2:*

InceptionResNetV2 model that is one of the popular training models in advanced convolutional neural networks is deployed in this study. Google came up with the InceptionResNetV2 model and the experimental result demonstrated its high effectiveness in image recognition tasks, which have often been demonstrated to be superior in many benchmarks.[18]. Due to its ability to be used with [ImageNet] as a pre-trained model and then given an additional augmentation and fine-tuning to support input images of size 224x224x3, the base model has become the foundation of the system. [35] The architecture consists of a set of convolutional layers, preferably multiple and in sequential order, with the final layer being the global average pooling layer for feature extraction. This thick layer has even softmax. Thus, it is suitable for the procedure of providing answers into two classes. It is the SGD model with a learning rate of 0.001 and momentum of 0.9 that is optimizing a categorical cross-entropy loss function. The question of model performance is monitored through the best weight saving system using a checkpoint mechanism. The training algorithm lasts for 20 epochs, and it helps the model converge and change the nature of refinement. [47]

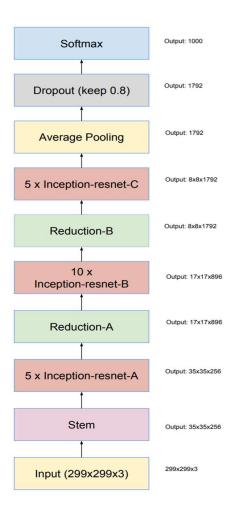


Fig. 3. InceptionResnetV2

## IV. RESULTS

The training process on the Kaggle platform equipped with P100 GPU acceleration with the accuracy and loss of training and validation datasets was kept recorder. Additionally, the extremely intensive computation nature of these models is the cause behind the hours-long training process. In Table 1 below, the table is dedicated to data particulars including the training accuracy, training loss, validation accuracy and validation loss respectively to three model variants: EfficientNetV2L, MobileNetV3Large, and InceptionResNetV2. The images from 4 to 9 explains the accuracy vs Epoch and Loss vs Epoch during complete Training process.

TABLE-1 MODEL METRICS

MODEL	Training Accurac y	Trainin g Loss	Validatio n Accurac y	Validatio n Loss
EfficientNetV2L	0.9696	0.0874	0.971	0.0865
MobileNetV3Larg				
е	0.99	0.001	0.973	0.1456
InceptionResNet				
V2	0.969	0.088	0.971	0.086

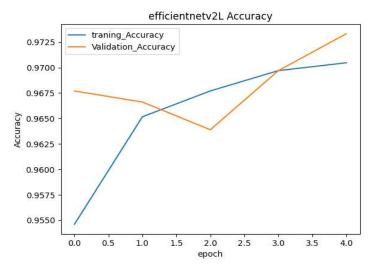


Fig. 4. Graph of Accuracy for efficientNetV2

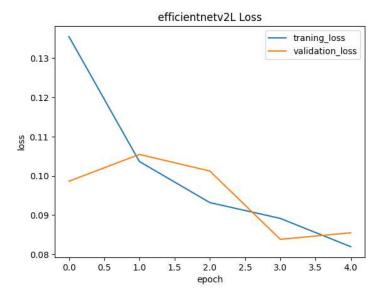


Fig. 5. Graph of Loss for efficientNetV2

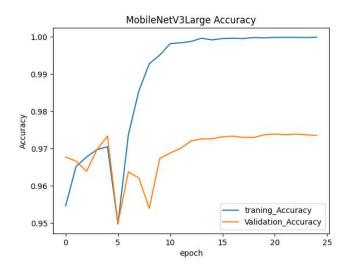


Fig. 6. Graph of Accuracy for MobileNetV3Large

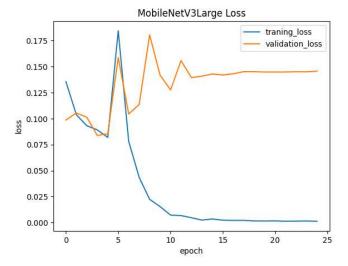


Fig. 7. Graph of Loss for MobileNetV3Large

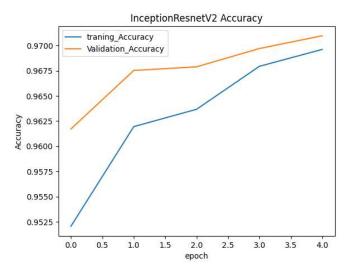


Fig. 8. Graph of Accuracy for InceptionResNetV2

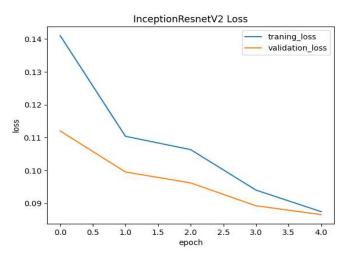


Fig. 9. Graph of Loss for InceptionResNetV2

## V. CONCLUSION

This study contributes to a new trend in diagnostics applications, which use CNNs, for the accurate detection of malaria from cell images. It utilizes a large dataset of 27,558 red blood cells images for demonstrating the ability of the deep learning algorithms to identify innocent cells. Thus, here, the power of deep learning in medical imaging is recognized based on the possibility of finding cancer.

The research leads to the conclusion that automated diagnostic system is a revolutionary advanced in detection of malaria diseases especially in poor areas. That way, it allows medical diagnostics to achieve much higher accuracy and efficiency.

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