AN INNOVATIVE ENSEMBLE LEARNING METHODOLOGY FOR THE IDENTIFICATION OF MALARIA USING MICROSCOPIC RED BLOOD CELL IMAGES

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ABSTRACT

Malaria is a potentially fatal parasite illness transmitted by female Anopheles mosquitoes that are infected. Microscopists are able to identify this disease by studying the sample of microscopic pictures of red blood cells.   The detection technique necessitates the expertise of a professional microscopist, which may take less time and yield subpar results when used to large-scale diagnosis.   Infectious and noninfectious erythrocyte images are collected and processed into models of transfer learning like as CNN, densnet201, Nasnet large, InceptionNet, Xception, Hybrid (CNN + DenseNet201 + NasNet Large + InceptionNet + Xception), KNN, SVM, Mobilenet, VGG16, Resnet50, InceptionV3, Densenet169, Resnet101, Lenet, efficientnetV2S which are all trained on the same dataset which is taken form Kaggle and augmented. The methodologies involving transfer acquisition and fine-tuning are utilized, and the results are compared. but the efficiency is very less, with individual method. Therefore, in this work we introduce an innovative methodology, utilizing ensemble learning in combination with deep learning techniques to accurately detect malaria parasites in red blood cells Images.   Resnet50(Residual Network), Inception (googlenet), and DenseNet201 are three techniques utilized in employing an weighted average ensemble method.   To decrease the variability in estimations, a technique called max polling cluster is employed together with weighted average collaborative models.   Diverse image processing approaches, such as the data expansion technique like augmentation, boost etc. are employed to improve dataset and address the issue of overfitting in the model.   Additionally, other methods such as tradition CNN, Transfer Knowledge, and CNN-ML classifier procedures are utilized to assess their effectiveness in comparison to ensemble learning pattern.   The model that has been suggested in this paper achieves better efficiency compared to other techniques discussed in literature survey, With a precision of 96.87%, it successfully distinguishes between parasitic and healthy cells.   Hence, the method employed for deep learning possesses the capability to precisely and autonomously detect malaria.

Keywords: *Analysis ,Deep Learning, Malaria Disease, Machine Learning and Classification*

1.   INTRODUCTION

Malaria is a debilitating disease that has potential to be lethal. The primary mode of disease transmission is by the act of being bitten by an infected Anopheles mosquito.   Mosquitos that are infected harbor plasmodium parasites.   Malaria is spread by the bite of a mosquito, who is diseased and subsequently bites another individual who is not afflicted. Once parasites reach maturity, they migrate to liver, the parasites swiftly enter the circulation and immediately begin the infection of blood vessels within a few of days.   Malaria may also be transferred via transplants of organs and blood transfusions. Transfusions and the use of contaminated syringes and needles.

Malaria is the predominant disease across tropical and subtropical areas. Regions characterized by fast proliferation of parasites.   Based on the The most recent edition of the Global Malaria Study anticipated that, In 2020, there were a total of 241 million reported cases of malaria.. Marginally more in comparison to 227 million in 2019.   An estimation was made that In 2020, the number of fatalities caused by malaria reached to 627,000. Children below the age of 5 are in the most precarious situation.   In 2020, the global mortality rate for children due to malaria was 80% [20]. The effect of the above disease on can be analyzed by performing Opinion Mining [41] on the data retrieved from Social Media platforms using varied methods [42].Malaria is caused by Plasmodium

parasites. There are five distinct malaria parasites that may infect humans. The following are the species of malaria parasites falciparum, pneumonia vivax, ovale, malariae, P. malariae, & P. knowlesi[1]. Malaria symptoms usually manifest after a period of 10 to 14 days following the first infection. In certain instances, there may be a delay of many months before symptoms manifest. Common symptoms of malaria include intense shivering, high fever, muscular discomfort, excessive perspiration, headache, vomiting, bloody stools, stomach pain, diarrhea and nausea[5]. Malaria can induce jaundice, a condition marked by the discoloration of the outermost layer of skin and eyes to a yellow hue as well as anemia, due to the depletion of red blood cells. Failure to immediately treat the infection might result in renal failure, cognitive impairment, unconsciousness, seizures, and mortality [9]. To determine whether someone has malaria or not Multiple tests are accessible.

Fig. 1 Proposed Methodology.

The most prevalent and precise examination refers to the process of doing a both thin and thick blood sample test. Microscopists using a microscope to identify parasites within red blood cells. This examination needs the expertise of skilled and seasoned microscopists. An alternative choice is a prompt diagnostic examination., sometimes known as an antigen test. In the absence of microscopy, a fast diagnostic test can be conducted as a substitute for blood cell. This diagnostic assay identifies malaria antigens present in an individual's bloodstream and signifies a positive conclusion by modifying the hue of the test result. Moreover, it does not possess the capability to differentiate the seriousness of the infection. An alternative choice is the Biochemical test, specifically the reaction

called Polymerase Chain Rxn (PCR). PCR is a molecular biology method employed in the laboratory to identify and distinguish various Plasmodium species by examining their DNA. In laboratories lacking expertise and proficiency in microscopic examination of malaria, employing a PCR test may be a more favorable choice to initiate treatment. The antigen test and the Susceptibility test are the two additional tests [38].
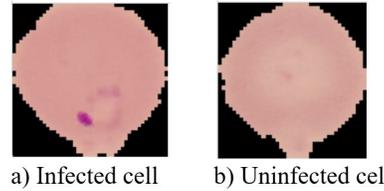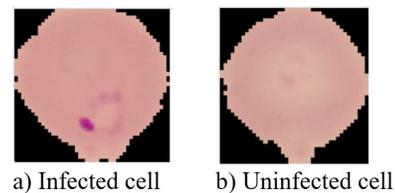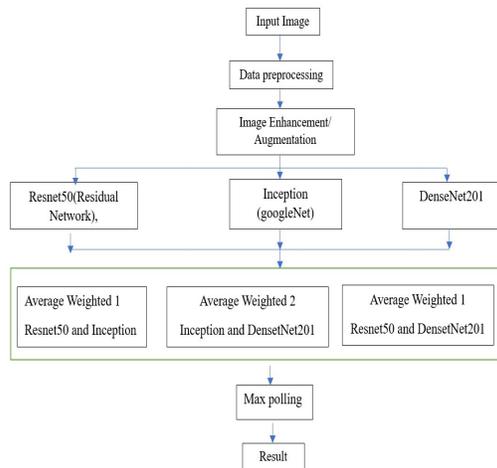

a) Infected cell   b) Uninfected cell

Fig.2 Images showing red blood cells a) Infected and b) uninfected.

a) Infected cell   b) Uninfected cell

Fig.3 Resized Images of 64x64.

Table 1 The dataset is partitioned into assessment, verification, and training sets..

Partitioned Type	Percentage %
Assessment	65%
Verification	15%
Training	20%

Hence, employing an automated malaria diagnosis procedure has several advantages. It yields far more precise outcomes in comparison to the manual procedure. It decreases the amount of work required to attend to a larger number of patients. Deep learning has the ability to deliver very precise and expedited results for detecting parasites[3]. Due to the severe nature of malaria, several researchers have dedicated several years to studying and addressing this illness. In the past, malaria was discovered by human knowledge. It was challenging for an unskilled individual to accurately identify the condition. However, researchers have achieved a remarkable outcome in this regard. Computer-aided diagnosis is the most powerful instrument in this field. Diverse methods for image processing are utilized to extract unique features from photographs, which are then analyzed

by a classifier to assess the presence of disease. The author in reference [33] presented a conventional image processing approach. The Otsu binarization process is employed to segment red blood cells. He manually derived statistical characteristics from the photographs. K-means clustering is utilized to group picture values into clusters. The illness is classified using a support vector machine (SVM) as a classifier. The author presented many methodologies for the diagnosis of malaria in reference [24]. Various approaches may be employed to do Image processing involves the manipulation and analysis of images. Cell segmentation refers to the process of identifying and separating individual cells within an image. Feature extraction involves identifying and extracting relevant characteristics or attributes from the segmented cells. Classification refers to the categorization or labeling of cells based on their extracted features. The preprocessing techniques discussed encompass the average filter, Laplacian filtering, Wiener filtering process, median filtering process, adaptive equalization of the histogram, contrast enhancement, and more methods[2]. Segmentation techniques encompass morphology operation, Fourier transformations, clustering using k-means, fuzzy segmentation, and several other methods. The study examines three distinct characteristics: a chromatic attribute, a textural attribute, and a morphological attribute. He used the two types of learning techniques into the classification process. Deep learning is the predominant method for disease detection.
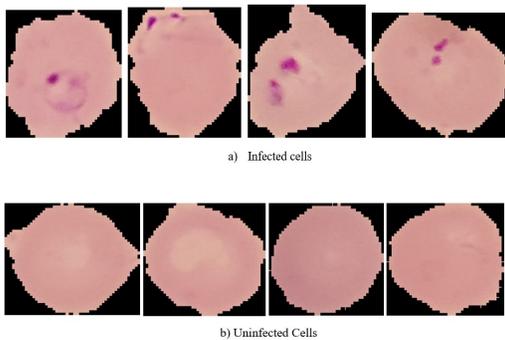

a) Infected cells

b) Uninfected Cells

Fig. 4 Augmented cell images.

Table 2 Augmented methods and their measures

Augmentation	Value
spin	0.3
Zoom	0.3
H-flip	yes
V- flip	yes
transform	1/256

In a mechanized and more precise method. The currently predominant technique is known as CNN. This system possesses the capability to automatically extract features from images [5]. The author in reference [22] presented a fast Convolutional Neural Network comprising of 6 convolutional layers, one completely linked layer, and a single classification layer. Furthermore, he evaluated alternative transfer learning approaches, such as AlexNet [15], RESNET50 (RESIDUAL NETWORK) [31], ResNet50 [11], and DenseNet121 [12]. In the end, he attained a thorough efficiency score of 95.70% throughout models while using the test dataset.

Transfer learning involves utilizing pre-trained neural networks. Employing the transfer learning approach, he discovered an accuracy of 95.9%. In reference [28], the author created a shallow convolutional neural network Achievement of a comparable performance with the RESNET50(RESIDUAL NETWORK) [31] and ResNet50 as its models [11]. The field of deep learning faces significant challenges due to its demanding computational complexity and significant computational cost. The CNN he proposes exhibits decreased computational complexity and lower computational runtime. The assessment criteria used in his research encompass accuracy, sensitivity, precision, F1 rating, and the MCC (Mathew's Composite coefficient). The researcher attained an accuracy rate of 94.32% in his investigation. The author in reference [7] presented a three-stage pipeline that includes the process of segmentation clipping and applying masking, and classification. A segment neural network (SNN algorithms) [9] has recently been designed exclusively for the purpose of dividing red blood cells (RBCs) during the segmentation stage. A unique CNN architecture consisting of 13 layers has been designed to categorize cases of malaria sickness. The CNN architecture he developed had an overall accuracy of 93.72%.The author in reference [9] presented a novel method for categorizing malaria sickness, known as CNN-SVM and CNN-KNN. In this methodology, a A Convolutional Neural Network (CNN) is employed for feature extraction, and SVM or KNN algorithm is utilized for classification of data[39]. Furthermore, he showcased a novel autoencoder methodology. An An autoencoder is a neural network which is trained to generate output that closely resembles its input. The author proposed a technique known as a pre-trained network in reference [8]. He employed LeNet [17], AlexNet

[15], and GoogLeNet [34] in his research. The pathologists connected with the School of Medicine of Alabama in Birmingham provided a unique dataset. Existing networks were used to extract features. Seven features were chosen optimally from a set of 72 characteristics utilizing the Kullback-Leibler (KL) proximity. He employed a classifier based on a Support Vector Machine, or S to classify malaria. The author presented a customized convolutional neural network, or CNN, architecture in reference [21]. The data preparation steps involved implementing a bilateral filter and employing data augmentation techniques.[40] The preprocessed input images were then fed into an CNN algorithm that was particularly designed for this task. The found accuracy was 96.82%. In their study, the author introduced a new neural network (CNN) structure called Alert Dense Circular Net (ADCN), which is detailed in Ref. [25]. ADCN was motivated by the design principles of ResNet [11] and DenseNet [12].

The ADCN architecture consists of three components. The initial section has a bespoke CNN model comprising of two compact block as well as an attention module. The dense block is composed of six thick convolutional blocks, each containing two convolutional layers. Every dense convolutional block is linked to another thick convolutional block. In essence, a focus module is comprised of two separate components. The network layout includes two layers: a 1x1 convolutional layer and a focus branch responsible for extracting the focus feature map. The attention branch utilizes down-sampling and up-sampling techniques to provide an even output size for the branch.. In reference [26], the author introduced three distinct methodologies: a customized convolutional neural network (CNN), transfer learning using the Resnet50(Residual Network) model [30], and a CN-SVM approach. Subsequently, he employed the ensemble learning technique to mitigate the variability in predictions and improve the overall accuracy of generalization. The outcomes The data from all three networks are combined, and the final forecast is calculated using a weighted average ensemble. The author presented a new approach called Incremental Modular Networks (IMNets) in Ref. [8] for the classification of malaria. This approach amalgamates multiple SubNets to offer supplementary information. Each SubNets unit is incrementally incorporated into the existing architecture, either in a sequential or parallel manner. The author in Ref. [10] examined several

methodologies for formulating protein sequences, including Discrete approaches, biochemical procedures, physiochemical methodologies, incorporating techniques of natural language processing.These classifications are subsequently combined to create an ensemble model utilizing the majority and genetic algorithms.

2. PROCEDURE

This research proposes a system based on ensemble learning to alleviate the workload of microscopists. Ensemble learning is a method in which many models are trained on a same dataset and then merged together. by utilizing their findings to enhance precision and minimize variability

The individual referred to is the model. The supplied data is initially scaled to a height of 64 pixels. A width of 64 pixels. Next, the dataset is splitted into a Assessment 65% of the data and a verification comprising 15% and 20% of the data is allocated for testing. Following the use of the data augmentation approach. The use of this technique spans across several fields in order to enhance the quantity of instruction. Data that improves the performance of the model. The models Resnet50(Residual Network)) and Inception (Googlenet) are being referred to. The DenseNet201 models are refined by adjusting several hyperparameters, including the optimization, learning rate, activation function, and others. Subsequently, these models undergo training to acquire knowledge of patterns within the data utilizing a Dataset used for training. Two models are selected from the particular model. Implemented an ensemble method called applied dynamic weighted average to enhance performance by mitigating the model's variation.
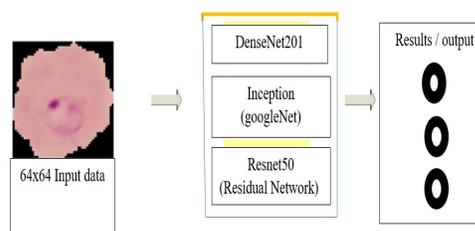

Fig. 5 Model promoting Transfer Learning.

This approach identifies the Automatically generate the result using the suitable weights. Resnet50(Residual Network)) and Inception (Googlenet) obtain superior performance with weights of 0.7 and 0.6 correspondingly. When using weight ratios of 0.6 and 0.5, Inception

(Googlenet) and DenseNet201(R) yield superior outcomes.

Table 3 Hyperparameters and their associated values using transfer learning

Variable Name	Value
Size of input image	64 x 64
Size of Batch	64
Distinct events	120
Optimizer	Adaam
Learn Rate	1^e-03
Objective Function	Thin category mutual entropy

When compared to alternative weight options, Resnet50(Residual Network)) and DenseNet201(R) demonstrate superior performance with weights of 0.4 and 0.5, respectively. After employing an adaptive weighted average approach, three ensembled models are obtained. Subsequently, a different ensemble strategy called max polling is employed, utilizing 3 ensembled algorithms with strong polling, in order to enhance the performance of the model and minimize the Uncertainty in the forecasts. The whole approach of this inquiry is depicted in Figure 1.

2.1 Dataset

The dataset used to conduct this study is obtained from Kaggle. [4]. The total number of cell pictures is 27,558. It is divided into two categories: A total of 13,779 individuals were parasitized, whereas an equal number of 13,779 individuals remained uninfected.
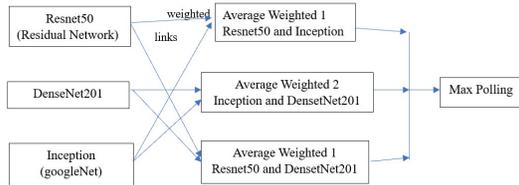

Fig.6 Aggregation of several ensemble methods.

The picture resolutions range from 110 to 150 pixels. During the preparation phase, the photos are resized to a standardized dimension of 64 pixels using online free tool zeeconvert.com[6]. Figure 2 displays the pictures of malaria-infected and uninfected microscopic red blood cells. Ref. [9] indicates the presence of data in the dataset with incorrect labels. Despite not being infected, a
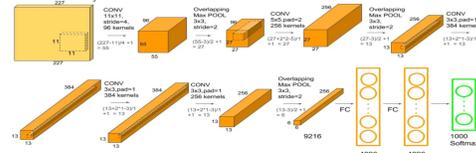
number of data points are classified as parasitized. Moreover, certain signals that come from cells that are not infected are recognized as parasitized. Additionally, the professional verified that some of the data had incorrect labels. 647 cases of incorrectly classified parasitized data and 700 cases of incorrectly labeled uninfected data have been identified overall [9]. The dataset contains about 5% of wrongly labeled data, which might potentially negatively impact the model's performance. The Google Colab platform was used for the experimentation.

Fig.7 proprietary Convolutional Neural Network (CNN).
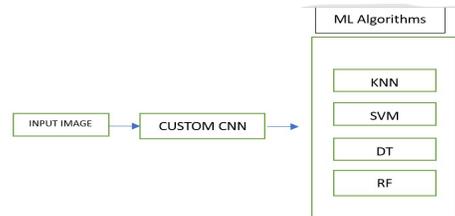

Figure 8 CNN-ML classifier model.

Table 4: Training and validation Accuracy and loss.

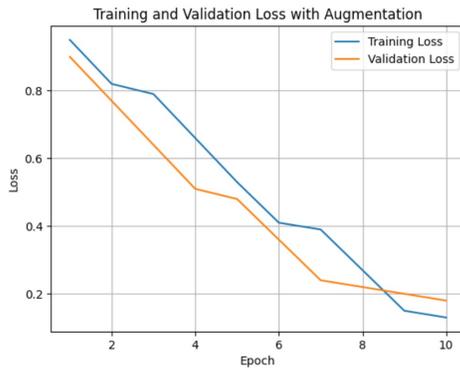| Epoch	Training Accuracy	Validation Accuracy	Difference
1	0.75	0.73	0.02
2	0.82	0.8	0.02
3	0.87	0.85	0.02
4	0.9	0.88	0.02
5	0.92	0.9	0.02

Fig 9 Augmented custom CNN model..

2.3. Data preprocessing and division

The dimensions of malaria images range from 110x150 pixels. The cell in this experiment are resized to dimensions of 64x64 pixels. Figure 3 displays the scaled-down cell pictures of malaria. Dataset splitting is an essential phase in the development of model. The size of data has an effect on how the dataset is divided [3]. The research uses a split dataset. Using the scikit-learn package, divide the data into three sets: 65% learning, 15% verification, and 20% Assessment. Using training set, an algorithm for machine learning is trained to find and examine patterns in the data. The validation sample set is utilized for evaluation of proposed model. while it is being trained. Ultimately, the model undergoes testing using a separate test set once it has finished the training process. The dataset splitting chart is displayed in Table 1.

Table 5: Efficiency of a CNN model with other optimization algorithms.

Enhancer	Precision	Recall	F1score	Accuracy
Adadealta	0.78	0.76	0.76	0.76
Proximal Gradient Descent	0.96	0.96	0.96	0.96
Follow the Regularized Leader	0.24	0.50	0.33	0.49
Nadam	0.97	0.97	0.96	0.96
Root Mean Square Propagation	0.96	0.95	0.96	0.96
Stochastic Gradient Descent	0.95	0.95	0.94	0.94
Adaptive Moment Estimation	0.96	0.98	0.97	0.97

2.4. Enhancing the dataset

Data augmentation involves generating synthetic data by manipulating the current data. It prevents the acquisition of unnecessary characteristics and enhances overall efficiency. Deep learning need a more extensive dataset for training in order to enable the model to discern a greater number of patterns from pictures and provide precise predictions[39]. Augmenting data is a technique that improves the effectiveness of a model by enlarging the dataset used for training through the application of diverse transformations. Data transformations encompass several operations, including rotation, zooming in and out , flipping, rescaling, shearing, and more. The present study utilizes Augmenting data, that improves the effectiveness of a model by enlarging the dataset used for training through the application of diverse transformations. Figure 4 illustrates implementation of data augmentation strategies on the training dataset, while Table 2 displays the corresponding values for each strategy. A stochastic rotation is applied using a value of 0.2, which represents a random rotation within the range of [-20% * 2pi, 20% * 2pi]. The generated picture is undergoing random rotational motion in both the clockwise and counterclockwise directions. Anticlockwise. The zoom transformation utilizes a value of 0.2, indicating random vertical zooming within a range of 20% with lower and upper limits [28]. The final image is depicted through the zooming in as well as out transformation. Horizontal and vertical flips are employed to horizontally mirror pictures and vertically invert them. The images are resized to match features within a range of zero to one by using a scaling factor of 1/4 to 1/255 in order to achieve quicker convergence.

2.5. Models for transfer learning

The proposed technique utilizes transfer learning models, specifically Resnet50(Residual Network)), Inception (Googlenet), And Densenet201, to implement the adaptive weighted average ensemble. In this process, models undergo retraining to update their weights, which helps the network learn and recognize characteristics related to new pictures. In this approach, the final dense layer is excluded when constructing transfer learning frameworks designed for 1000 categories. A fresh dense layer, comprising two neurons, is added to the output layer., with the purpose of classifying cells as either parasitized or uninfected. In order to optimize the results, hyperparameters are employed to finely adjust the transfer learning frameworks.

The Adam optimizer is a hyperparameter used to update weights and biases in order to decrease error. It is often employed with a learning rate of 1e-04.

The sparse classified cross-entropy is utilized as a loss function to compute the discrepancy amidst the real and projected values. Batch size is 32 and the number of epochs is 100. The architecture is shown, including all transfer learning models seen in Figure 5, along with their corresponding hyperparameters mentioned in Table 3.

2.6. Aggregation of several ensemble methods

During this stage, a collection of ensemble methods is utilized to achieve optimal performance. The adaptive weighted average approach is applied by combining two models at a time, after using three distinct transfer learning models. Consequently, three distinct adaptive weighted average models are identified. The first weighted average model is created by merging Resnet50(Residual Network)) And Inception (Googlenet), The second weighted average model is formulated by combining Inception (Googlenet) and Densenet201[39]. The construction of the weighted average model involves utilizing the Resnet50 (Residual Network) and DenseNet201 (R) architectures. In the standard weighted average approach, it is necessary to establish weights in order to achieve optimal results. The outcome. Nevertheless, the adaptive weighted average approach automatically selects suitable weights depending on the data. In the weighted average model 1, Resnet50(Residual Network)) and Inception (Googlenet)(R) yield superior results with weights of 0.7 and 0.6 correspondingly. Inception (Googlenet)(R) and DenseNet201(R) provide superior performance in the weighted average model 2, with weights of 0.6 and 0.5 wt, respectively. The diagram illustrating the collection of ensemble methods is presented in Figure 6.

Table 6 Behavior of a personalized CNN model at distinct learning rates.

Frequency of learning	Recall	Accuracy	Precision	F1 score
1E-02	0.51	0.51	0.24	0.34
1E-03	0.94	0.96	0.95	0.96
1E-04	0.96	0.96	0.96	0.95

Table 7 Different CNN-Based Machine Learning (ML) Filter Performance.

Model	Recall	Accuracy	Precision	F1 score
CN-SVM	0.82	0.82	0.82	0.82
CN–KN	0.62	0.62	0.63	0.58
CN-DT	0.76	0.74	0.74	0.74
CN-RF	0.80	0.82	0.82	0.82

2.7. Additional Architectures

2.7.1. Customized Convolutional Neural Network structure

The CNN architecture is composed of an overall of 16 layers, which are proprietary. The layers are structured into three blocks, whereby each block comprises the convolutional layers., stimulation, max pooling, then batch normalization layers. In addition, there is a single flatten layer and a single dropout layer. The architecture is finalized using two thick or completely interconnected layers. The starting convolutional layer conducts convolutions utilizing 32 cores to extract information from the source images. The kernel is convolved with a 5x5 matrix while applying identical padding. A stride of 1 pixel is employed to maintain the initial size of the map of features.. The convolution layer's output is subsequently fed into a ReLu activation function, which introduces non-linearity. This aids in expediting training and achieving faster convergence [30].The ReLu activation function, represented by Equation (1), transforms negative values to zero and leaves positive values unchanged.

$$R(x) = max\ (0,\ x) \quad ----- (1)$$

Here, R represents the outcome obtained by introducing non-linearity to matrix x.

Subsequently, the maximum pooling layer is applied utilizing a matrix of three by three and an offset of 2 to reduce the size of the image Derived from the result of a layer of convolution.. Furthermore, it reduces the computing cost by

$$\mu = \frac{1}{n}\sum_i N^{(i)} \tag{2}$$

$$\sigma = \frac{1}{n}\sum_i (N^{(i)} - \mu) \tag{3}$$

$$N_{norm}^{(i)} = \frac{N^{(i)} - \mu}{\sqrt{\sigma^2 - \varepsilon}} \tag{4}$$

$$N = \gamma * N_{norm}^{(i)} + \beta \tag{5}$$

$$Cost\ function = Loss + \frac{\lambda}{2m} * \sum \|w\|^2 \tag{6}$$

decreasing the number of parameters. Afterwards, a layer of batch normalization is utilized to normalize numerical information to a consistent scale while maintaining the original shape of the data.. It addresses the issue of overfitting and enhances the speed and stability of the neural network.

The Batch adjustment layer calculates the average μ and the average variation σ from the activation levels across the entire batch utilizing calculations (2) and (3). The activating vector N(i) then undergoes normalization utilizing equation (4). The output of layer N(i) is determined by applying the linear transformation utilizing two configurable variables, γ and β, using equations (5) [13]. The second and tertiary convolutional layers consist of 32 and 64 the kernels, correspondingly, each with a three by three matrix. The matrix represents the ReLu function of activation employed to introduce non-linearity to the linear output of convolutional operations. The system incorporates maximum pooling & group normalization techniques. layer with identical values thereafter every convolutional layer.

The feature extraction phase has been concluded In the preceding section. The subsequent section will now elucidate the process of categorizing malaria parasites through the acquisition of knowledge about parameters. Previously, the data was kept in the form of a three-dimensional feature vector. In order to categorize parasitized and uninfected cells, it is necessary to turn it into a one-dimensional array. The flatten layer is utilized to convert a 3-dimensional array into a 1-dimensional linear array, which is then used to input data into a fully linked layer. The layer is comprised of 4096 neurons and serves as the initial completely Connected or compact layer within the model. The output produced by the layer that is flattened is thereafter transmitted to the following dense layer. The concealed layer consists of 1024 units. Neurons employ a modified linear unit (the ReLu algorithm) activation function to transform proportional input into an unpredictable format. The layer incorporates L2 regularization to reduce the weighted metrics. Therefore, it tackles the problem of overfitting by reducing the weights allocated to the variables.. The cost function, as represented by equation (6), is modified by these values.

In this context, λ represents the regularization parameter.Drop out is an additional regularization approach that is bundled with the next thick layer will have a deactivation rate of 20%, meaning that 20% of the nodes will be randomly deactivated with a value of 0.2. Additionally, it aids in

mitigating the issue of overfitting. Finally, a thick layer for classification is included, consisting of 2 neurons, which is used to categorize parasitized and uninfected cells based on micro red blood cell pictures. In that layer, a softmax activation function is utilized as a classifier to provide results expressed as the probability distribution.
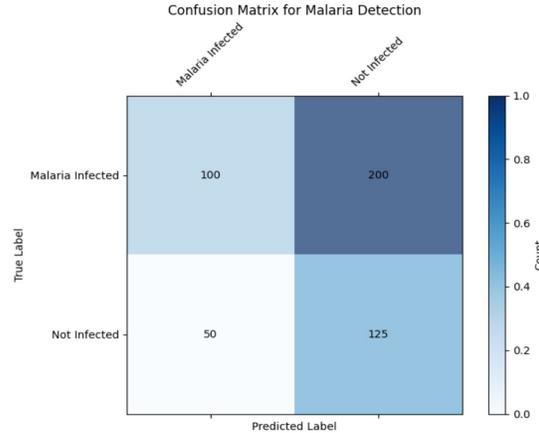

Figure 10 depicts the diagram of the CNN-ML classifier

The model undergoes fine-tuning utilizing The Adam optimizer is used with a rate of learning of 1e-04. to update weights and biases in order to minimize losses.

Table 8 The statistics of several transfer learning models.

S.No	Method/Algorithm	The Recall	F1 score	The Accuracy	The Precision
1	VG16	.92	.91	.92	.93
2	VG19	.89	.9	.94	.92
3	DesNet201	.92	.9	.93	.88
4	ResNet50	.87	.9	.95	.94
5	CNN SVM	.91	.91	.92	.9
6	PROPOSED MODEL	0.94	0.94	0.97	0.95

The loss function employed for binary categorization is sparse category crossover entropy. It calculates the discrepancy between the expected values and the actual values002E.The efficiency is shown in table5.

2.7.2. Convolutional Neural Network Multi-Layer classifier

With in this part, the proprietary The utilization of an CNN structure serves as a means to extract

features. Additionally, multiple machine learning methods are applied as classifiers in order to assess their performance with that of the softmax classifier [32].

This study utilizes machine learning algorithms like SVM, KNN, DT(Decision Tree), and RF(Random forest). The Support Vector Machine (SVM) is a type of supervised learning technique that performs well when the volume of dimensions is greater than the volume of samples.

3. ANALYSIS OF RESULTS

The objective of this work is to assess many deep learning methods to find a more accurate and efficient model for red blood cell image-based malaria diagnosis. A variety of optimization techniques, training rates, transferable learning simulations, deep learning classification algorithms, and ensemble learning strategies are taken into account while evaluating the results. Every experiment is carried out using a batch count of 32 and a rate of learning of 1e-04.. The model's performance is evaluated using recall, precision, F1 score, and accuracy as performance measures. There exist four significant parameters. The four categories are true positives (TP), false positives (FP), true negatives (TN), and a false negative (FN). A true positive refers to infected cells that are appropriately recognized as infected. A false positive occurs when cells that are actually infected are mistakenly labeled as uninfected. A true negative refers to uninfected cells that are accurately recognized as such, whereas a false negative refers to the opposite scenario. The equations (9)–(12) display several assessment measures.

SVM classifier, where its value is determined by the distance from the origin. Equation (8) presents the mathematical formulation of the RBF kernel.

Table 9 Comparison of results between the suggested ensemble approach and the current models

prototype	Recall	Accuracy	Precision	F1 score
Otsu segmentation, K-means clustering [33]	0.93	0.946	0.9607	0.945
CNN [22]	-	0.96	-	-
VGG16 [29]	-	0.9615	-	-
CNN [21]	0.9633	0.9682	0.9682	0.9682
VGG16 [26]	0.972	0.9777	0.9719	0.9709
VGG16 [35]	0.956	0.96	-	0.956
CNN [19]	0.9699	0.9737	0.9773	0.9736
Proposed Ensemble model	0.9792	0.97	0.9791	0.9792

This study aims to evaluate several deep learning techniques in order to discover a more precise and effective model for malaria detection using red blood cell pictures. The evaluation of the outcomes is conducted by considering various optimizers, learning rates, transfer learning models, machine learning classifiers, and ensemble learning techniques. All experiments are conducted with a learning rate of 1e-04 and a batch size of 32. The model's performance is evaluated using recall, precision, F1 score, and accuracy as performance measures. There exist four significant parameters. The four different categories consist of true positives (TP), true negatives (TN), false positives (FP) & false negatives (FN). A true positive denotes to infected cells that are appropriately recognized as infected. A false positive occurs when cells that are actually infected are mistakenly labeled as uninfected. A true negative refers to uninfected cells that are accurately recognized as such, whereas a false negative refers to the opposite scenario. The equations (9)– (12) display several assessment measures.

$$K(X_1, X_2) = exp\left(-\gamma \|X_1 - X_2\|^2\right) \qquad (8)$$

$$Precision = \frac{TP}{TP + FP} \qquad (9)$$

$$Recall = \frac{TP}{TP + FN} \qquad (10)$$

$$F1\ Score = \frac{2 \times Precision \times Recall}{Precision + Recall} \qquad (11)$$

$$Accuracy = \frac{TP + TN}{TP + FP + TN + FN} \qquad (12)$$

3.1. Efficiency

3.1.1 Performance Evaluation of A Customized Convolutional Neural Network (CNN)

The exclusive Convolutional Neural Network (CNN) network attains an initial training proficiency of 96.4% and validation efficiency of 96.6%. Applying the data augmentation strategy eliminates the issue of overfitting. In the absence of data augmentation, the training accuracy is measured around 98% approximately and the validation accuracy is recorded as 95 %.

Table 10 The efficiency for various transfer learning models.

collaborative method	The model	The value of the weight	Precision	Recall	F1 score	Accuracy
Scalable Weighted Average	Resnet50 (Residual Network), Inception (Googlenet)	0.7, 0.6	0.97	0.975	0.96	0.97
	Inception (Googlenet), Densenet201	0.6, 0.5	0.97	0.97	0.97	0.97
	Resnet50(Residual Network)), Densenet20	0.4, 0.5	0.97	0.97	0.96	0.97
	Resnet50 (Residual Network)), Inception (Googlenet)& Densenet201	0.1, 0.9, 0.8	0.97	0.97	0.977	0.97
Max polling	Resnet50 (Residual Network)), Inception (Googlenet) & Densenet201	–	0.97	0.97	0.98	0.97
Adaptive Weighted Average & Max polling	Resnet50 (Residual Network), Inception (Googlenet) & Densenet201		0.97	0.97	0.98	0.97

It is evident that there is a significant disparity between the training and validation accuracy scores. This phenomenon is referred to as overfitting, in which The model demonstrates solid results on the initial training data but lacks effective generalization on the test data. Figure 9 displays the Evaluation of the custom CNN model's performance regardless of augmentation.

The method remains unchanged when the gradients are rescaled diagonally and is particularly well-suited for applications involving vast amounts of data or parameters [14]. Table 6 displays the performance outcomes of the customized Convolutional Neural Network (CNN) model under various optimization algorithms.

A learning rate of 1e-04 is necessary to achieve the global minimum point optimally. Currently, the level of loss is minimal and allows for more precise identification of malaria parasites. Due to very high values of the other two learning rates, they are incapable of reaching the global minimum point. Table 7 displays the performance outcomes of the bespoke Convolutional Neural Network (CNN) model at various learning rates.

3.1.2. Evaluation of The Performance of CNN-ML Classifier

The results of several machine learning algorithms are now under investigation. Shown in table 11.

Table 11 ML Algorithms accuracy based on classifiers

Description	Classifier	Test Accuracy
A customized Convolutional Neural Network (CNN)...	CNN-SVM	81.67%
The CNN-SVM classifier is outperforming the other...	-	-
The SVM classifier achieved a test accuracy of 81.67%.	SVM	81.67%
In contrast to the softmax classifier...	-	-

3.1.3. Performance of transfer learning

Based on data, models utilize known weights exhibit subpar performance. However, models that have undergone retraining exhibit exceptional performance due to the training of all layers and the

acquisition of new characteristics linked with novel pictures and categories by the networks. INCEPTION (GOOGLENET) (R) surpasses the other models by attaining an accuracy of 96%. accuracy Figure 11 illustrates the data, while Table 9 presents the performance results of several learning models..
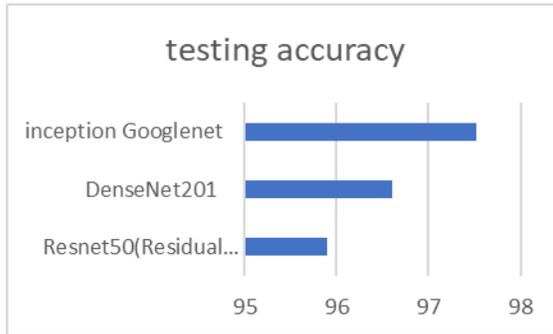

Figure 11 testing accuracy of different proposed models

3.1.4. Evaluation of ensemble learning

Figure 10 presents the confusion matrix depicting the classification outcomes for the parasitized and uninfected classes, employing the recommended ensemble method. This proposed ensemble strategy merges the adaptive average weighted and max polling ensemble techniques. The approach accurately categorized 2678 photos as parasitized and 2723 images as uninfected. The ensemble approach achieved a testing accuracy of 97.92%.

Table 10 showcases the results of various ensemble learning approaches. The adaptive average weight technique autonomously generates the best result for a specific weight set. The proposed method amalgamates two ensemble strategies: adaptive average weighting and max voting. This combined ensemble approach produces the most favorable outcome when compared to alternative tactics.

3.2. Comparative Analysis

3.2.1. Comparing the results with various models

At present, the outcomes are under evaluation against diverse deep learning models, encompassing the recommended ensemble learning method. Surpassing other models, the ensemble model attains an impressive testing accuracy of 97.92%. Table 9 provides a performance evaluation, comparing the proposed ensemble model with alternative models using various assessment metrics..

3.2.2. Comparison of results with already established methodologies

This part involves a comparison of the outcome with previous studies using various performance indicators.Numerous researchers have introduced the transfer learning model and the Convolutional Neural Network (CNN) model in their studies.Nevertheless, the outcomes do not match the effectiveness of the suggested approach. The suggested ensemble model attains a remarkable testing accuracy of 96.52% and demonstrates enhanced precision and efficiency in detecting malaria. The performance of the suggested ensemble approach is compared to current methods in Table 9.

4. OBSERVATION AND DISCUSSION

This research paper introduces a novel method for malaria parasite identification by combining two ensemble learning approaches to construct a model. In the past, several models have been constructed by various researchers. The authors explored both a Convolutional Neural Network (CNN) model and a transfer learning model. Additionally, they endeavored to construct an ensemble learning model. Nonetheless, their model employed only a single ensemble strategy for malaria detection, resulting in subpar accuracy.

Nevertheless, this work integrates two ensemble methodologies to form a unique design. In the initial phase, transfer learning models are utilized to execute a weighted average ensemble.Subsequently, the weighted average models are subjected to the max polling ensemble technique in order to provide more precise outcomes. In comparison to prior research, this distinctive model demonstrates superior performance and increased accuracy, as seen in Table 9.

5. CONCLUSIONS AND FUTURE INVESTIGATION

This research introduces a deep neural network that uses ensemble learning to accurately diagnose malaria parasites in tiny red blood cell pictures. Furthermore, the performance of several deep learning techniques, such as the custom CNN model, the transfer learning method, and The effectiveness of the CNN-ML classifier model is evaluated to compare its performance with the proposed ensemble approach. The suggested ensemble learning model attains a testing accuracy of 96.52%in classifying malaria parasites, making it the most effective model. Additionally, it reduces the spread of forecasts and enhances the efficiency of the model. The dataset for this investigation was taken from Kaggle.com Various preprocessing

approaches are being implemented to enhance the performance of the model. Data augmentation is a strategy used to address the issue of overfitting. The model is optimized by adjusting several hyperparameters in order to minimize the classification error. Hence, the ensemble model exhibits remarkable performance and considerably expedites the detection procedure. The suggested composite model might undergo additional validation and be included into clinical environments. Engaging in partnerships with health care providers and practitioners might facilitate the implementation of the model for practical diagnosis, potentially enhancing the effectiveness of malaria detection. The effectiveness of the ensemble learning technique may be evaluated using datasets pertaining to different illnesses that present comparable diagnostic complexities. This might illustrate the adaptability and applicability of the suggested methodology in the wider domain of image analysis in medicine.

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