Research Article

Deep learning-based computer assisted detection techniques for malaria parasite using blood smear images

Shankar Shambhu[1*], Deepika Koundal[2] and Prasenjit Das[1]

Chitkara University School of Engineering & Technology, Chitkara University, Himachal Pradesh, India[1]
School of Computer Science, University of Petroleum and Energy Studies, Dehradun, India[2]

Abstract
Malaria remains a significant global health concern, impacting various regions worldwide. Achieving effective treatment and reducing mortality rates hinges on early and accurate diagnosis. In the year 2021, the World Health Organization (WHO) reported a staggering 619,000 deaths attributed to malaria. Additionally, approximately 214 million individuals were afflicted by this disease during that period. Hence, this study introduces two distinct deep-learning algorithms tailored for malaria disease classification. The first method employs a binary classifier convolutional neural network (CNN) model, attaining an accuracy (ACC) of 90.20%. The second method introduces a customized CNN model that exhibits even greater ACC, reaching an impressive 96.02%. These advanced deep learning (DL) techniques hold the potential to enhance the precision (PRE) and efficiency of malaria diagnosis, ultimately facilitating early disease detection. The study provides comprehensive insights into the proposed models. Model 1 involves malaria disease classification employing a CNN-based binary classifier, while Model 2 adopts a customized CNN architecture. The methodology section elucidates the details of these models, their design, and the execution of experiments undertaken to evaluate their performance. Notably, the proposed method is juxtaposed with the state-of-the-art approach, demonstrating superior results in accurately discerning infected and uninfected malaria blood cell images.

Keywords
Malaria classification, Deep learning, Binary classifier, Customized CNN model, Image classification, Parasite detection.

1.Introduction
Malaria is a deadly infectious disease that affects humans. Malaria is caused by the parasite protozoan plasmodium, which may infiltrate erythrocytes and lead to a wide range of symptoms in humans. In accordance with World Health Organization (WHO), over 619, 000 people died from malaria in 2021, with an estimated 214 million people affected [1]. Over 90% of these deaths happened in Africa, followed by over 6% in the South East Asia Region, Eastern Mediterranean, and 4% in the Western Pacific. In 2020 there were an expected 241 million cases of malaria and 627000 casualties caused by malaria. In 2019, there were 229 million confirmed cases of malaria and an estimated 409000 deaths. In 2018, 228 million malaria cases were detected, and causalities reached to 411000 [1].

In 2016, around 1.09 million and in 2017, approximately 0.84 million cases of malaria were documented in India, the majority of which were caused by the P. falciparum species [2].

Dr. Ronald Ross first discovered malaria transmission in the human body by mosquitoes in 1897 [3]. The main reason for malaria is a protozoan parasite. The plasmodium genus infects the red blood cells (RBC) of the human body, which causes malaria [4]. Generally, female anopheles mosquitoes and human beings are the two main hosts infected by the parasite. When female Anopheles mosquitoes desire to foster their eggs, they bite and draw blood from the human body. If a parasite infects that person, then that same infected parasite blood is found in the mosquito, and that parasite reproduces and develops in the mosquito's body. When that infected mosquito bites another person, parasites containing the salivary gland are transferred into that person's blood [5]. After transferring parasites into the human body by the mosquito, malaria parasites grow at a very high

---
*Author for correspondence

speed in the liver and RBC of that infected person. Malaria symptoms appear after one or two weeks. Primary symptoms that appear are headache, vomiting, fever, and chills. If malaria is not treated early and properly, it is very harmful to the human body. It may be a reason for kidney failure, low blood sugar, respiratory distress, enlargement of the spleen etc. [6]. Malaria can kill a person by destroying their RBC. Malaria during pregnancy is very dangerous, and it is one of the reasons for abortion [7].

Control and eliminating malaria requires global awareness and the availability of effective interventions, such as gene drives and medication treatments. Effective and timely malaria extinction faces several issues to build a malaria-free world, and the possible supervision of the WHO 3 T (test, treat, and track) policy might be a rising ride [5]. Antimalarial medications, innovative insecticides, potent vaccinations, sustainable domestic and international funding, and worldwide awareness programs were created to promote effective implementation. While these initiatives were successful early on, the gradual modifications in the unusual climate patterns, the developing resistance of vaccines, and the late delivery of enormous quantities of pharmaceuticals and medical staff meant an emerging roadblock to eliminating malaria [8]. Funding per malaria-risk individual in 41 high-burden nations is below US$ 2, according to surveys [1]. Malaria is a chronic disease that primarily affects poor people. It imposes a significant burden on society, the economy, and people's health, and it is inextricably related to poverty [9]. This presented a difficulty for the early diagnosis and fast effective treatment of malaria, which was necessary to ensure that patients did not serve as a reservoir for parasites anywhere in the world.

Following several years of deliberation, the malaria research and development (R&D) alliance decided to collaborate with the WHO in the hunt for innovative and more effective strategies to fight malaria [5]. As a result, the malaria R&D alliance led to the multidisciplinary teamwork of clinical experts in the diagnostic and research research engineers in the field of malaria R&D [10]. The productive collision of the two disciplinary has resulted in the development of digital technologies with guaranteed levels of quality as well as a significant rise in the use of automated computer vision tools for the treatment of malaria, which has facilitated both the diagnosis and the implementation of a monitoring system [11].

With automated malaria diagnosis, it's possible to provide a patient's disease history, disease stage, speedy diagnostic test results, effective care, and accurate disease detection. Today, these automated computational models are unique initiatives of malaria R&D alliances that help reach the surveillance aim of early detection rate by implementing smart malaria diagnosis systems [12]. Malaria may be prevented, controlled, and treated more effectively if a more precise and effective diagnostic technology was available. As part of the standard malaria diagnostic technique, a competent microscope checks blood smears for infected erythrocytes. This approach is inefficient since it relies on the skill of the microscopists to provide an accurate diagnosis. In contrast to microscopy, rapid diagnostic methods are more costly and provide less information. Since 2005, thick and thin malaria blood smears have been exposed to automatic image identification approaches for microscopic diagnosis based on machine learning (ML) [13].

Through the study of medical images, deep learning (DL) has emerged as a potential tool for the accurate detection and diagnosis of diseases, including malaria. Yet, the application of DL in malaria diagnosis remains a difficult task due to the complexity of blood smear images, which include variable parasite size and shape, low contrast, and overlapping cells [14].

The purpose of this work is to build a DL-based computer-assisted detection method for the precise and automated detection of the malaria parasite in blood smear images. The suggested method leverages convolutional neural network (CNN) for effective feature extraction and classification, thereby overcoming the issues associated with the analysis of complicated blood smear images.

Early and precise malaria diagnosis is critical for efficient treatment and disease management. Malaria diagnosis is now based on manual evaluation of blood smear pictures, which takes time and requires expert workers [15]. The absence of qualified workers and laboratory equipment exacerbates the problem in resource-limited settings, such as rural areas, where the incidence of malaria is highest [16]. DL techniques, such as CNN, have emerged as a promising approach for automated malaria diagnosis in response to these problems [17]. These approaches have demonstrated tremendous promise in reliably categorizing blood smear pictures as malaria parasite-infected or uninfected. DL can significantly reduce

the strain of healthcare staff, accelerate the diagnosis process, and enhance diagnosis accuracy (ACC), resulting in timely and effective treatment [18].

DL models may also be trained on huge datasets, which improves their ACC and robustness, and they can be readily scaled up to analyse large amounts of data [19]. These models, which may be incorporated into healthcare systems and distributed on mobile devices, make diagnosis more accessible, particularly in distant and resource-constrained situations.

As a result, the motivation for diagnosing malaria using blood smear images using DL techniques is to enhance the ACC, efficiency, and accessibility of malaria diagnosis, thereby contributing to the decrease of the worldwide malaria burden.

The objective of this study is to design and implement a DL-based technique for malaria parasites that is accurate, efficient, and minimizes losses. Evaluate the proposed technique's performance using a variety of performance measures, compare the suggested technique's performance to other state-of-the-art techniques, and demonstrate the effectiveness of the proposed technique in clinical situations. This also expedites the diagnosis and classification of malaria by medical professionals. To forecast the result of such medical events, medical specialists must exert tremendous effort. The objective of the research procedure is to acquire certain outcomes. The significance of the research is as follows:

Research for community
The disease with the highest mortality incidence is malaria. Children under five years old were the most vulnerable [2], with an estimated 214 million cases and 619,000 fatalities in 2021 and 241 million cases and 627,000 deaths in 2020 [1]. Delay in detection is the primary cause of the elevated mortality rate. By spreading knowledge and enabling quick treatment, early detection of malaria can significantly lower the fatality rate. To reduce the mortality rate, an automated computer-assisted technique is necessary for precise and early detection. With such a method, there would be a greater possibility for an early diagnosis and appropriate treatment, which would increase the likelihood that malaria patients would survive. Digital thin and thick blood smear images can be used to automatically identify malaria parasites, giving a more effective and accurate diagnosis, when computer vision and ML techniques are used.

Technical aspect for the healthcare industry
Algorithms for DL and ML are generally acknowledged as powerful tools for image analysis. These models work better than other cutting-edge models in a variety of applications, increase disease diagnosis speed and ACC, and lower error rates generally. This kind of model can assist medical professionals in making crucial decisions, which in turn can help save lives.

This research paper's contributions include the development of a novel DL-based computer-assisted detection technique for the automated detection of malaria parasites in blood smear images, a comprehensive evaluation of the performance of the proposed technique, and a comparative analysis with other state-of-the-art techniques. The proposed method has the potential to aid physicians in making precise and timely diagnoses, leading to improved disease treatment and patient outcomes.

In this work, DL is employed to detect RBC parasite infection in thin smears on conventional microscope slides. For this purpose, used CNN, a field of DL that excels at handling two-dimensional input like photos and movies. It was motivated by research into the brain mechanisms responsible for object identification in felines [20]. The studies motivate a pattern recognition model to mimic how the brain interprets visual data. CNN models have the benefit of being trained robustly owing to their hierarchical structure of learning layers after the model's topology has been matched to the feature input. Using the spatial correlations of the visual patterns, the model may effectively minimize the number of parameters that need to be learned. This improves the precision (PRE) of the feedforward-backpropagation training technique. A CNN provides a learning approach that, unlike traditional classifiers, does not require feature extraction and fine-tuning in advance because DL represent exceedingly complex data.

The paper is organised as follows: in the section 2, the existing work done for malaria detection has been summarised. Section 3 describes the material and methods used in the current work for implementation. The proposed models evaluation and result analysis have been done in section 4. The comparison of proposed models with state-of-the-art techniques and limitations of the present work has been summarised in section 5. Furthermore, conclusion, along with the future scope, have been discussed in section 6.

2.Related work

In order to identify the malarial parasite in thin blood smear images, Raj et al. [21] suggested a DL-based image classification approach that makes use of a CNN for effective feature extraction and precise classification. It's possible that the suggested CNN model might automatically extract unique and fundamental features from given images. Using CNN for image data is a great idea. Using data from three distinct optimizers for both training and validation, this research evaluates the proposed model's apparent ACC.

Minarno et al. [22] emphasise the seriousness of malaria as a worldwide public health concern and the significance of early identification and fast treatment to avoid serious results, including death. The purpose of this study was to categorise malaria cell images using the Inception-V3 architecture. The study indicated that the model with the RMSprop optimizer got the maximum ACC of 97% and the lowest loss value across three given scenarios. The findings suggest that the Inception-V3 model accurately identifies malaria cells, indicating that DL techniques might be used to diagnose malaria.

Silka et al. [23] emphasise the vital need of early identification and treatment in controlling the potentially fatal illness of malaria. Researchers have achieved a stunning 99.68% ACC in identifying malaria from blood samples by adding a revolutionary CNN architecture. The researchers' proposed CNN exceeds existing approaches in ACC and speed, providing a viable alternative for malaria detection, particularly in resource-limited areas. The model's outstanding performance in categorising infected and uninfected samples with high sensitivity (SEN) and specificity (SPE) highlights its potential to assist healthcare professionals in properly detecting malaria and its subtypes using DL techniques. These findings have important implications for the application of artificial intelligence in infectious illness diagnosis.

Razin et al. [12] suggest a DL strategy for the detection of malaria parasites using CNN and the YOLOv5 (you only look once version 5) algorithm. This is done in order to solve the constraints that are present in existing medical science malaria detection techniques. When it comes to identifying infectious blood images, the CNN model that has been trained achieves an astounding ACC of 96.21%. This novel approach has the potential to improve malaria

diagnosis and reduce the burden of the disease all over the world.

Krishnadas et al. [24] show that DL models, specifically YOLOv5 and scaled YOLOv4 (you only look once version 4), can automate the identification and categorization of malaria parasites, as well as their stage of advancement. The manual diagnostic method that has been used for malaria in the past takes a significant amount of time and is prone to mistakes. In contrast, the automated models that have been developed provide findings that are both quicker and more accurate. The performance of the model was significantly improved by the addition of augmented images and the usage of annotated datasets. Scaled YOLOv4 showed greater ACC for the categorization of parasites, achieving a score of 83%. YOLOv5 came in a close second, with 78.5%. These findings suggest that these models have the potential to assist medical practitioners with accurate diagnosis and stage prediction of malaria, which might lead to more successful management and treatment techniques.

Sifat et al. [25] developed an automated approach for identifying malaria parasites and their phases from a blood smear, which is an early use of DL algorithms. Using visual geometry group (VGG) 16, infected RBC parasites were identified. It was possible to identify malaria and its different stages automatically. 97.67% of their segmentation was accurate. The ACC of U-Net's model was 92.05%. Using the CNN model, the SPE was 95%. The median ACC of the VGG16 model was 95.55%, and its SPE was 94.7%. Sampathila et al. [26] has implemented a computer technique for detecting malaria that involves categorising the malaria parasite from microscopy of a blood smear. It demonstrates how image segmentation and extraction of features may be used to detect malaria in blood smear images under a microscope. To eliminate distracting backdrops and objects, researchers examined the HSV (hue saturation value) of each image's colour space. Then, a neural network was used to identify and extract attributes from the data, such as colour and texture. The research yielded a training ACC percentage of 97.2%.

Recent methodologies were used in the study work carried out by Li et al. [27]. The authors investigated a hybrid model known as reinforced stream-based active learning (RAL) - convolutional neural networks with a support vector machine (CNNSVM), which was made up of numerous modules of residual

attention learning networks, a global average pooling block, and a classifier that was trained using a support vector machine (SVM). It was discovered that the model significantly improved prediction ACC without requiring any extra complicated calculations to be performed.

Roy et al. [28] used image processing to detect malaria parasites in blood smear microscope images. This was done by using a model that used a colour pixel-based discriminating method and a segmentation technique. In their method, both watershed and HSV color segmentation were used. Next, they used morphological techniques to highlight the parasite in RBC microscopic images. Their efforts boosted the detection rate of the disease-causing parasite to 90.0%.

Nayak et al. [29] examined the effectiveness of several deep-learning algorithms for diagnosing malaria. With a training ACC of 97.55%, the ResNet 50 model performed quite well. Maduri et al. [30] implemented the CNN network and image datasets in this work. This model's primary focus is image processing with the Keras image generator to produce the results. The trained model efficiently differentiates the between positive and negative images of the dataset. Image processing does not need expert expertise, image processing makes malaria diagnosis rapid and accurate. The primary goal of incorporating image processing into trained model is to allow it to classify positive and negative RBC from a huge dataset of microscope images of thin blood smears. DL is also used to classify human blood cells.

Francies et al. [31] described the development of the YOLO technique and YOLOv5 as a cutting-edge object identification method in their study. The study explains how a single neural network was able to reframe the object identification issue using the YOLO approach. Setyawan et al. [32] used CNN to automatically categorise malaria parasites from blood smear images, and a positive result was found. This made a quick diagnosis possible, which saved the patient's life. This research focuses on the technologies, data collection, initial processing, and classification of the CNN algorithms that are already being utilised to diagnose malaria. This research also talks about problems that will need to be handled in the future and why it's hard to compare current tactics. Second, researchers analyse into the CNN techniques that are being used to classify malaria in research publications that have been published. Then,

the suggested CNN techniques are spoken about and rated based on how well they work and what kind of features they have.

Hung and Carpenter [33] used bright-field microscopy images of malaria-infected blood to identify cells and characterize their phases using an object detection algorithm previously applied to natural images. They compare it to a baseline technique that comprises cell segmentation, the acquisition of a number of single-cell attributes, and categorization using random forests. One of the greatest models for identifying objects in recent years, faster R-CNN, was utilised. It was learned using ImageNet and then tuned using the image dataset.

Var and Tek [34] used images from Giemsa-stained blood smears to identify the parasites that cause malaria. (Plasmodium sp.). In this study, the scientists used transfer learning to detect and classify malaria parasites. They use the well-known CNN model VGG19, which has already been trained. Over 20 iterations, they used 1428 samples of P. Vivax, 1425 samples of P. Ovale, 1446 samples of P. Falciparum, 1450 samples of P. Malariae, and 1440 samples with no parasites.

Yang et al. [35] built the first DL system that works on mobile devices and can find parasites caused by malaria in thick blood smear images. This approach has two stages of processing. Start by using an intensity based iterative global minimum screening (IGMS) on a thick smear imagine to identify for possible parasites. The next stage is to use a customized CNN to classify each candidate as a parasite or a backdrop.

Iradukunda et al. [36] develop a realistic model to aid in the detection of malaria. The dataset used, made accessible by the National Institute of Health (NIH) in the United States, contained a total of 27,560 photos of red RBC, including an equal number of images of infected and uninfected RBC. The extreme learning machine (ELM) model of single hidden layer feedforward neural networks was used to categorise and forecast whether a patient has malaria or not.

Sifat and Islam [25] proposed that malaria parasites and their stages may be detected automatically from blood smears. An online database was used to identify images of blood smears from people with malaria. After some initial processing, U-Net was

used to separate RBC from blood smear images. CNN was then used to find RBC that were infected with malaria parasites. Finally, an outstanding neural network called VGG16 was used to find the different kinds and stages of malaria.

Prakash et al. [37] build a deep CNN that can detect the presence of the malaria parasite in the thin blood smear images dataset. The malaria dataset can be obtained at the Lister Hill National Center for Biomedical Communications, which is located in the United States and houses the National Library of Medicine (NLM). The CNN model has an F1 score (FS) of more than 94% and is resistant to overfitting. Shekar et al. [38] proposed a CNN-based ML approach that automatically detects and predicts infectious cells in thin blood smears on traditional microscope slides. A ten-fold cross-validation layer of the CNN is applied to 27,558 single-cell images to understand the cell parameter. By comparison, the most accurate of three different CNN model types— Basic CNN, VGG-19 Frozen CNN, and VGG-19 Fine Tuned CNN—is determined. The model with the best ACC rate is then picked by comparing the ACC rates of the three models.

Umer et al. [39] examined infected red cells under a microscope. This diagnosis is based on the pathologists' expertise and experience, and manual examination results may differ between laboratories. Alternatively, various ML methods have been used to help blood stains identify themselves. Yet, modifying positional and morphological features is a tough task that requires skill. Without considering the hand-crafted features, in this paper, a new stacked based CNN design is proposed that makes it easier for computers recognize malaria.

Joshi et al. [40] present a CNN-based DL technique for diagnosing malaria from microscopic cell images in their publication. In terms of ACC and other evaluation criteria, the suggested CNN model, which uses a 5-fold cross-validation approach, does better than all other methods presently in use and gives the greatest results for DL for diagnosing malaria.

Paul and Bania [41] built three CNN models to predict malaria from RBC images of infected parasite RBC and uninfected parasite RBC.

To detect malaria parasites, Aimi et al. [42] employed k-means clustering with red, green, blue (RGB), hue, saturation, intensity (HSI), and cyan, yellow (C-Y) colour models. The colour models were used to determine the optimum segmentation component. Following the selection of the best colour component, median filtering and seeded region growing area extraction were used to remove unwanted artifacts from the segmented image.

Savkare and Narote [43] employed a statistical SVM classifier to detect malaria parasites in erythrocytes automatically. SVM, Naive Bayes, and multilayer perceptron were utilised to classify malaria-infected erythrocytes utilising textural and morphological information in a recent study.

According to a review of numerous state-of-the-art studies, one of the key issues provided by the current study is that the results of kit-based procedures are less exact, and any wrong result may have an impact on the medication given to the patient. Another big obstacle that must be overcome utilising the technologies that are currently accessible is determining whether or not a patient has malaria. It is unable to distinguish between different types of malaria. Numerous scholars have conducted experiments and then disseminated their findings through scholarly publications within the same field of study. However, there is a need to enhance an automated computational-based computer vision approach to efficiently and effectively detect the malaria parasite from blood smear images, in accordance with the demands of the community.

The community necessitates: The usage of standardised imagine datasets is limited in research due to the prevalent lack of standardisation across researchers' datasets. The quality and features of the microscope play a crucial role in the digital blood smear dataset, as it is via the use of a digital camera mounted to the microscope that all digital photographs of blood smears are captured. A standardised dataset has significant importance for a machine-learning system aimed at automating the detection of malaria. In the field of literature, the existing methodologies are capable of identifying just a singular strain of the malaria parasite. However, it is possible for the patient to be impacted by many types of parasites. Therefore, it is imperative to develop a model capable of accurately identifying various strains of malaria parasites. The authors employed several models and methodologies to train the machines for the purpose of classifying malaria parasites from blood smear images. The learning process of the training model is experiencing a significant duration. Therefore, it is imperative to minimise the duration required for training

classification models. In the field of literature, some academics have formulated models to analyse digital photographs of blood smears captured by a microscope-mounted camera. Hence, the development of an automated methodology is imperative to enhance the PRE of malaria parasite identification, facilitating early diagnosis and ultimately mitigating the future death rate associated with malaria.

3.Material and methods

Blood smear images are often used to detect malaria at an early stage. Medical professionals, such as medical laboratory technicians or pathologists, who are well-versed in the identification and classification of the different species and stages of malaria parasites under a microscope, do the grading of blood smear images. Accurate analysis of microscopic blood smear images is influenced by the expertise of pathologists. It takes too much effort and can produce inaccurate results. Hence, a computer aided diagnosis (CAD) system is critical for the automatic classification of malaria diagnoses and for assisting medical professionals and pathologists by providing a

tool for a second opinion. As a result, an autonomous malaria detection system is being developed to ensure proper disease analysis and evaluation while also increasing ACC.

3.1Dataset

The malaria dataset is collected from the NIH website, which is publicly available [44]. This dataset has originated from Giemsa-stained slides of thin blood smears from 50 healthy patients and 150 P. falciparum infected patients who were screened for malaria. At the MOTM Research Unit of Bangkok, image specialists use slide readers to manually annotate images that are included in a dataset. After then, the NLM gathers all of these images together. *Table 1* shows that there are an equal number of infected and healthy RBC in the 27558 images in the dataset. *Figure 1* shows that uninfected blood image samples do not have plasmodium and (b) infected blood cell image samples have plasmodium. During pre-processing, the colored patches on RBC, which range in size from 110 to 150 pixels, are resampled to 64×64 pixels to meet the needs of the classifier.

Table 1 Dataset description

Dataset	Number of Healthy Patients	Number of falciparum infected patients	Total Images	Number of Parasitized Images	Number of Uninfected Images
[44]	50	150	27558	13779	13779

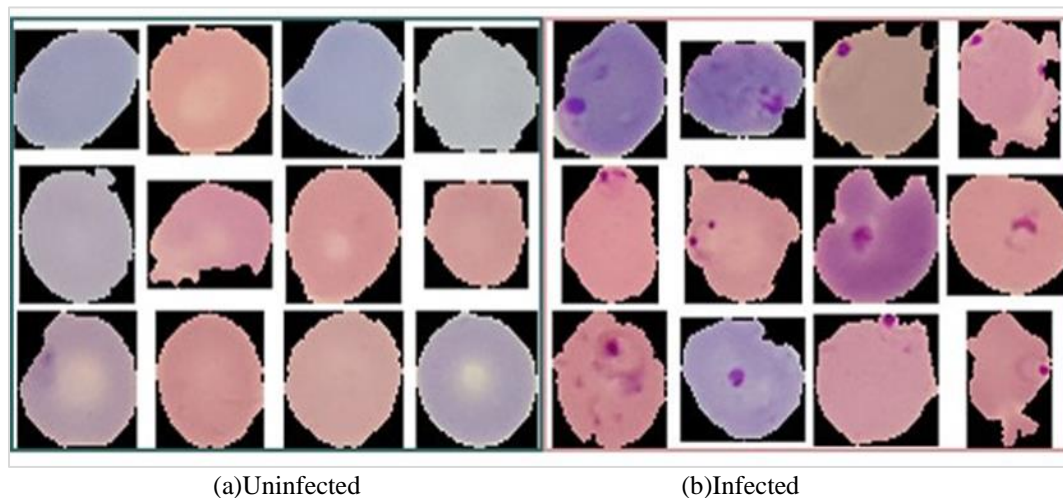(a)Uninfected   (b)Infected

Figure 1 Malaria dataset sample images

3.2Hardware and software requirements

Training DL models demands a central processing unit (CPU), graphics processing unit (GPU), and random access memory (RAM) with high performance. As the dataset utilized in this study

consists of 27558 blood smear images, it is a relatively large dataset. *Table 2* explains all the all the required hardware resources and *Table 3* explain all software tools needed for this research study.

Table 2 Required hardware resources for this study

CPU	GPU	RAM	STORAGE
Xeon CPU 2.20 GHz	Nvidia K80 12 GB RAM 8.7 TFLOP@FP16	16GB	128GB

Table 3 Software tools needed for this research

Programming language	Libraries	Software tools	Integrated development environment (IDE)
Python 3.7	Tensorflow, Pandas, Kearas, Matplot, Numpy, os, Pickle, Scikit-Image, Scikit-Learn, OpenCV Seaborn, PIL, Sklearn, Pillow, CV2,	Anaconda 3, Google Collab, Google Drive	Spyder

3.3 Block diagram of methodology

The block diagram of the research methodology is shown in *Figure 2*. The proposed methodology is divided into three sections: data pre-processing and segmentation, architecture of proposed classifiers models, and evaluation of proposed models.

3.4 Data pre-processing and segmentation

Malaria blood smear images are taken from the NIH website consisting of 27558 images of malaria diseases [44]. In which 13779 images are parasitized Images and 13779 images are uninfected images. All of the images are in portable network graphics (PNG) format and RGB. The size of the original images is 110 to 150 pixels. During the pre-processing stage, the colored patches on RBC, which range in size from 110 to 150 pixels, are resampled to 64×64. After that segment the RBC for the detection of the malaria parasite using blood smear images to facilitate the classification process.

3.5 Proposed classification models

The procedure for dealing with malaria diseases involves classifying them using two different models. In the first model, classification is carried out with the proposed CNN model-based binary classifier. In the second model, classification is carried out with the help of the proposed customized CNN model.

3.5.1 Proposed Model 1 - malaria disease classification with CNN model-based binary classifier

A CNN model based binary classifier was created for malaria diagnosis using blood smear microscopic images. The model is implemented by resizing every image in the dataset to 64×64 and labelling them with 0s and 1s. In addition, there is a 30% testing portion and a 70% training portion, with both of these portions being normalized between 0 and 1. In order to enhance Malaria detection ACC, binary classification algorithms based on CNN on a set of parameters have been used. In order to fine-tune the algorithm's PRE, it was trained and evaluated using a wide range of epoch sizes and batch sizes. By combining the most effective optimizer strategy, loss function, activation function, and binary classification, the CNN model improved its ACC to 90.2%. The logic flow diagram of a binary classifier based on a CNN model is shown in *Figure 3*.

Architecture of proposed model 1

The proposed CNN model-based binary classifier design is made up of many convolutional and pooling layers, followed by a fully connected (FC) layer for classification. The pooling layers minimize the spatial dimensions of the feature maps while the convolutional layers extract and manipulate data from input images. The model employs the rectified linear unit (ReLU) activation function to induce nonlinearity, which improves the model's discriminative capability. To prevent overfitting, 0.5 dropout regularization is utilized. To obtain the binary classification prediction, the output of the last layer is passed via a sigmoid function. The cross-entropy loss between true labels and predicted labels is computed using the binary cross entropy loss function and the rmsprop optimizer. Because of its capacity to learn complex characteristics from images, the suggested architecture has exhibited good performance in binary image classification tasks. *Table 4* shows the various characteristics of the proposed classifier.

Components of proposed model 1 architecture convolutional layer

The first and most important part of a CNN is the convolutional layer. It uses a mathematical process called "convolution" on the image it is given to find and learn key features or patterns in the image. Convolution is done with a set of filters, which are also called kernels or weights. These filters slide over the input image and multiply and add each element to make feature maps [45]. Then, these feature maps are sent through activation functions and pooling layers

to reduce the size of the network and make it deeper. As seen in *Figure 4*, this layer includes filters that can be learned. Convolutional layers are crucial in enabling CNNs to effectively process and analyze visual information, making them popular for image classification and other computer vision tasks. Equation 1 is used to calculate output parameters in the convolution layer. Where w represents the width, h is the height, d is the dimension of the input image, and N is the number of filters.

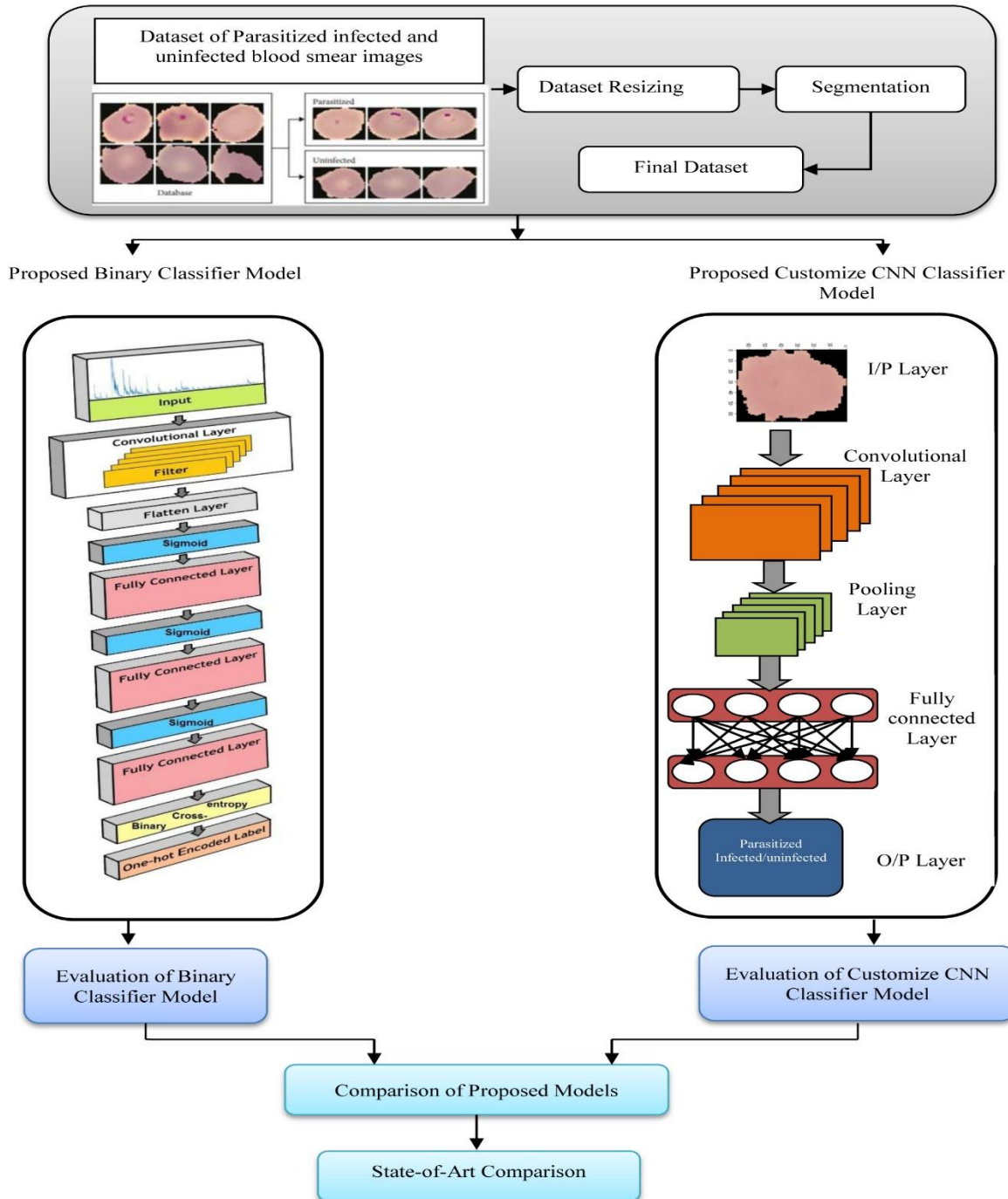$$No. \, of \, output \, parameters = (((w \times h \times d) + 1) \times N) \quad (1)$$

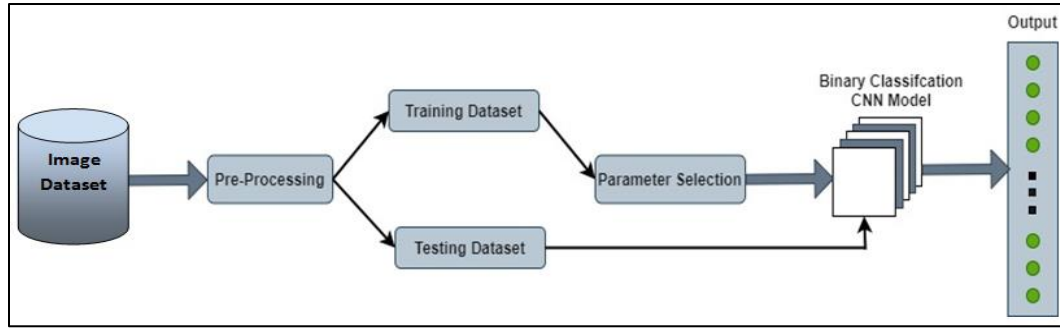**Figure 2** Block diagram of proposed research methodology

998

Figure 3 CNN Model based binary classifier

Table 4 Parameters of the proposed model 1 - CNN model based binary classifier

| S. No.	Layers	Input Image size	Filter size	No. of filter	Activation function	Output	Parameters
1	Input Image	64×64×3	--	--	--	--	--
2	Convolutional	64×64×3	3×3	32	ReLu	62×62×32	896
3	Maxpooling	62×62×32	Poolsize (2×2)	--	--	31×31×32	0
4	Convolutional	31×31×32	3×3	32	ReLu	29×29×32	9248
5	Maxpooling	29×29×32	Poolsize (2×2)	--	--	14×4×32	0
6	Convolutional	14×14×32	3×3	32	ReLu	12×12×64	18496
7	Maxpooling	12×12×64	Poolsize (2×2)	--	--	6×6×64	0
8	Flatten	6×6×64	--	--	--	6×6×64	0
9	Dense	2304	64	--	ReLu	64	147520
10	Dense	64	1	--	Sigmoid	1	65
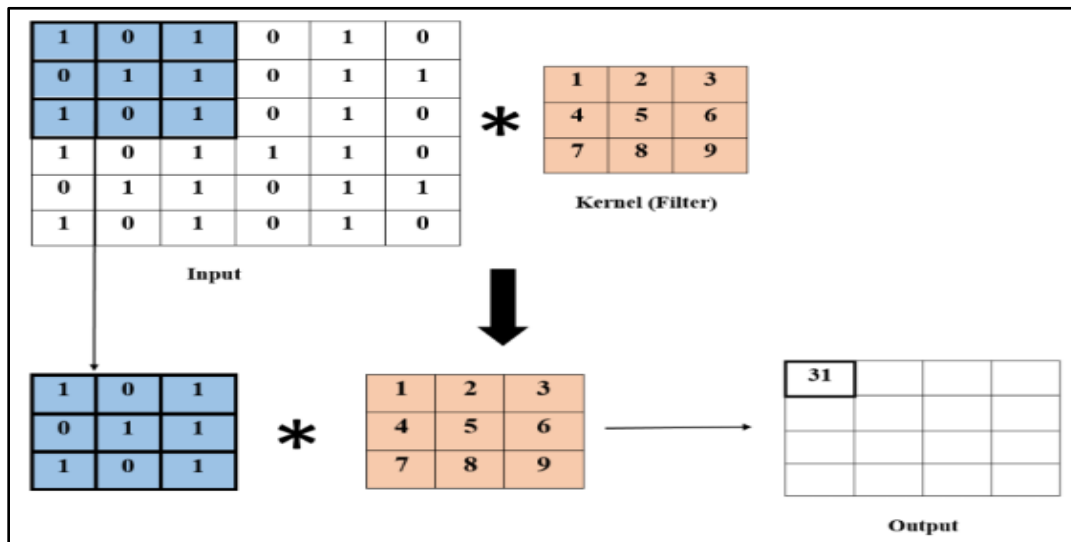
Figure 4 Convolutional layer

Rectified linear unit (ReLU) layer
ReLU activation functions avoid the vanishing gradient problem in DL networks, especially CNNs. DL networks often use this activation function to avoid the vanishing gradient issue, which is common in deep networks, it replaces all negative input values

with zero. Mathematically, the function is written in Equation 2, where i is the input and t are the output. ReLU activation functions are simple, easy to compute, and have been shown to make many DL models work better. In addition to ReLU, there are other types of activation functions, such as leaky

ReLU, which lets small negative values through, and parametric ReLU, where the slope of the function can be learned through training.

$$t = maximum(0, i) \qquad (2)$$

Batch normalization

Batch normalization normalizes neural network layer activations. It processes layer inputs before the activation function. Batch normalization reduces internal covariate shift and stabilizes and optimizes training. It reduces the variance of layer inputs, which makes the optimization process smoother and reduces the network's SEN to initialization. Batch normalization normalizes activations for each mini-batch of data during training and scales and shifts them using learned parameters. Normalization makes the network more robust and faster learning by preventing it from being excessively sensitive to large or small inputs. The calculation of output parameters is shown in Equation 3.

$$Parameters = (d \times 4) \qquad (3)$$

Here, d represents the value of the dimension that was output by the layer before it. For instance, if the input image for the batch normalization layer is 3×3×32, then d=32.

Pooling layer

CNN frequently employ the pooling layer to reduce the size of the feature images produced by the convolutional layers. Its main goal is to make network processes simpler while keeping the crucial data in the feature maps. The two most widely used pooling techniques are maximum pooling and average pooling. As seen in *Figure 5*. The size of the feature maps and the number of parameters and computations needed by the network are both reduced by max pooling in CNN, which outputs the maximum value in a particular region of the feature map. In average pooling, the output is the average value of the same region. Pooling helps prevent the network from overfitting by reducing the number of parameters and computational resources needed. It also increases the network's spatial invariance, making it less sensitive to small changes in the input image.
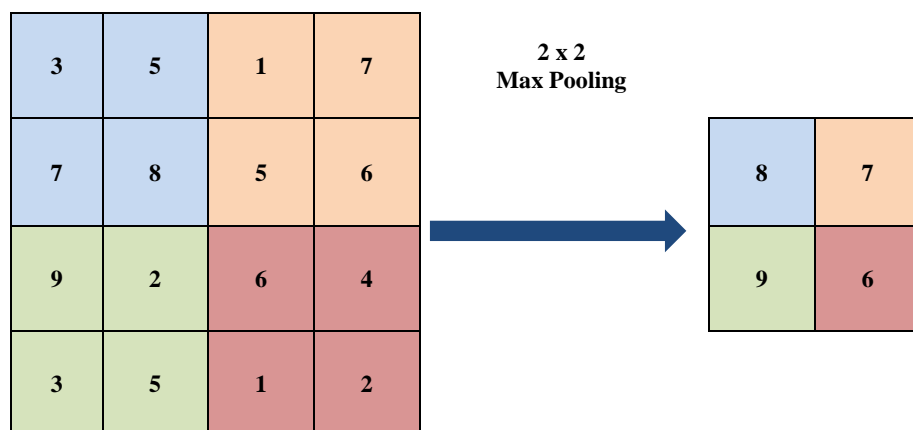

Figure 5 Pooling layer (2×2 Max pool)

Dropout layer

It is a regularization technique used to prevent overfitting in DL neural networks as shown in *Figure 6*. During training, the dropout layer sets a predefined proportion of input units to 0, compelling the network to learn numerous distinct representations of the input data. This prevents the network from remembering the training data and failing to generalize to new input. Typically, the dropout rate, or the proportion of input units set to 0, is between 0.5 and 0.8. During

testing, all input units are used, and their activations are scaled by the inverse of the dropout rate to compensate for the decreasing number of active units during training. Dropout is commonly utilized to enhance model performance and stability in several neural network types, including CNNs and recurrent neural networks. The major purpose of this layer is to eliminate some arbitrary group of functions in the layer by assigning a value of zero to each of those functions.
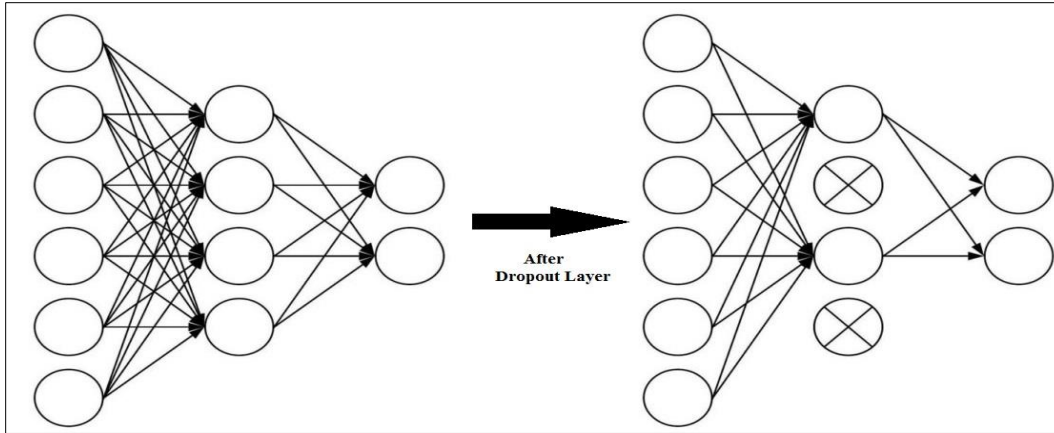
Figure 6 Dropout layer

FC layer

A deep neural network (DNN) completely connected layer is its brain. Every neuron in this layer is linked to every neuron in the layer above, as shown in *Figure 7*. Every neuron in a FC layer receives information from the layer below it, weights those inputs, and then sums them. After that, an activation function like ReLU, Sigmoid, or Tanh is applied to each neuron's output. By combining several fundamental characteristics from the layer before it, these layers in DL models are used to extract high-level features from the raw input data. By combining the features that were picked up in the previous layer, this is achieved. Class probabilities can be generated from the output of the final FC layer for use in classification challenges.
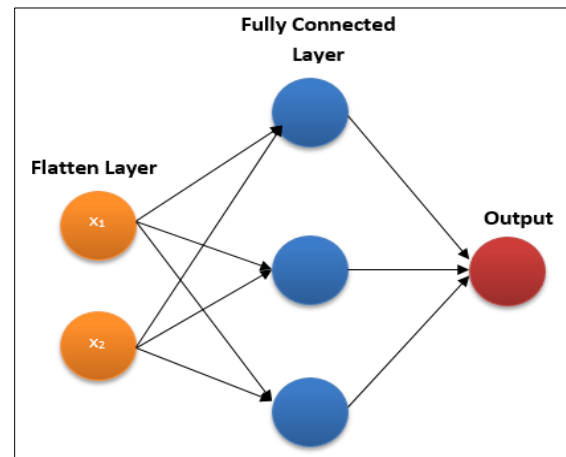

Figure 7 FC layer

Activation functions

Activation functions are utilized in neural networks to apply a mathematical operation on the output of each neuron to determine the neuron's output signal. This signal is used to determine if the neuron should be "activated" and pass information to the next layer in the network. Activation functions are critical in enabling neural networks to model complex, nonlinear relationships between input and output data. Common activation functions include Sigmoid, ReLU, and Tanh. Each of these functions has its unique characteristics and is best suited for particular types of neural networks or specific problems. They add complexity and nonlinearity to the model, which lets it learn complex ways to represent the data it is given. ReLU, Sigmoid, Tanh, and Softmax are all common activation functions. They are important design decisions that can have a significant effect on how well a neural network works.

Sigmoid

It is one of the most common non-linear activation functions. Sigmoid changes the values between 0 and 1 in a certain way. The mathematical function of the sigmoid function is shown in Equation 4 and a graph of the Sigmoid function is shown in *Figure 8*.

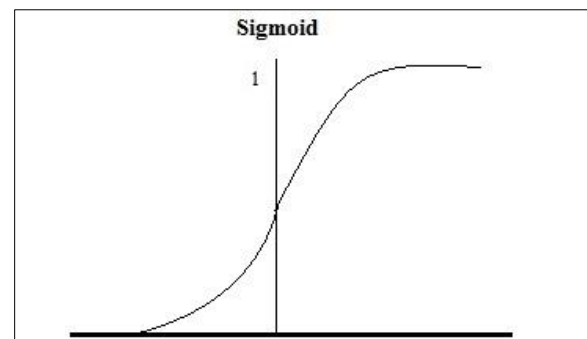$$S = \frac{1}{(1+e^{\wedge}-k)} \tag{4}$$

Figure 8 Sigmoid function

3.5.2 Proposed Model 2 - malaria disease classification with customize CNN model

In recent years, DL has become increasingly widespread for use in the classification of medical images. Mostly, DL refers to a type of neural network that has several layers between the input and the output. Although a normal neural network has between one and two hidden layers, DNN include multiple layers. For the purpose of performing malaria disease classification in blood smear images, a customized CNN model has been proposed. There is no provision for the manual extraction of features in DNN. Using a wide range of different convolutional building components is required in order to successfully develop a customize CNN. The architecture of each convolutional block includes both convolutional layers and max pooling layers. After that, the proposed customized CNN model is evaluated with regard to a number of various factors.

A customized CNN has been built to detect malaria parasites using blood smear images. In this model, two convolutional layers and four hidden layers were built consecutively. Each convolutional layer's output was added to the max-pooling layer, and the max-pooling layer's output was added for batch normalization. A dropout layer has been added at the end of each convolutional layer. Dropout causes certain neurons in the network to be turned off at random, forcing the data to seek other pathways. As a result, overfitting is reduced. Following the convolutional layers, four dense layers were added at the end for class prediction.

Finally, the model was built with a categorical cross entropy loss function, an Adam optimizer, and an ACC metric. The dataset was then fitted to the model, i.e. the proposed model was trained for different epochs and batch sizes. After training the model, evaluated the loss and ACC of the model on the test dataset.

Architecture of proposed model 2

The proposed customized CNN model is put to use in order to classify blood smear images collected from microscopy in order to determine whether or not they are infected of the malaria disease. The CNN model has a number of distinct convolution blocks, each of which is composed of convolution layers and max pooling layers. The size of the image being input is 64 x 64 pixels. The image that was provided as input is then sent on to the first convolution block of the proposed customized CNN model. One convolutional layer and one max pool layer are included in the first convolution block. Detail architecture of proposed customized CNN model is following:

Proposed customized CNN model is developed using the Keras API. The model is designed to classify images into one of two classes, and the input shape of the images is (64, 64, 3). Following is a brief explanation of each layer in the model:

Input Layer: The input layer is defined using the Input class from Keras, with the shape of the input images specified as (64, 64, 3).

Convolutional layers: Two convolutional layers are defined, each with a kernel size of (3, 3) and 32 filters. The activation parameter is set to 'relu', and the padding parameter is set to 'same'. The first convolutional layer takes the input layer as its input, while the second takes the output of the first layer.

Max pooling layers: Two max pooling layers are defined, each with a pool size of (2, 2). The first max pooling layer takes the output of the first convolutional layer as its input, while the second takes the output of the second convolutional layer.

Batch Normalization Layers: 4 batch normalization layers are defined, each with the axis parameter set to -1. The output of the first max pooling layer is the input for the first batch normalization layer, whereas the output of the second max pooling layer is the input for the second batch normalization layer. The remaining two batch normalization layers are connected to the FC layers.

Dropout layers: Six dropout layers are defined, each with a rate parameter of 0.2. The first dropout layer takes the output of the first batch normalization layer as its input, while the remaining five are connected to the FC layers.

Flatten layer: The flatten layer is used to flatten the output of the second max pooling layer, which is a 3D tensor, into a 1D tensor that can be fed into the FC layers.

FC layers: Four FC layers are defined, with 512, 256, 128, and 64 units respectively. The activation function for each of these layers is set to 'relu'. The first FC layer takes the output of the flatten layer as its input, while the remaining three are connected to the output of the preceding dropout and batch normalization layers.

Output layer: The output layer is a FC layer with 2 units and the activation function set to 'sigmoid', which is used for classification. It takes the output of the final dropout and batch normalization layer as its input.

Model compilation: Finally, the model is compiled using the compile method. The optimizer parameter

is set to 'Adam', which is a popular optimizer for training neural networks. The loss parameter is set to 'categorical_crossentropy', which is the loss function for classification problems. The metrics parameter is set to ['ACC'], which means that the ACC metric will be used to evaluate the performance of the model during training and testing.

Model summary: The model summary is printed using the summary method of the Keras model. The block diagram of the proposed customized CNN model is shown in *Figure 9* and the proposed model architecture is shown *Figure 10* It displays the layers of the model, their output shapes, and the number of trainable parameters in the model.
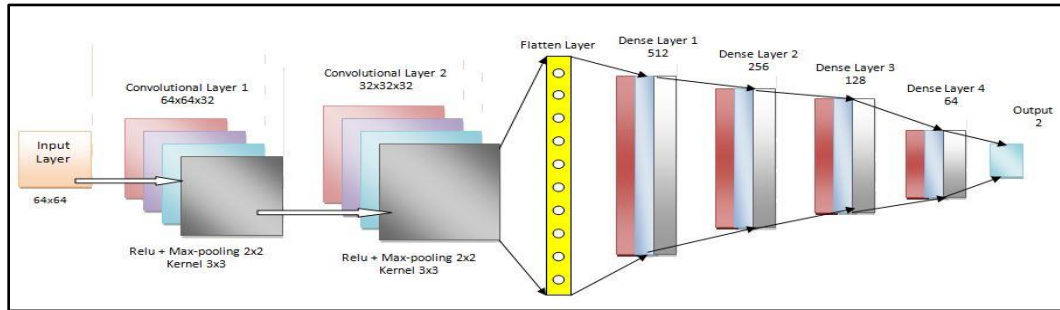

Figure 9 Block diagram of proposed customized CNN model

Figure 10 Proposed customized CNN model architecture

Model: "model"

Layer (type)	Output Shape	Param #
input_1 (InputLayer)	[(None, 64, 64, 3)]	0
conv2d (Conv2D)	(None, 64, 64, 32)	896
max_pooling2d (MaxPooling2D)	(None, 32, 32, 32)	0
batch_normalization (BatchNo	(None, 32, 32, 32)	128
dropout (Dropout)	(None, 32, 32, 32)	0
conv2d_1 (Conv2D)	(None, 32, 32, 32)	9248
max_pooling2d_1 (MaxPooling2	(None, 16, 16, 32)	0
batch_normalization_1 (Batch	(None, 16, 16, 32)	128
dropout_1 (Dropout)	(None, 16, 16, 32)	0
flatten (Flatten)	(None, 8192)	0
dense (Dense)	(None, 512)	4194816
batch_normalization_2 (Batch	(None, 512)	2048
dropout_2 (Dropout)	(None, 512)	0
dense_1 (Dense)	(None, 256)	131328
batch_normalization_3 (Batch	(None, 256)	1024
dropout_3 (Dropout)	(None, 256)	0
dense_2 (Dense)	(None, 128)	32896
batch_normalization_4 (Batch	(None, 128)	512
dropout_4 (Dropout)	(None, 128)	0
dense_3 (Dense)	(None, 64)	8256
batch_normalization_5 (Batch	(None, 64)	256
dropout_5 (Dropout)	(None, 64)	0
dense_4 (Dense)	(None, 2)	130

Total params: 4,381,666
Trainable params: 4,379,618
Non-trainable params: 2,048

4.Results

For the evaluation of proposed models, different evaluation metrics are used that are discussed below. After this, trained models are compared with state-of-art techniques.

Evaluation metrics

The different parameters that are used for performance measurement for classification are PRE, SEN, SPE, FS and ACC. After considering all the parameters from the confusion matrix, the actual values and the predicted values are presented in *Table 5*.

The term "true positive" (TP) refers to the situation in which both the observed and projected classes for a given data item are true. The term "false positive" (or "FP") refers to a situation in which the actual class of the data point is inaccurate, whereas the class that was predicted was accurate. A "true negative (TN)," abbreviated as "TN," indicates that both the observed and projected classes of the corresponding data item are false. False negative (FN) occurs when the real class of the data point is different from the projected class.

PRE: is measured by dividing the number of TP by the combined total of TP and FP, as seen in Equation 5.

$$\text{Precision(PRE)} = \frac{TP}{TP+FP} \qquad (5)$$

SEN: is defined as the ratio of TP to the sum of TP and FN as shown in Equation 6. Range of SEN is between 0 and 1.

$$\text{Sensitivity (SEN)} = \frac{TP}{TP+FN} \qquad (6)$$

SPE: is defined as the ratio of TN to the sum of positive as shown in Equation 7. Range of SPE is between 0 and 1.

$$\text{specificity (SPE)} = \frac{TN}{FP+TN} \qquad (7)$$

FS: A statistic for ML that can be utilized in classification models is referred to as the FS. In order to calculate the FS, one should combine the PRE and recall metrics into a single measure, as illustrated in the Equation 8.

$$\text{F1 Score (FS)} = \frac{2 \times TP}{2*(TP+FP+FN)} \qquad (8)$$

ACC: is computed by dividing the total number of true events, which is the sum of TP and TN, by the sum of TP, FP, TN, and FN, FP, as illustrated in Equation 9.

$$\text{Accuracy (ACC)} = \frac{TP+TN}{TP+FN+FP+FN)} \qquad (9)$$

Table 5 Confusion matrix

		Actual	
		+ve	-ve
Predicted	**+ve**	TP	FP
	-ve	FN	TN

4.1 Result analysis of proposed model 1

The proposed classifier was put into place to train and test it on a set of 27558 images of blood smears. 70% of the 27558 blood smear images were used to train the model while 30% were used to test the model. The last layer of output gives back a single number between 0 and 1. If the result of the final output layer of the trained model is near to 0, then the image has been parasitized; however, if it is close to 1, then the image has not been parasitized. After the different hyper-parameters of the proposed model were set up, the final trained model had an ACC of 90.20 percent, and it took the proposed model 207 minutes to train.

Hyper-parameter Configuration

The system must be trained with a number of parameters, each of which must be optimized at different training levels. After examining and assessing the outcomes at various phases, the batch size, epoch size, loss function, optimizer configuration algorithm, and activation function were configured. Batch size, epoch size, activation function, loss function, and optimizer settings all have default setup options of 32, 30, Sigmoid, binary crossentropy, and AdaDelta. The results are shown in *Figure 11* according to various epoch sizes. Training loss decreased from 0.510 to 0.0102 and training ACC increased from 0.609 to 0.9892 as seen in *Figure 12* for models trained and tested with varying epoch sizes. Increasing the epoch count resulted in a decrease in Val Loss from 0.441 to 0.160. This model achieved a best-in-class 75% Val ACC across 30 epochs.

The epoch size parameter was set to 30 with the validation ACC 75%, and successive CNN models were trained and tested on varied batch sizes. Overfitting was found in models trained and tested with 96, 128, and 160 batches, while models trained and tested with 32 and 64 batches generated the best results. *Figure 13* shows the best performance with a batch size of 32.

```
Model: "sequential"
Layer (type)                 Output Shape              Param #
=================================================================
conv2d (Conv2D)              (None, 62, 62, 32)        896
activation (Activation)      (None, 62, 62, 32)        0
max_pooling2d (MaxPooling2D) (None, 31, 31, 32)        0
conv2d_1 (Conv2D)            (None, 29, 29, 32)        9248
activation_1 (Activation)    (None, 29, 29, 32)        0
max_pooling2d_1 (MaxPooling2 (None, 14, 14, 32)        0
conv2d_2 (Conv2D)            (None, 12, 12, 64)        18496
activation_2 (Activation)    (None, 12, 12, 64)        0
max_pooling2d_2 (MaxPooling2 (None, 6, 6, 64)          0
flatten (Flatten)            (None, 2304)              0
dense (Dense)                (None, 64)                147520
activation_3 (Activation)    (None, 64)                0
dropout (Dropout)            (None, 64)                0
dense_1 (Dense)              (None, 1)                 65
activation_4 (Activation)    (None, 1)                 0
=================================================================
Total params: 176,225
Trainable params: 176,225
Non-trainable params: 0
```

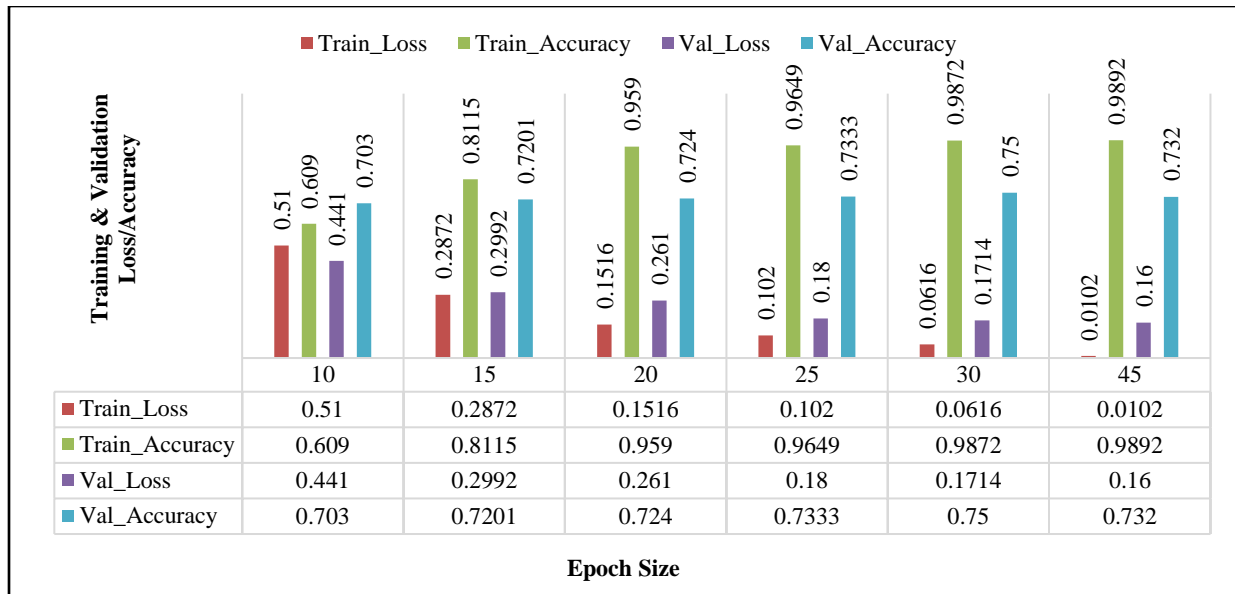**Figure 11** Screenshot of the proposed model 1 architecture

	10	15	20	25	30	45
■ Train_Loss	0.51	0.2872	0.1516	0.102	0.0616	0.0102
■ Train_Accuracy	0.609	0.8115	0.959	0.9649	0.9872	0.9892
■ Val_Loss	0.441	0.2992	0.261	0.18	0.1714	0.16
■ Val_Accuracy	0.703	0.7201	0.724	0.7333	0.75	0.732

Epoch Size

Figure 12 Training & validation loss / ACC for different epoch sizes

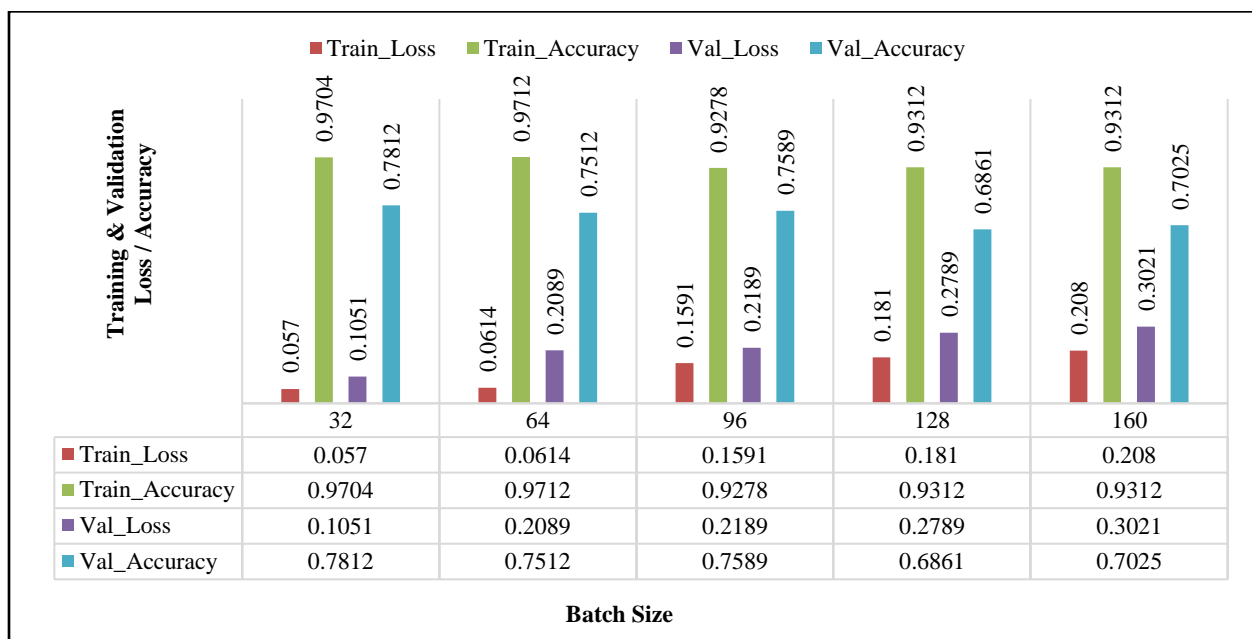|	32	64	96	128	160
■ Train_Loss	0.057	0.0614	0.1591	0.181	0.208
■ Train_Accuracy	0.9704	0.9712	0.9278	0.9312	0.9312
■ Val_Loss	0.1051	0.2089	0.2189	0.2789	0.3021
■ Val_Accuracy	0.7812	0.7512	0.7589	0.6861	0.7025

Batch Size

Figure 13 Training & Validation Loss / ACC for different Batch sizes

After determining the best epoch and batch size, the dataset is trained and tested on several optimizer algorithms, which serve as DL standards. *Figure 7* presents the results of various optimizers. According to the findings, the AdaGrad optimizer algorithm has a low training ACC and a high training loss. Both RMSProp and stochastic gradient descent (SGD) are overfitted when it comes to optimizers. Based on the values of Val Loss and Val ACC in *Figure 14*, Adam is the best optimizer method for

this model, followed by AdaDelta. As shown in *Figure 15*, the suggested model is trained and assessed using a range of activation functions in an attempt to increase classification PRE. According to the results of the activation function analysis, the Relu activation function, Softmax activation function, and Elu activation functions are not well-matched for binary classification but are matched for multi-class classification. Although having a high Val ACC, the Tanh activation function is an overfit model. A

sigmoid activation function with a Val loss of 0.171% yields the best PRE. Considering this, the diagram below depicts our conclusion that the sigmoid activation function is the best fit activation function for our suggested model. Finally, the optimal model has been determined by experimenting with various loss functions.
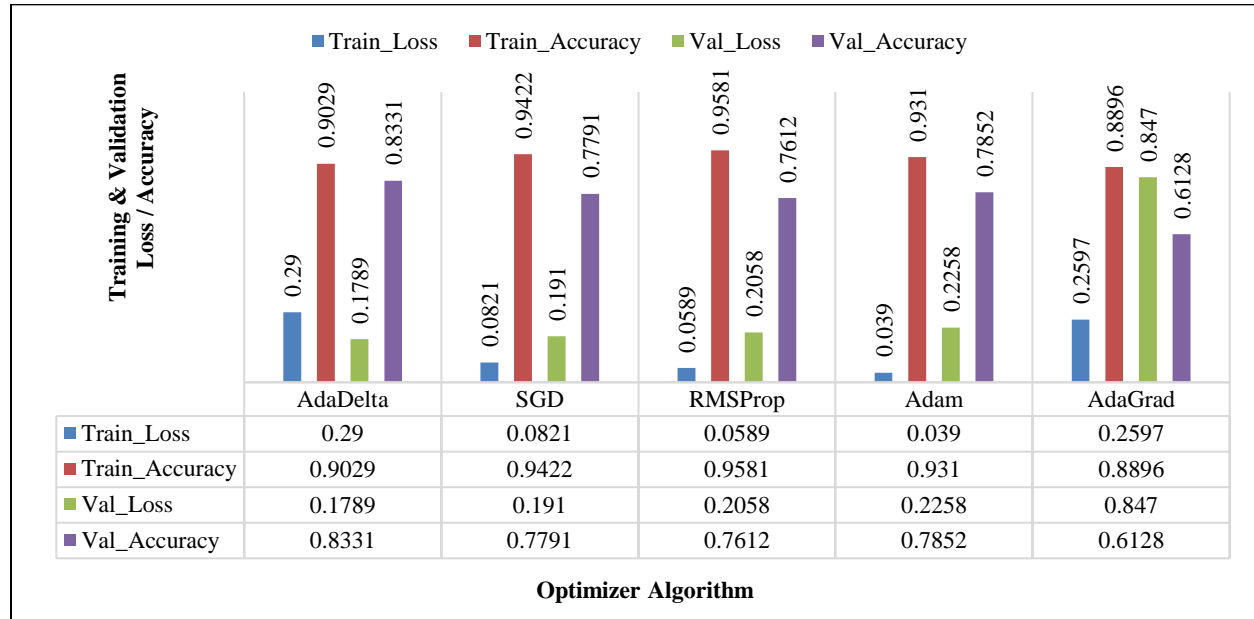
	AdaDelta	SGD	RMSProp	Adam	AdaGrad
Train_Loss	0.29	0.0821	0.0589	0.039	0.2597
Train_Accuracy	0.9029	0.9422	0.9581	0.931	0.8896
Val_Loss	0.1789	0.191	0.2058	0.2258	0.847
Val_Accuracy	0.8331	0.7791	0.7612	0.7852	0.6128

Optimizer Algorithm

Figure 14 Training & validation loss / ACC for different optimizer algorithms

Tabulated in *Figure 16* are the outcomes obtained using various loss functions. The findings of the Categorical Hinge model are found to be inferior when compared to those of other models after reviewing *Figure 16*. It was discovered that different models yielded different results but within the same numeric range. In terms of Val ACC, mean absolute percentage error (MAPE) achieved 86.6% and Binary loss functions achieved the best ACC of 90.2%. Visualize results are shown in the *Figure 16*.
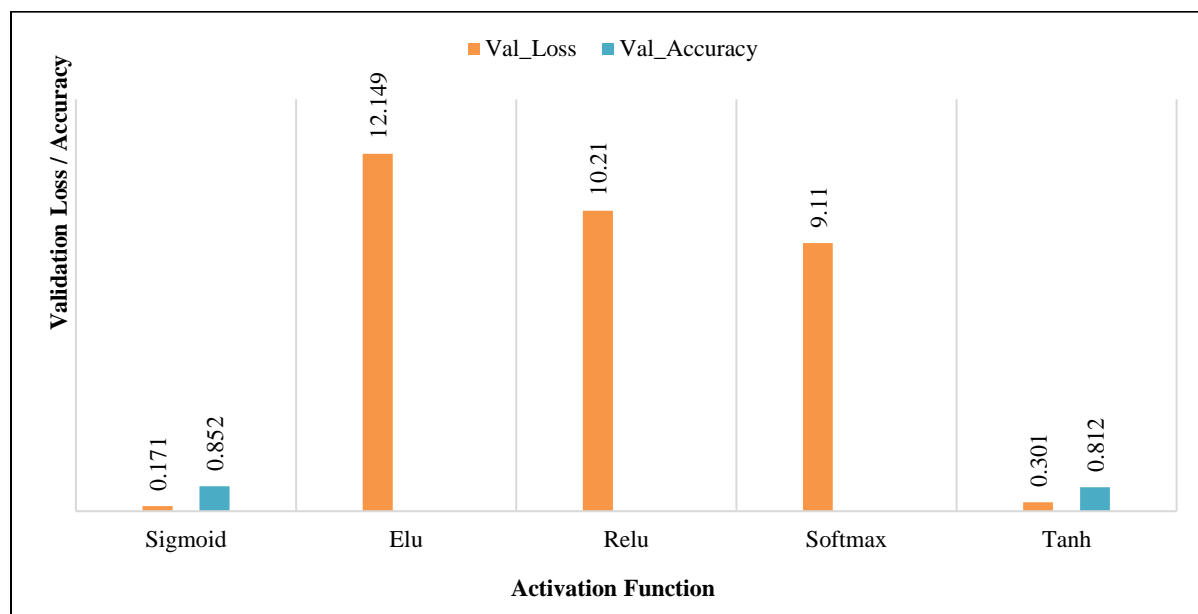
Figure 15 Training & validation loss / ACC for different activation functions
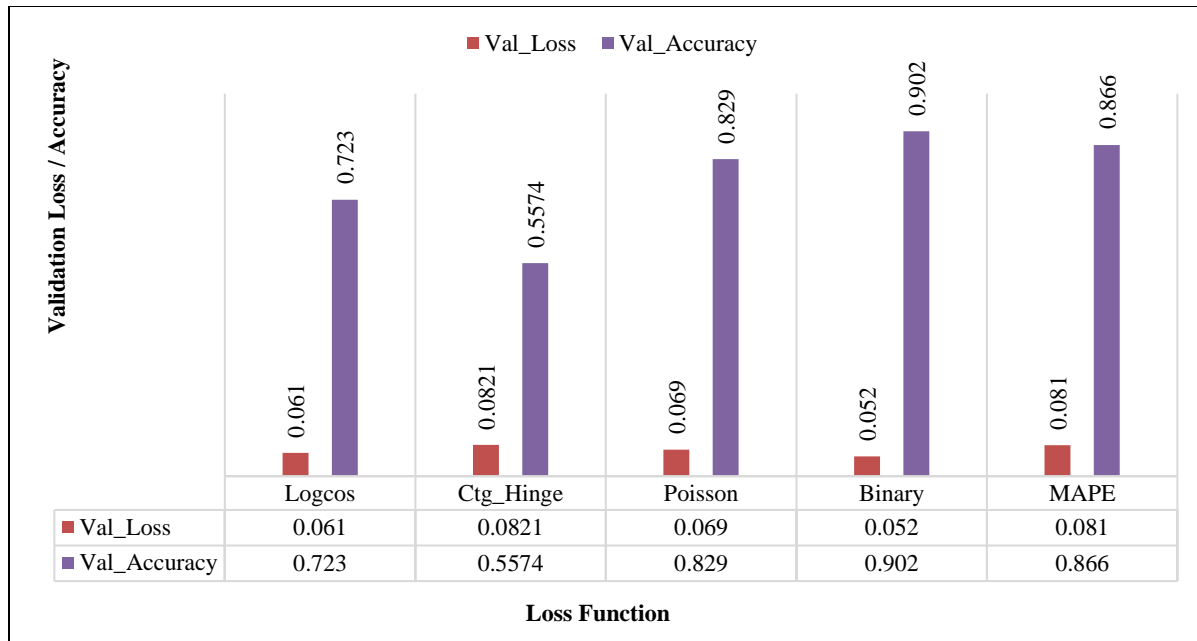
Figure 16 Training & validation loss / ACC for different loss functions

Result analysis based on confusion matrix
Several simulation parameters are used to test the proposed Binary classifier algorithm. A confusion matrix, which is a table that displays the number TP, TN, FP, and FN produced by a suggested binary classification algorithm, summarizes the classification results. *Figure 17* depicts the confusion matrix for the suggested binary classification method. In *Figure 17*, TP denotes the number of parasitized positively labelled instances, which in this case is 4058. The number of infectious negative cases appropriately labelled as negative, TN, is 3449. The number of parasitized tagged individuals that were incorrectly classed as negative is 305. The number of uninfected people that were incorrectly labelled as positive is 510.
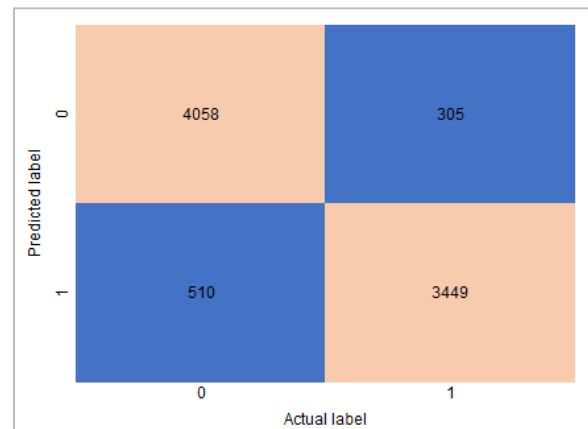
The parameters of the confusion matrix tell us a lot about how well a proposed classification technique works. Some of the most common metrics that can be worked out from the parameters of the confusion matrix are shown in *Table 6*.

Table 6 Proposed binary classification technique results

Classification report				
PRE	Recall	SPE	ACC	F1 score
0.930	0.888	0.919	0.902	0.909

Figure 17 Confusion matrix for the proposed binary classification technique

4.2 Result analysis of proposed model 2
Malaria blood smear images are used to test the suggested customized CNN model using simulated settings. Batch size, optimizer, and epochs are the different simulation parameters employed in the analysis. For the evaluation of the proposed CNN model with the Adam optimizer, a batch size of 64, and epoch size of 20 is used. An analysis of the proposed model is carried out based on the confusion matrix parameters, the model's ACC, and the findings of an analysis of the model's loss.

Analysis based on model ACC and model loss

Figure 18 and *Figure 19* depict the model ACC and model loss lines respectively, as they relate to classification using the proposed CNN model. The value of ACC improves as the number of epochs increases, while the value of loss falls as the number of epochs rises. The analysis was carried out on a total of 20 epochs. *Figure 18* demonstrates that the proposed customized CNN model has a model ACC of 96.02% throughout a maximum of 20 epochs. The value of the model's ACC is roughly 92.51% when it is evaluated on the 9th epoch. The value of ACC also increases in parallel with the epoch value as it goes higher.

The proposed model loss values are displayed in *Figure 19* for a total of 20 epochs. While the value of the epoch continues to increase, the value of loss continues to decrease. As the number of epochs increases, it can be seen from the graph that the highest value of loss is around 1.1, and that this value goes down as the number of epochs increases.

Result analysis based on confusion matrix

The confusion matrix for the proposed customize CNN classification technique is shown in *Figure 20.* In the shown confusion matrix, the model has made a total of 8267 predictions, out of which 4429 are TP and 3509 are TN. This means that the model correctly predicted 4429 positive cases and 3509 negative cases.

However, the model has also made some incorrect predictions. It has predicted 197 cases as malaria positive that are actually negative, which are FP. Similarly, it has predicted 132 cases as malaria negative that are actually positive, which are FN.

Along with these results, some other important metrics have also been calculated, including PRE, SEN, SPE, ACC and FS as shown in *Table 7.*

How much of the model's positive predictions were accurate is referred to as PRE. It is calculated as TP/(TP+FP), which in this case is 0.957. This means that 95.7% of the positive predictions made by the model were actually positive, and only 4.3% were FP. A high PRE value indicates that the model is good at identifying TP, with few FP.

Recall, also called as SEN, is a measurement of how many real positive instances the model accurately recognized. In this instance, it is computed as TP/(TP+FN), which is 0.971%. This indicates that the model successfully detected 97.1% of the real positive instances. A high recall score shows that the model accurately identifies all positive situations while producing a few FN.

SPE is the proportion of real negative instances that were accurately detected by the model. In this case, it is computed as TN/(TN+FP), which is 0.947%. This indicates that 94.7 percent of negative situations were accurately detected by the model. A high SPE score suggests that the model accurately identifies all negative situations while producing minimal false positives.
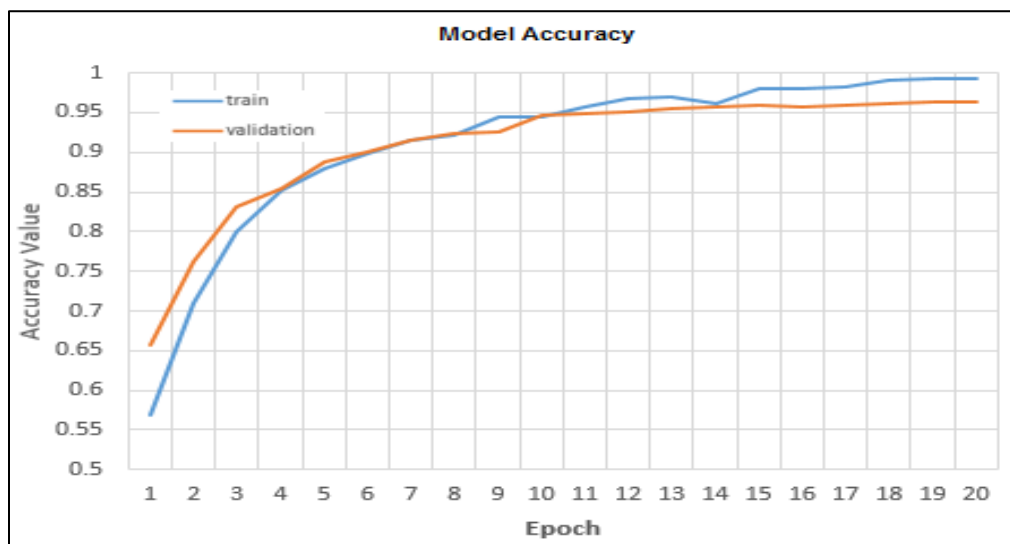

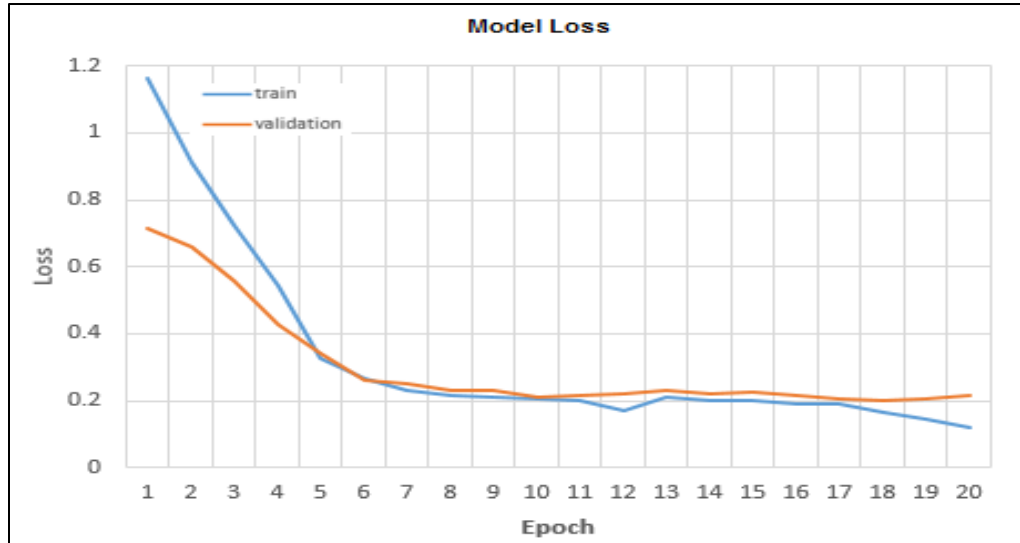**Figure 18** Training & validation ACC of proposed model 2

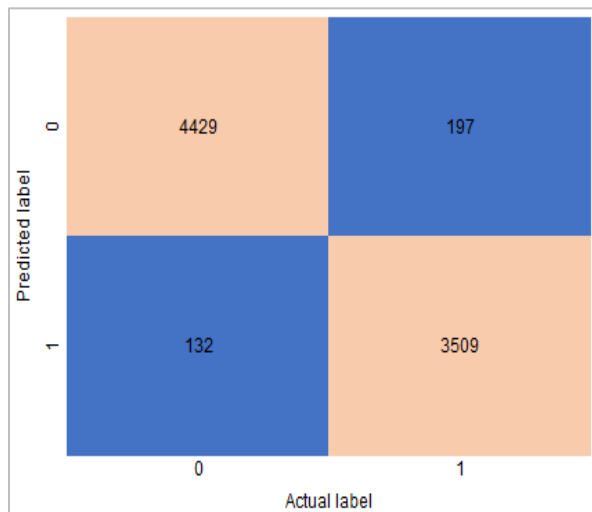**Figure 19** Training & validation loss of proposed model 2

Figure 20 Confusion matrix for the proposed customize CNN technique

ACC is the proportion of total predictions produced by the model that were accurate. In this case, it is computed as (TP+TN)/(TP+TN+FP+FN), which is 0.9602. This indicates that the model's predictions were true in 96.02 percent of instances. A high ACC number implies that the model is effective at distinguishing positive and negative situations.

The FS is a weighted average of the ACC and recall values, and it accounts for both false positives and FN. The model's FS is 0.964%. A high FS shows that the model is effective at recognising genuine positives as well as avoiding false positives and FN.

Table 7 Proposed customize CNN classification technique results

Classification report				
PRE	**Recall**	**SPE**	**ACC**	**F1 score**
0.957	0.971	0.947	0.960	0.964

5.Discussion

In the presented research, two approaches for binary categorization of malaria blood smear images are thoroughly analysed. The performance of the models is depicted by the confusion matrices in *Figure 15*. Using the first method, 4058 TP and 3449 TN are obtained, yielding a 90.2% ACC rate. However, it incorrectly categorized 510 non-infected patients as positive and 305 parasite-infected ones as negative. With a greater ACC of 96.02%, the second technique—a customized CNN model—performs better than the first. There are fewer errors made, with 197 parasite-infected patients labelled as negative and 132 non-infected cases tagged as positive, but it accurately detects 4429 positive and 3509 negative cases.

The ACC and loss curves for both approaches are shown in *Figure 16*, which indicates that as the number of epoch's rises, ACC rises and loss falls. The customized CNN model achieves 96.02% ACC and consistently performs well over all 20 epochs. The customised CNN model outperforms existing methodologies when compared to state-of-the-art models (*Table 8*), indicating its efficacy for classifying malaria parasites in microscopy blood smear pictures.

Overall, the study emphasizes the importance of the personalized CNN model, which offers a significant advancement in the field of malaria diagnosis by image classification.

Comparison of proposed models based on confusion matrix

The confusion matrix gives a very clear representation of both the actual labels and the predicted labels. *Figure 21(a)* shows the confusion matrix of the binary classification technique used on the malaria blood smear dataset. 4058 cases were correctly labelled as positive, and 3449 cases were correctly labelled as negative, even though they were not infected. There were 305 labels with parasites that were wrongly labelled as negative, and there were 510 labels without parasites that were wrongly labelled as positive. After analysis of confusion matrix it is clearly stated that the proposed technique achieved an ACC of 90.2%. The confusion matrix for the binary classification method used on the malaria blood smear dataset is shown in *Figure 21(b)*. 4429 cases were correctly labelled as positive, and 3509 cases were correctly labelled as negative, even though they were not infected. There were 197 labels with parasites that were wrongly marked as negative, and 132 labels without parasites that were wrongly marked as positive.

After looking at the confusion matrix, it is clear that the proposed method has a 96.02% ACC rate.

Result analysis of proposed models based on ACC and model loss

Figure 22 shows the ACC and loss curves for the proposed techniques. A binary classification technique is presented for the classification of malaria blood smear images. Results of the presented technique are shown in *Figure 22(a)* and *Figure 22(b)*. After analysis of the graph, it is observed that as the value of the epochs increases, the ACC of the proposed technique is increased and as with the value of epochs, the loss value decreases. After the completion of the 30 epochs proposed technique achieved an ACC of 90.2%.

Figure 22(c) and *Figure 22(d)* depict the model ACC and model loss lines respectively, as they relate to classification using the proposed CNN model. The value of ACC improves as the number of epochs increases, while the value of loss falls as the number of epochs rises. The analysis was carried out on a total of 20 epochs. *Figure 22(c)* demonstrates that the proposed customized CNN model has a model ACC of 96.02% throughout a maximum of 20 epochs. The value of the model's ACC is roughly 92.51% when it is evaluated on the 9th epoch. The value of ACC also increases in parallel with the epoch value as it goes higher. The proposed customize CNN model loss values are displayed in *Figure 22(d)* for a total of 20 epochs. While the value of epoch continues to increase, the value of loss continues to decrease. As the number of epochs increases, it can be seen from the graph that the highest value of loss is around 1.1, and that this value goes down as the number of epoch's increases.
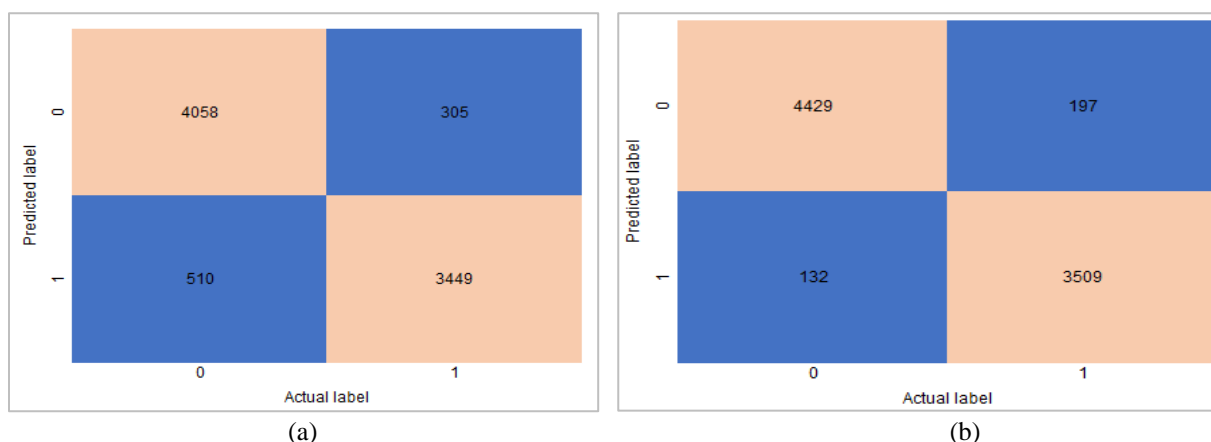

(a)   (b)

Figure 21 Confusion matrix (a) Proposed binary classification technique (b) Proposed customize CNN technique
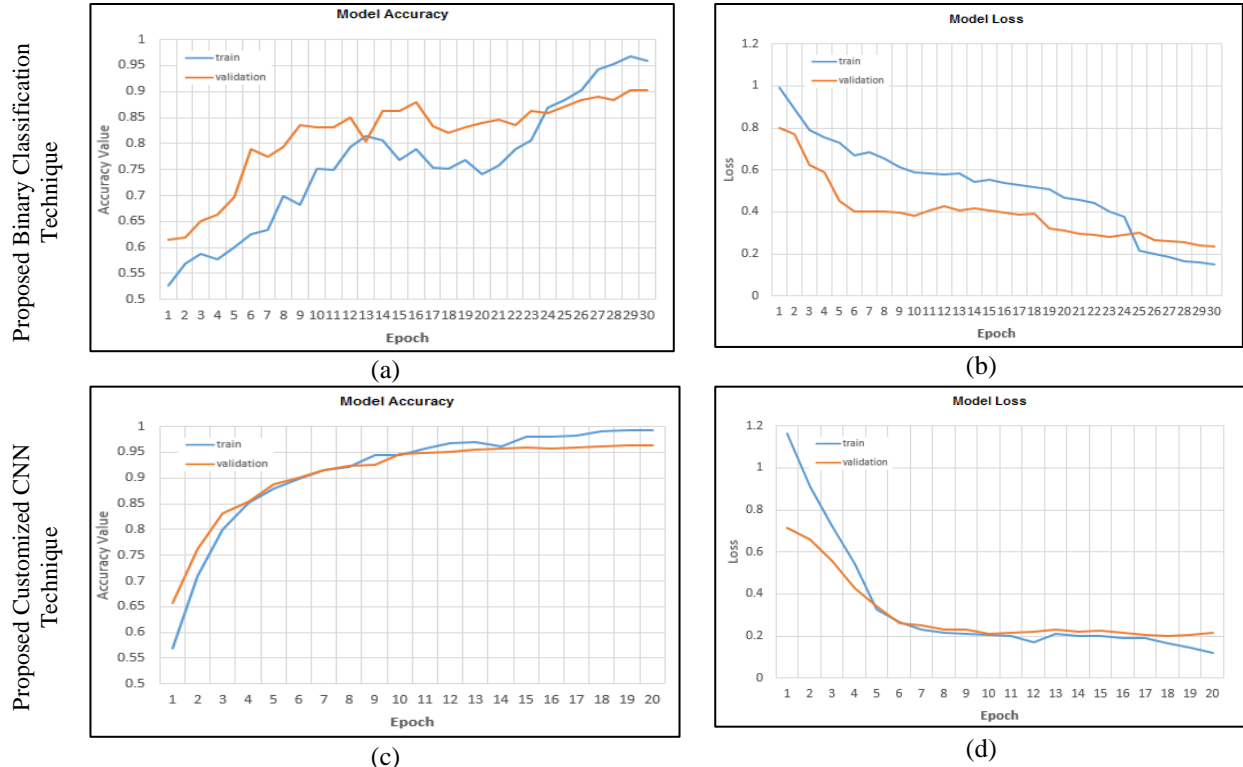
Figure 22 (a) ACC of Binary Classification Technique (b) Loss of Binary Classification Technique (c) ACC of Customize CNN Classifier (d) Loss of Customize CNN Classifier

Comparison of proposed techniques with state-of-the-art techniques

In order to test and validate the proposed techniques, *Table 8* depicts a comparison between the proposed techniques and state-of-the-art techniques. Using 27556 blood smear images, Jameela et al. employed ResNet-50 and VGG-16 DL techniques to classify malaria parasite [46]. With ResNet-50, the performance parameters indicated an ACC value of 95.82%, while for VGG-16, the ACC value was

96.00%. Yang et al. used 27,558 blood smear images and CNN technique to get a 93.46% ACC [35]. Shah et al. also applied CNN to 17460 blood smear images and achieved a 95.00% ACC [47]. The proposed customize CNN model achieved an ACC of 96.02%. Using microscopy blood smear images, a comparison of the SEN and ACC of the proposed DL techniques to other state-of-the-art techniques was conducted. This analysis demonstrates that the proposed customize CNN technique achieves greater overall ACC than existing techniques. A complete list of abbreviations is shown in *Appendix I*.

Table 8 Comparison of different techniques

Publication	Number of Images	Dataset Name	Technology Used	Performance Parameters				
				PRE	SEN	SPE	F1	ACC
Proposed 1	27558	Blood Smear Images	Binary Classifier Based on CNN	93.00%	88.80%	91.90%	90.90%	90.20%
Proposed 2	**27558**	Blood Smear Images	**Customize CNN**	**95.70%**	**97.10%**	**94.70%**	**96.40%**	**96.02%**
[46]	27558	Blood Smear Images	ResNet-50	-	96.64%	94.97%	-	95.82%
[48]	27558	Blood Smear Images	Morphological Image Processing	94.66%	88.60%	95.00%	91.53%	91.80%
[35]	27558	Blood Smear Images	Customize CNN	94.25%	92.59%	94.33%	93.41%	93.46%
[47]	17460	Blood Smear Images	Customize CNN	-	-	-	-	95.00%
[49]	27558	Blood Smear Images	VGG Net-16	-	-	-	-	95.03%
[50]	1530	Blood Smear Images	VGG16-SVM	84.47%	89.80%	88.81%	87.05%	89.21%
		Blood Smear Images	VGG19-SVM	89.95%	93.44%	92.92%	91.66%	93.13%
[51]	27558	Blood Smear Images	Pre-trained CNN with VGG-16	-	94.70%	97.20%	95.90%	95.9%

Limitations

One significant limitation in the field of malaria classification and research is the absence of a standard dataset (i).The lack of a standardized collection of malaria-infected blood smear images with varying magnification factors and photo counts makes it challenging to develop accurate algorithms and hampers the comparison of results among different researchers. This limitation not only impedes the progress in developing robust CAD systems but also restricts the ability of histologists and ML professionals to introduce new algorithms that could potentially improve the classification ACC for malaria diagnosis.

Another limitation arises from the existing models' inability to identify multiple malaria parasite species (ii).Given that malaria infections can involve different parasite species, the current models' limitations could lead to misdiagnoses, particularly in cases with co-infection. Accurate identification of parasite species is crucial for appropriate treatment, and the inability of these models to distinguish between multiple types of parasites hinders the effectiveness of diagnostic efforts.

Furthermore, the unreliability of current microscopy-based methods for malaria detection (iii) poses a serious challenge to accurate diagnosis. To improve the ACC and efficiency of parasite detection in malaria-infected blood smear images, fully automatic and precise techniques are required. Relying on manual microscopy-based methods alone can result in missed diagnoses and delayed treatment, thereby impacting patient outcomes.

Another practical limitation is the lengthy training time for ML models in malaria parasite classification (iv).Researchers have explored various methods and techniques to train these models, but the extended training time remains a bottleneck in developing more efficient and timely classification models. Addressing this issue is critical to expedite the development and deployment of advanced diagnostic tools that can aid in malaria detection and treatment.

Additionally, the manual counting of affected cells in blood smear examination is both time-consuming and subjective (v).Histologists and clinicians may need to manually count thousands of cells, leading to a tedious and error-prone process. To overcome this limitation, there is a pressing need for an automated cell counting model that can accurately and efficiently count the affected cells, thereby

streamlining the diagnosis and enabling faster patient care.

Moreover, the lack of a model specifically designed to diagnose malaria using smartphone-captured thin blood smear images (vi) Presents a significant limitation. Integrating smartphones as diagnostic tools can enhance accessibility and convenience, especially in resource-limited settings. A dedicated model that can accurately interpret images obtained from smartphones would facilitate widespread adoption and improve early detection and treatment of malaria.

Furthermore, the invasive nature of current malaria detection techniques (vii), such as taking blood samples with an injection syringe, poses a concern. There is a growing demand for non-invasive alternatives to make the diagnosis process less discomforting for patients and reduce the risk of infections associated with invasive procedures. Developing and implementing non-invasive malaria detection techniques would improve patient compliance and overall diagnostic efficacy.

Lastly, inter-observer and intra-observer variability in malaria diagnosis (viii) pose challenges to consistent and accurate diagnoses. Differences in interpretations among multiple pathologists or even within the same pathologist can lead to diagnostic discrepancies. To address this issue, automated detection methods are needed to reduce variability and ensure more reliable and standardized malaria diagnosis, enabling timely and appropriate patient management.

6.Conclusion and future work

This study introduced two DL algorithms that utilize blood cell images for malaria diagnosis. The binary classifier CNN model achieved an ACC of 90.20%, whereas the customized CNN model yielded significantly improved ACC at 96.02%. These proposed methods hold the potential to enhance the PRE and efficiency of malaria diagnosis, thereby contributing to early detection and more effective treatment. The outcomes highlighted the viability of DL techniques for swift and accurate malaria diagnosis, potentially saving lives and bolstering healthcare systems' resilience against the disease's impact. Moreover, the proposed models possess applicability beyond malaria diagnosis, offering potential benefits for diagnosing various infectious diseases, thereby enhancing global healthcare.

In the future, avenues can be explored to develop hybrid models that integrate DL with other ML

approaches. Additionally, research could delve into the feasibility of implementing the proposed models in resource-limited regions where malaria prevails. Deployment of these models within healthcare systems has the potential to expedite malaria detection and diagnosis, ultimately leading to improved treatment outcomes and alleviating the global malaria burden.

Acknowledgment
None.

Conflicts of interest
The authors have no conflicts of interest to declare.

Author's contribution statement
Shankar Shambhu: Investigation, data curation, experiment setup, writing – original draft, writing – review and editing. **Deepika Koundal:** Supervision, writing – original draft, analysis and interpretation of results. **Prasenjit Das:** Supervision, investigation on challenges and draft manuscript preparation, writing - original draft.

References
[1] https://www.who.int/news-room/fact-sheets/detail/malaria. Accessed 10 December 2022.
[2] https://www.malariasite.com/malaria-india/. Accessed 3 May 2023.
[3] Centers for disease control and prevention. Ross and the discovery that mosquitoes transmit malaria parasites. https://www.cdc.gov/malaria/about/history/ross.html. Accessed 3 May 2023.
[4] May Z, Aziz SS. Automated quantification and classification of malaria parasites in thin blood smears. In international conference on signal and image processing applications 2013 (pp. 369-73). IEEE.
[5] https://www.who.int/news-room/questions-and-answers/item/do-all-mosquitoes-transmit-malaria. Accessed 3 May 2023.
[6] Gilles HM. Management of severe and complicated malaria. A practical handbook. World Health Organization; 1991.
[7] Murphy SC, Breman JG. Gaps in the childhood malaria burden in Africa: cerebral malaria, neurological sequelae, anemia, respiratory distress, hypoglycemia, and complications of pregnancy. The Intolerable Burden of Malaria: A New Look at the Numbers: Supplement to Volume 64 (1) of the American Journal of Tropical Medicine and Hygiene. 2001.
[8] Sachs J, Malaney P. The economic and social burden of malaria. Nature. 2002; 415(6872):680-5.
[9] Chahar R, Dubey AK, Narang SK. A review and meta-analysis of machine intelligence approaches for mental health issues and depression detection. International Journal of Advanced Technology and Engineering Exploration. 2021; 8(83):1279-314.
[10] Rosado L, Correia DCJM, Elias D, S CJ. A review of automatic malaria parasites detection and segmentation in microscopic images. Anti-Infective Agents. 2016; 14(1):11-22.
[11] Tek FB, Dempster AG, Kale I. Computer vision for microscopy diagnosis of malaria. Malaria Journal. 2009; 8:1-4.
[12] Razin WR, Gunawan TS, Kartiwi M, Yusoff NM. Malaria parasite detection and classification using CNN and YOLOv5 architectures. In 8th international conference on smart instrumentation, measurement and applications 2022 (pp. 277-81). IEEE.
[13] Poostchi M, Silamut K, Maude RJ, Jaeger S, Thoma G. Image analysis and machine learning for detecting malaria. Translational Research. 2018; 194:36-55.
[14] Alharbi AH, Lin M, Ashwini B, Jabarulla MY, Shah MA. Detection of peripheral malarial parasites in blood smears using deep learning models. Computational Intelligence and Neuroscience. 2022; 2022:1-11.
[15] Marques G, Ferreras A, De LTI. An ensemble-based approach for automated medical diagnosis of malaria using EfficientNet. Multimedia Tools and Applications. 2022; 81(19):28061-78.
[16] Fuhad KM, Tuba JF, Sarker MR, Momen S, Mohammed N, Rahman T. Deep learning based automatic malaria parasite detection from blood smear and its smartphone based application. Diagnostics. 2020; 10(5):1-22.
[17] Simon A, Vinayakumar R, Sowmya V, Soman KP, Gopalakrishnan EA. A deep learning approach for patch-based disease diagnosis from microscopic images. In classification techniques for medical image analysis and computer aided diagnosis 2019 (pp. 109-27). Academic Press.
[18] Dubey A, Gupta U, Jain S. Medical data clustering and classification using TLBO and machine learning algorithms. Computers, Materials and Continua. 2021; 70(3):4523-43.
[19] Maqsood A, Farid MS, Khan MH, Grzegorzek M. Deep malaria parasite detection in thin blood smear microscopic images. Applied Sciences. 2021; 11(5):1-19.
[20] Rajaraman S, Silamut K, Hossain MA, Ersoy I, Maude RJ, Jaeger S, et al. Understanding the learned behavior of customized convolutional neural networks toward malaria parasite detection in thin blood smear images. Journal of Medical Imaging. 2018; 5(3):1-11.
[21] Raj M, Sharma R, Sain D. A deep convolutional neural network for detection of malaria parasite in thin blood smear images. In 10th international conference on communication systems and network technologies 2021 (pp. 510-4). IEEE.
[22] Minarno AE, Aripa L, Azhar Y, Munarko Y. Classification of malaria cell image using inception-V3 architecture. JOIV: International Journal on Informatics Visualization. 2023; 7(2):273-8.
[23] Siłka W, Wieczorek M, Siłka J, Woźniak M. Malaria detection using advanced deep learning architecture. Sensors. 2023; 23(3):1-21.

Shankar Shambhu et al.

[24] Krishnadas P, Chadaga K, Sampathila N, Rao S, Prabhu S. Classification of malaria using object detection models. Informatics. 2022; 9(4):1-18.

[25] Sifat MM, Islam MM. A fully automated system to detect malaria parasites and their stages from the blood smear. In region 10 symposium 2020 (pp. 1351-4). IEEE.

[26] Sampathila N, Shet N, Basu A. Computational approach for diagnosis of malaria through classification of malaria parasite from microscopic image of blood smear. Biomedical Research. 2018; 29(18):3464-8.

[27] Li D, Ma Z. Residual attention learning network and SVM for malaria parasite detection. Multimedia Tools and Applications. 2022; 81(8):10935-60.

[28] Roy K, Sharmin S, Mukta RM, Sen A. Detection of malaria parasite in Giemsa blood sample using image processing. International Journal of Computer Science and Information Technology. 2018; 10(1):55-65.

[29] Nayak S, Kumar S, Jangid M. Malaria detection using multiple deep learning approaches. In 2019 2nd international conference on intelligent communication and computational techniques 2019 (pp. 292-7). IEEE.

[30] Maduri PK, Agrawal S, Rai A, Chaubey S. Malaria detection using image processing and machine learning. In 3rd international conference on advances in computing, communication control and networking 2021 (pp. 1789-92). IEEE.

[31] Francies ML, Ata MM, Mohamed MA. A robust multiclass 3D object recognition based on modern YOLO deep learning algorithms. Concurrency and Computation: Practice and Experience. 2022; 34(1):e6517.

[32] Setyawan D, Wardoyo R, Wibowo ME, Murhandarwati EE, Jamilah J. Malaria classification using convolutional neural network: a review. In sixth international conference on informatics and computing 2021 (pp. 1-9). IEEE.

[33] Hung J, Carpenter A. Applying faster R-CNN for object detection on malaria images. In proceedings of the IEEE conference on computer vision and pattern recognition workshops 2017 (pp. 56-61).

[34] Var E, Tek FB. Malaria parasite detection with deep transfer learning. In 3rd international conference on computer science and engineering 2018 (pp. 298-302). IEEE.

[35] Yang F, Poostchi M, Yu H, Zhou Z, Silamut K, Yu J, et al. Deep learning for smartphone-based malaria parasite detection in thick blood smears. IEEE Journal of Biomedical and Health Informatics. 2019; 24(5):1427-38.

[36] Iradukunda O, Che H, Uwineza J, Bayingana JY, Binimam MS, Niyonzima I. Malaria disease prediction based on machine learning. In international conference on signal, information and data processing 2019 (pp. 1-7). IEEE.

[37] Prakash SS, Kovoor BC, Visakha K. Convolutional neural network based malaria parasite infection detection using thin microscopic blood smear samples. In second international conference on inventive research in computing applications 2020 (pp. 308-13). IEEE.

[38] Shekar G, Revathy S, Goud EK. Malaria detection using deep learning. In 4th international conference on trends in electronics and informatics (48184) 2020 (pp. 746-50). IEEE.

[39] Umer M, Sadiq S, Ahmad M, Ullah S, Choi GS, Mehmood A. A novel stacked CNN for malarial parasite detection in thin blood smear images. IEEE Access. 2020; 8:93782-92.

[40] Joshi AM, Das AK, Dhal S. Deep learning based approach for malaria detection in blood cell images. In region 10 conference 2020 (pp. 241-6). IEEE.

[41] Paul A, Bania RK. Malaria parasite classification using deep convolutional neural network. In international conference on computational intelligence and computing applications 2021 (pp. 1-6). IEEE.

[42] Aimi SAN, Yusoff M, Zeehaida M. Colour image segmentation approach for detection of malaria parasites using various colour models and k-means clustering. WSEAS Transactions on Biology and Biomedicine. 2013; 10(1):41-55.

[43] Savkare SS, Narote SP. Automatic detection of malaria parasites for estimating parasitemia. International Journal of Computer Science and Security. 2011; 5(3):310-5.

[44] https://lhncbc.nlm.nih.gov/LHC-downloads/dataset.html. Accessed 04 May 2020.

[45] Patel M, Shah M. Transfer learning with fine-tuned deep CNN model for COVID-19 diagnosis from chest X-ray images. International Journal of Advanced Technology and Engineering Exploration. 2023; 10(103):720-40.

[46] Jameela T, Athota K, Singh N, Gunjan VK, Kahali S. Deep learning and transfer learning for malaria detection. Computational Intelligence and Neuroscience. 2022; 2022:1-14.

[47] Shah D, Kawale K, Shah M, Randive S, Mapari R. Malaria parasite detection using deep learning:(beneficial to humankind). In 4th international conference on intelligent computing and control systems 2020 (pp. 984-8). IEEE.

[48] Fatima T, Farid MS. Automatic detection of Plasmodium parasites from microscopic blood images. Journal of Parasitic Diseases. 2020; 44(1):69-78.

[49] Sharma A, Vaishampayan C, Santlani K, Sunhare M, Arya M, Gupta S. Malaria parasite detection using deep learning. International Journal for Research in Applied Science & Engineering Technology. 2020; 8(V):163-8.

[50] Vijayalakshmi A. Deep learning approach to detect malaria from microscopic images. Multimedia Tools and Applications. 2020; 79:15297-317.

[51] Rajaraman S, Antani SK, Poostchi M, Silamut K, Hossain MA, Maude RJ, et al. Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images. Peer J. 2018; 6:e4568.

Shankar Shambhu earned his PhD degree in Computer Science and Engineering from Chitkara University, Himachal Pradesh, India. He currently holds a position at Chitkara University, Himachal Pradesh, India, where he serves as an Assistant Professor at the School of Engineering and Technology. With over 13 years of experience in teaching and research, Shankar has authored and co-authored numerous research papers in well-regarded SCI and Scopus indexed journals and conferences. He has also taken on the role of a reviewer for several esteemed journals and conferences. His areas of expertise encompass Artificial Intelligence, Machine Learning / Deep Learning, Biomedical Imaging and Signals, as well as Soft Computing and Image Processing.
Email: shankar.shambhu@chitkarauniversity.edu.in

Deepika Koundal is currently associated with University of Petroleum and Energy Studies, Dehradun. She received the recognition and honorary membership from Neutrosophic Science Association from University of Mexico, USA. She received the Master and Ph.D. degrees in computer science & engineering from the Panjab University, Chandigarh in 2015. She received the B. Tech. degree in computer science & engineering from Kurkushetra University, India. She is the awardee of research excellence award given by Chitkara University in 2019. She has published more than 40 research articles in reputed SCI and Scopus indexed journals, conferences and two books. She is currently a guest editor in Computers & Electrical Engineering and Internet of Things Journals. She also has served on many technical program committees as well as organizing committees and invited to give guest lectures and tutorials in Faculty development programs, international conferences and summer schools. She has also served as reviewer in many repudiated journals of IEEE, Springer, Elsevier, IET, Hindawi, Wiley and Sage. Her areas of interest are Artificial Intelligence, Biomedical Imaging and Signals, Image Processing, Soft Computing, Machine Learning/ Deep Learning.
Email: dkoundal@ddn.upes.ac.in

Prasenjit Das received his PhD degree in Computer Science and Engineering from Chitkara University, Himachal Pradesh, India. His Ph.D. thesis is focused on malware detection using data mining. He received his MCA degree from Thapar Institute of Engineering & Technology, Patiala, India. He has more than 15 years of teaching and research experience. He has also served as a reviewer in many reputed journals and conferences. His areas of interest are Machine Learning, Malware Detection, Software Engineering, Cloud Computing and image processing.
Email: pdas47@gmail.com

Appendix I

S. No.	Abbreviation	Description
1	ACC	Accuracy
2	CAD	Computer Aided Diagnosis
3	CNN	Convolutional Neural Network
4	CNNSVM	Convolutional Neural Networks with a Support Vector Machine
5	CPU	Central Processing Unit
6	C-Y	Cyan, Yellow
7	DL	Deep Learning
8	DNN	Deep Neural Network
9	ELM	Extreme Learning Machine
10	FC	Fully Connected
11	FN	False Negative
12	FP	False Positive
13	FS	F1 Score
14	GPU	Graphics Processing Unit
15	H S I	Hue, Saturation, Intensity
16	HSV	Hue Saturation Value
17	IDE	Integrated Development Environment
18	IGMS	Iterative Global Minimum Screening
19	MAPE	Mean Absolute Percentage Error
20	ML	Machine Learning
21	NIH	National Institute of Health
22	NLM	National Library of Medicine
23	PNG	Portable Network Graphics
24	PRE	Precision
25	R&D	Research and Development
26	RAL	Reinforced Stream-Based Active Learning
27	RAM	Random Access Memory
28	RBC	Red Blood Cells
29	RGB	Red, Green, Blue
30	SEN	Sensitivity
31	SGD	Stochastic Gradient Descent
32	SPE	Specificity
33	SVM	Support Vector Machine
34	TN	True Negative
35	TP	True Positive
36	VGG	Visual Geometry Group
37	WHO	World Health Organization
38	YOLOv4	You Only Look Once Version 4
39	YOLOv5	You Only Look Once Version 5