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A novel transfer learning-based model for diagnosing malaria from parasitized and uninfected red blood cell images

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ABSTRACT

Malaria represents a potentially fatal communicable illness triggered by the Plasmodium parasite. This disease is transmitted to humans through the bites of Anopheles mosquitoes that carry the infection. This disease has significant and devastating consequences on the health systems of fragile countries, particularly in sub-Saharan Africa. Malaria affects red blood cells by invading and replicating within them, destroying them, and releasing toxic byproducts into the bloodstream. The parasite's ability to stick and modify the surface of red blood cells can cause them to become sticky, obstructing blood flow in vital organs such as the brain and spleen. Therefore, efficient approaches for the early detection of malaria are critical to saving patients' lives. The main aim of this study is to develop an efficient model for early malaria diagnosis. We used malaria images based on parasitized and uninfected red blood cells for the study experiments. We applied neural network-based approaches such as Neural Search Architecture Network (NASNet) and compared its performance with machine learning techniques. Moreover, we proposed a novel NNR (NASNet Random forest) method for feature engineering. The proposed NNR approach first extracts spatial features from input malaria images, then class prediction probability features are extracted from these spatial features. The feature set obtained from the data extraction trains machine learning models. Our comprehensive experiments show that the support vector machine outperformed state-of-the-art models, achieving a high-performance score of 99% and having an inference time near 0.025 s. We validated the performance using k-fold cross-validation and optimized the hyperparameters through tuning. Our proposed research has improved the early diagnosis of malaria and can assist medical specialists in reducing the mortality rate.

1. Introduction

Malaria is a severe illness caused by the Plasmodium parasite. It is mainly spread through the bite of infected females of Anopheles mosquitoes [1]. The disease is caused by various species of Plasmodium, such as Plasmodium vivax and Plasmodium falciparum. These parasites invade and multiply inside the red blood cells of humans [2,3]. Malaria remains a major health concern worldwide, notably in tropical and subtropical countries, affecting millions annually and causing serious damage to their economies. Typical indications of malaria encompass elevated body temperature, shivering, aching head, queasiness, retching, muscular discomfort, weariness, and chest discomfort. If patients are left untreated, malaria can cause serious complications to them and even lead to mortality.

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The late diagnosis of malaria can pose critical risks, potentially leading to the death of the patient. In 2016, the World Health Organization (WHO) reported that there were 212 million cases of malaria worldwide. By 2019, this number had increased to 229 million [4]. The annual mortality rate from malaria is estimated to be 409 thousand [5,6]. Studies indicate that malaria primarily affects young children under the age of five [7,8]. However, traditional microscopic examinations for accurate diagnosis take longer. The accuracy of malaria diagnosis depends on factors such as test costs, the sensitivity of the technique, attention to detail, the time required for the test, and the expertise of the person conducting it [9]. Therefore, there is a need for an advanced automated artificial intelligence-based model that can early and accurately detect malaria from human red blood cells.

In recent years, artificial intelligence (AI) has significantly improved early diagnosis of various critical and chronic diseases in the medical domain [10–13], saving and improving patients' lives [14]. Since traditional methods of malaria diagnosis, such as microscopic examination, can be time-consuming and require skilled personnel, AI-based models offer the potential alternative for faster and more accurate detection, aiding in timely diagnosis and treatment [15]. AI models can analyze digital images of red blood cells and identify malaria parasites with high precision. To accomplish this, we can employ deep learning approaches, such as convolutional neural networks (CNN) [16], to classify blood cells and effectively filter out infected cells. This approach is particularly valuable in rural areas where microscopic tests for malaria detection may be unavailable. These learning methods can be turned using several optimization methods, such as in [17–20].

This study proposes a transfer learning-based mechanism for efficiently diagnosing malaria. Transfer learning has emerged as a promising approach for malaria diagnosis using red blood cell images, explicitly focusing on spatial features [1]. Transfer learning allows for extracting significant traits from images and capturing low-level and high-level representations by exploiting pre-trained deep-learning models [21]. This approach facilitates the transfer of learned knowledge to new datasets, reducing the need for extensive labeled data and computational resources [22]. By incorporating transfer learning into diagnosing malaria, we can leverage the spatial features of red blood cell images, thereby enhancing the accuracy and efficiency of the diagnostic process. Ultimately, this can aid in the early detection and treatment of this life-threatening disease.

The primary research contributions of the study for the early diagnosis of malaria are summarized followed as:

- A novel approach called NASNet Random forest (NNR) is proposed based on features extracted from fine-tuning of pre-trained models following a transfer learning approach. The NNR technique extracts spatial features from input malaria images, specifically based on parasitized and uninfected red blood cells. These spatial features are then used to extract class prediction probability features, which are further utilized in building the applied machine learning methods.
- We evaluate the performance impact of using the NNR method on various machine learning and neural network techniques. All applied approaches are hyperparameter-tuned, and performance assessment is confirmed using k-fold cross-validation. Computational complexity analysis was also conducted to assess the efficiency of the applied techniques. Our study's results outperformed the state-of-the-art approaches.

The remaining sections of this research are formulated as follows: Section 2 presents an analysis of the related literature. Section 3 outlines our proposed methodology. Section 4 presents the comparative results of applied AI techniques. Finally, the study findings are summarized in Section 5.

2. Related work

In recent years, researchers have explored the potential of using automated image analysis techniques to aid in malaria diagnosis. Various studies have employed machine learning algorithms and image processing techniques to distinguish between parasitized and uninfected red blood cells based on their morphological characteristics and staining patterns. This literature analysis underscores the importance of continuing research in this field to develop robust and accessible diagnostic tools that can help healthcare providers identify malaria infections promptly and accurately. The summary of the analyzed literature is provided in Table 1.

In [1], Vijayalakshmi et al. employed a transfer learning strategy for recognizing the illness caused by the Falciparum malaria parasite using a unique Deep Neural Network (DNN) model. The study utilized the Support Vector Machine (SVM) and geometry group network to identify the severe form of the malaria parasite. Their evaluation data set consisted of microscopic images of stained blood smears. The proposed VGG-19 SVM model outperformed the CNN model. However, the performance score obtained from the VGG-19 SVM project model was 93. 13%, which is considered relatively low.

In [23], the study presented a framework for identifying malaria caused by the Plasmodium falciparum parasite. The experiments used a dataset obtained from the Parasitology laboratory at Gadjah Mada University. To identify the malaria parasite, an advanced feature extraction strategy based on histogram-based texture features was applied to the image data. The acquired characteristics were subsequently inputted into an Artificial Neural Network (ANN) [24] model to undergo training and testing. The algorithm used for training the ANN was the backpropagation algorithm of a multilayer perception [25]. The experimental performance results demonstrated that the proposed ANN achieved a performance accuracy score of 87.8% with a computation time of 0.55 s. However, the performance scores of the study were relatively low, indicating the need for more accurate diagnostic techniques.

Suraksha et al. [31] focused on classifying blood smear images of malaria parasites. The dataset used in their study is the protozoal red blood cells obtained from the National Library of Medicine. An investigation involving the categorization of malaria images employs a Convolutional Neural Network (CNN) model, which relies on principles of deep learning methodologies. Additionally, a hybrid model [32] combining a pre-trained VGG-19 and CNN is utilized. The VGG-19-CNN model achieves satisfactory results compared to other models, with an accuracy of 96.02%. However, there is still a need for further performance enhancement.

In [26], the study presented a segmentation strategy designed to identify microscopic images of the malaria parasite. The dataset of the images was obtained from the Eijkman Institute for Molecular Biology in Indonesia. The dataset consists of thirty images of microscopic blood smears for patients with malaria. The empirical findings demonstrate the significance of the deep segmentation method in handling different image and histogram conditions, resulting in improved overall performance. The proposed approach achieved an overall metric score of 86%. However, when compared to other studies, the performance results of their approach were relatively poor.

Alassaf et al. [33] developed a unique strategy called IDTL-MPDC, and accurately detected the malarial parasites in blood smear images. The dataset used for the study has blood smear images. Their approach includes different sub-steps: preprocessing based on median filtering (MF), feature mining based on Res2Net, hyperparameter tuning based on the differential evolution (DE) algorithm, and ranking based on K-nearest neighbor (KNN) results. The DE algorithm achieved an excellent accuracy score of 95.86%, which can be further improved.

In [28], Masud et al. used mobile clinical systems and deep learning to identify lethal malaria in patients. The main focus of their study was to utilize a CNN structure to effectively and accurately diagnose malaria using a mobile application. The dataset used for to evaluate

Table 1
Related literature summary analysis.

Ref.	Year	Dataset	Proposed technique	Performance accuracy
[23]	2016	Data from Parasitology laboratory of Gadjah Mada University	ANN deep learning with Feature extraction	87.8%
[1]	2020	Microscopic images from stained blood	DNN + VGG-19 SVM	93.13%
[26]	2019	Images of microscopic organized at the Eijkman Institute for Molecular Biology, Indonesia	Deep learning Segmentation method	86%
[27]	2022	Open source blood smear images dataset	Deep learning IDTL-MPDC	95.86%
[28]	2020	Malaria dataset from NIH	Deep learning + cyclical-SGD	97.30%
[29]	2020	National library of medicine dataset	DL-Xception with mish	98.86%
[30]	2022	Malaria blood sample images of balanced class dataset	DL-DAGNN	94.79%
[31]	2023	National library of medicine dataset	VGG-19-CNN	96.02%

their approach is publicly available on Kaggle and was obtained from Chittagong Medical College Hospital in Bangladesh, consisting of two hundred patient records. The suggested model achieved an accuracy score of 97.30% through performance evaluation of a traditional CNN model using cyclical-SGD.

Sriporn et al. [29], utilized malaria disease images to identify and detect malaria based on a CNN model. The dataset used in the study was obtained from the National Library of Medicine and consisted of 151 infected patients and 50 non-infected individuals. The Xception model was employed with the activation algorithm Mish and optimizer Nadam to improve the accuracy of ranking malaria illness in thin blood smear images. The approach utilized a total of 7000 images, with 4500 contaminated images and 2500 non-contaminated images. The efficacy achieved by Xception with Mish was 98.86%.

Oyewola et al. [30], introduced a novel method of deep learning named as data augmentation convolutional neural network (DACNN), which focuses on analyzing blood smear images of Plasmodium parasites to aid in identifying malaria illness in humans. The dataset used in the study is an open-source dataset downloaded from Kaggle. A comparative analysis is conducted between the suggested model and various CNN-based models to evaluate its performance. The results of this research indicate that the suggested approach exhibited superior performance compared to alternative deep learning models, achieving an optimum accuracy score of 94.79%. However, it should be noted that this accuracy score is relatively low when compared to other studies.

2.1. Research gap

Through this literature analysis, we have determined the following major research gaps that need to be covered:

- Although classical deep and machine learning approaches have been used extensively in malaria diagnosis, it is crucial to adopt advanced learning approaches such as transfer learning techniques. These advanced methods show remarkable performance, where they efficiently reuse pre-existing models, alleviating the challenge of limited patient data, and enhancing the stability of the diagnosis system.
- The current performance scores for malaria detection can be significantly improved by proposing novel transfer learning-based feature engineering mechanisms.

3. Proposed methodology

In this section, we discuss our novel research methodology for the Malaria diagnosis step-by-step (see Fig. 1). The proposed methodology utilizes malaria images of parasitized and uninfected red blood cells. We introduce a novel approach called NNR for feature engineering from malaria image data. This feature engineering process creates a new feature set, which is divided into training and testing sets using an 80:20 split ratio. We have applied advanced machine learning and neural network approaches with hyper-parameter optimization for comparison. The applied approaches are trained and tested to evaluate their performance. The model that outperforms the others is then used for diagnosing malaria from red blood cell images.

3.1. Parasitized and uninfected red blood cells data

This study utilized a benchmark dataset [34] that includes images of parasitized and uninfected red blood cells related to malaria. The sample images corresponding to each class are illustrated in Fig. 2. The dataset has 27,601 malaria images, as depicted in Fig. 3. The dataset has been carefully balanced to facilitate experimental analysis.

3.2. Novel proposed approach

This study introduces a unique NNR approach aimed at enhancing the feature engineering process using a transfer learning-based approach, as shown in Fig. 4. The image data of parasitized and uninfected red blood cells related to malaria are input to a pre-trained NASNet model for extracting spatial features. The spatial features obtained are subsequently utilized as inputs for the random forest technique to derive class prediction probability features [35]. The resulting features are used to build deep machine-learning models for malaria diagnosis. As we discuss later in Section 4.3, the study results show that the employed method demonstrated excellent performance results through the utilization of the suggested transfer features.

Transfer learning-based feature engineering presents significant advantages over classical methods in diagnosing malaria from parasitized and uninfected red blood cell images. Traditional feature engineering approaches often rely on handcrafted features that may not capture all the relevant information in the images, leading to limited discriminatory power. In contrast, transfer learning leverages pre-trained deep neural networks, enabling them to learn generic features that are broadly applicable across different tasks. This empowers our proposed

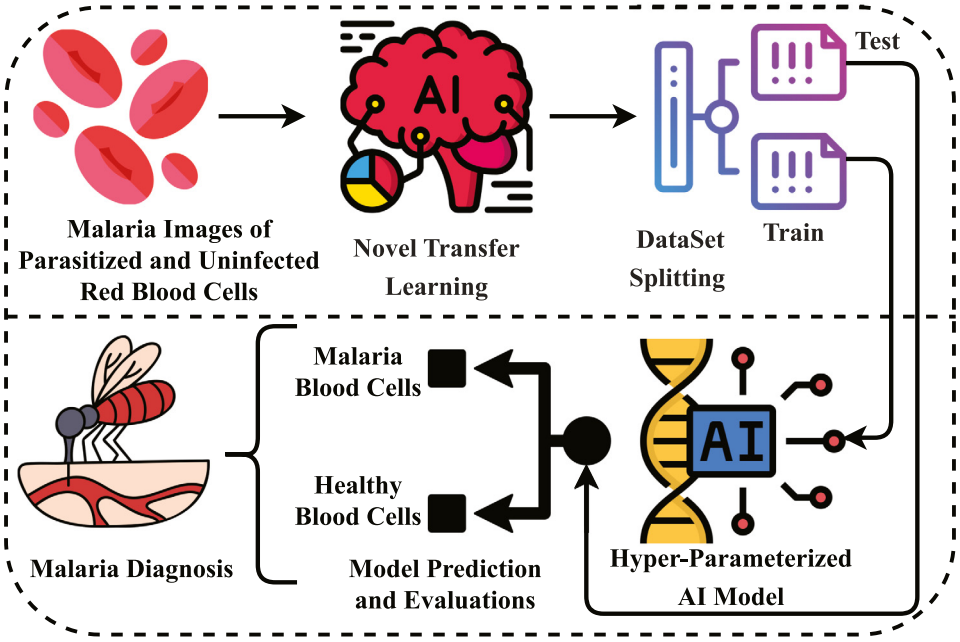


Fig. 1. Architecture of the proposed Malaria Diagnosis Method.

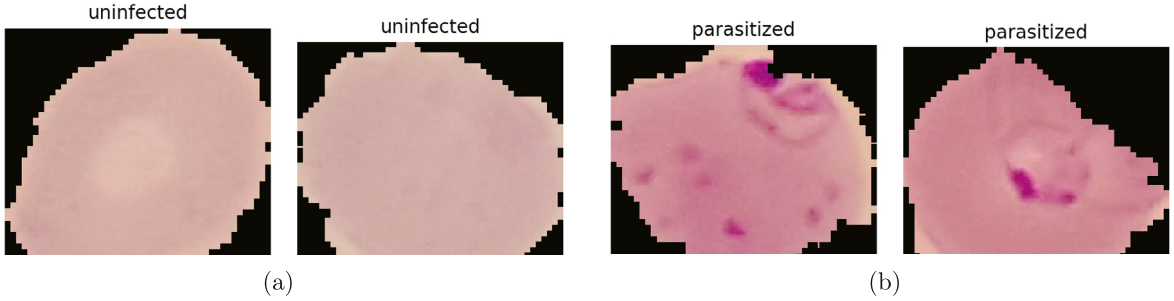


Fig. 2. The red blood cell images data analysis with the target class.

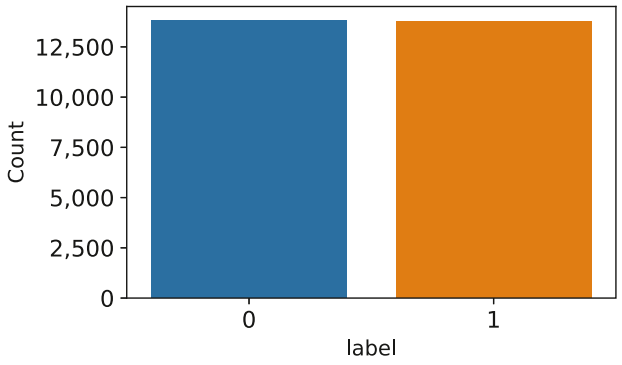


Fig. 3. Distribution of target labels based on the images of red blood cells in the benchmark dataset.

model to extract highly discriminative features from the red blood cell images, thereby enhancing its ability to distinguish between parasitized and uninfected cells. Overall, the implementation of our proposed transfer learning-based feature engineering represents a powerful approach to improving the accuracy and robustness of malaria diagnosis from red blood cell images.

Algorithm 1 shows the step-by-step flow of the proposed feature engineering approach.

Algorithm 1 NNR Method

Input: Malaria images.

Output: New transfer features for detecting malaria.

initiate;

1- $F_{nasnet} \longleftarrow NASNet_{prediction}(MiS)$ // $MiS \; \epsilon \; Malaria \; images$, here MiS is input image data and F_{nasnet} is newly obtained spatial feature set.

2- $F_{rf} \longleftarrow RF_{probabilities\ prediction}(F_{nasnet})$ // here F_{rf} represents the collection of probabilistic-based features that are extracted.

3- $F_{Prob} \longleftarrow F_{rf}$ // hereF_{Prob} represents the conclusive set of probabilistic-based features employed for the identification of malaria.

end;

3.3. Machine learning techniques

Artificial intelligence techniques [36], such as deep and machine learning, have emerged as powerful tools for the diagnosis of malaria using images of red blood cells. These techniques leverage advanced algorithms to extract meaningful features from the images, enabling accurate classification of infected and uninfected cells. By training models on large datasets, artificial intelligence can learn complex patterns and variations associated with malaria, enabling early and precise detection. This automated approach not only reduces the

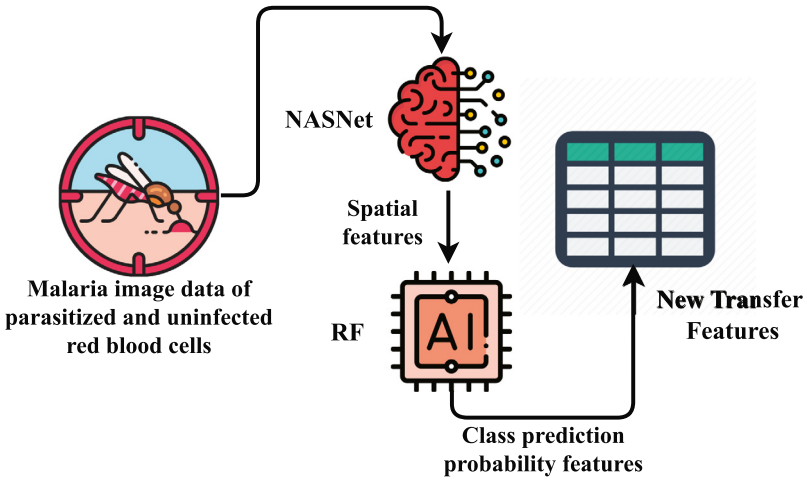


Fig. 4. Architecture of the proposed NNR method for feature engineering.

dependence on manual inspection but also enhances diagnostic efficiency and accuracy, potentially revolutionizing the field of malaria diagnosis.

3.3.1. K-Neighbors Classifier

The K-Neighbors Classifier (KNC) is a supervised machine learning algorithm used for classification tasks [37]. In the context of malaria diagnosis using images of red blood cells, we can utilize KNC to classify the cells as infected or uninfected based on specific features extracted from the images.

Let us denote our training dataset as X and the corresponding class labels as y. The feature vector of each image can be represented as $\mathbf{x}_i = (x_{i1}, x_{i2}, \ldots, x_{id})$, where i indicates the index of the image and d represents the number of features.

To classify a new image, we calculate the distance between its feature vector $\mathbf{x}$ and the feature vectors of all the training images. The most common distance metric used is the Euclidean distance, given by:

$$\text{Euclidean Distance}(\mathbf{x}, \mathbf{x}_i) = \sqrt{\sum_{j=1}^{d} (x_j - x_{ij})^2} \tag{1}$$

After obtaining the distances, the k closest neighbors are chosen by considering the smallest distances. The selection of the value for k is crucial as it acts as a hyperparameter and should be predefined in advance. We can then assign a class label to the new image based on the majority vote of the class labels of its k nearest neighbors. If most neighbors are infected, the new image is classified as infected; otherwise, it is classified as uninfected.

This classification process can be summarized as follows:

1. Calculate the Euclidean distances between $\mathbf{x}$ and all training images $\mathbf{x}_i$.
2. Select the k nearest neighbors with the smallest distances.
3. Determine the majority class label among the k neighbors.
4. Classify the new image as infected or uninfected based on the majority class label.

3.3.2. Random Forest

Random Forest (RF) can be described as an ensemble learning technique that merges numerous decision trees to generate predictive models [38]. It is commonly used in machine learning for classification tasks, including medical diagnosis. Here is the basic mathematical work for Random Forest in diagnosing malaria using images of red blood cells.

Consider a training dataset D containing N samples, where each sample is denoted by a feature vector $\mathbf{x}_i$ along with its corresponding label y_i. In this context, a label of 1 signifies the presence of malaria, while a label of 0 indicates its absence.

Random Forest (RF) is a technique that entails constructing an ensemble of M decision trees, with each tree being built using a randomly selected subset of the training data. For each tree T_m in the ensemble, the following steps are performed:

1. Randomly select a subset of features to consider at each split. This helps introduce diversity among the trees. Let K be the number of features considered at each split.
2. Build a decision tree using the selected subset of training data. Each internal node within the tree represents the splitting condition of a chosen feature, while each leaf node corresponds to a class label.
3. Repeat steps 1 and 2 to create M decision trees in the forest.

Once the RF is trained, it can be used to make predictions on new, unseen data. Given a test sample $\mathbf{x}_{\text{test}}$, the following steps are performed:

1. Pass $\mathbf{x}_{\text{test}}$ through each decision tree T_m in the forest, and collect the predictions from all trees.
2. Each tree's prediction is weighted by its performance (e.g., accuracy) on the training data. This weighting can be determined by metrics such as Gini impurity or information gain.
3. Combine the weighted predictions to obtain the final prediction. For binary classification, a common approach is to use majority voting, where the class with the most votes among the trees is selected as the predicted class.

3.3.3. Logistic Regression

The Logistic Regression (LR) model [39] for diagnosing malaria using images of red blood cells can be represented mathematically as follows:

Let X be the input image features (e.g., pixel intensities, texture features, etc.), and Y be the binary output variable indicating the presence or absence of malaria.

We define the sigmoid function as:

$$h_\theta(X) = \frac{1}{1 + e^{-\theta^T X}} \tag{2}$$

where $h_\theta(X)$ represents the predicted probability that the input image X belongs to the positive class (malaria present).

The logistic regression hypothesis is given by:

$$h_\theta(X) = P(Y = 1 | X; \theta) = \frac{1}{1 + e^{-\theta^T X}} \tag{3}$$

We need to define a cost function to estimate the parameters θ of the LR model. The cost function measures the model's performance and determines how well it predicts the output variable Y.

The cost function for LR is given by:

$$J(\theta) = -\frac{1}{m}\sum_{i=1}^{m}\left[y^{(i)}\log(h_\theta(x^{(i)})) + (1-y^{(i)})\log(1-h_\theta(x^{(i)}))\right] \tag{4}$$

Where variable m represents the total count of training data points. The symbol $y^{(i)}$ denotes the real output value corresponding to the ith training example, while $x^{(i)}$ indicates the input features associated with the same ith training example.

We can use gradient descent to find the optimal parameters θ that minimize the cost function. The parameter update rule is:

$$\theta_j := \theta_j - \alpha\frac{\partial J(\theta)}{\partial \theta_j} \tag{5}$$

Where α is the learning rate, and $\frac{\partial J(\theta)}{\partial \theta_j}$ is the partial derivative of the cost function with respect to the jth parameter θ_j.

To prevent overfitting, we can add a regularization term to the cost function:

$$J(\theta) = -\frac{1}{m}\sum_{i=1}^{m}\left[y^{(i)}\log(h_\theta(x^{(i)})) + (1-y^{(i)})\log(1-h_\theta(x^{(i)}))\right] + \frac{\lambda}{2m}\sum_{j=1}^{n}\theta_j^2 \tag{6}$$

Where λ is the regularization parameter, and n is the number of features.

3.3.4. Support Vector Machine

The Support Vector Machine (SVM) approach for the diagnosis of malaria disease using images of red blood cells is used in this study [40]. The SVM algorithm is designed to discover the most suitable hyperplane for distinguishing between infected and healthy red blood cells. Let us define the following variables:

$$\begin{aligned}
\text{Training dataset:}\quad & D = \{(x_1, y_1), (x_2, y_2), \ldots, (x_n, y_n)\}\\
\text{Feature vector:}\quad & x_i = [x_{i1}, x_{i2}, \ldots, x_{id}]\\
\text{Class label:}\quad & y_i \in \{-1, +1\}\\
\text{Hyperplane equation:}\quad & f(x) = \text{sign}(w \cdot x - b)
\end{aligned}$$

To find the optimal hyperplane, we solve the following optimization problem:

$$\begin{aligned}
\min_{w,b}\quad & \frac{1}{2}\|w\|^2 + C\sum_{i=1}^{n}\xi_i\\
\text{subject to}\quad & y_i(w \cdot x_i - b) \geq 1 - \xi_i, \quad \forall i = 1, 2, \ldots, n\\
& \xi_i \geq 0, \quad \forall i = 1, 2, \ldots, n
\end{aligned}$$

Here, C is the regularization parameter that controls the trade-off between maximizing the margin and minimizing the classification errors. The variables ξ_i represent the slack variables that allow for some misclassification.

After solving the optimization problem, we can classify a new image x_{new} by evaluating the sign of $f(x_{\text{new}})$.

3.3.5. Convolutional Neural Network

A potent instrument for medical diagnosis is the Convolutional Neural Network (CNN), which has risen to prominence [41,42], including diagnoses of malaria using images of red blood cells [43]. By leveraging its ability to learn hierarchical features from raw pixel data automatically, CNN can effectively capture intricate patterns and variations in infected red blood cells. By applying convolutional layers, activation functions, and pooling operations, CNN can extract discriminative features, reduce dimensionality, and highlight important regions within the images. The layered architecture of applied CNN is demonstrated in Table 2. The following steps elaborate on the mathematical working of CNN for image diagnosis:

Table 2
Architecture analysis of applied CNN model.

Layer	Output shape	Param #
Conv-2D	(None, 126, 126, 32)	896
Max pooling-2D	(None, 63, 63, 32)	0
Dropout	(None, 63, 63, 32)	0
Flatten	(None, 127008)	0
Dense Output	(None, 1)	127 009
Total params	127, 905	

Step-1: Input Image

Let X represent the input image of a red blood cell.

Step-2: Convolutional Layer

Apply a set of many learnable filters to the input malaria image:

$$Z^{[l]} = W^{[l]} * X + b^{[l]} \tag{7}$$

where $W^{[l]}$ is the filter weights, $b^{[l]}$ is the bias term, and $Z^{[l]}$ is the output feature map.

Step-3: Activation Function

Apply an activation function (e.g., ReLU) element-wise to introduce non-linearity:

$$A^{[l]} = \text{ReLU}(Z^{[l]}) \tag{8}$$

Step-4: Pooling Layer

Downsample the activation maps to reduce dimensionality and extract dominant features:

$$A^{[l+1]} = \text{MaxPooling}(A^{[l]}, \text{pool\_size}, \text{stride}) \tag{9}$$

Step-5: Flattening

Flatten the pooled feature maps into a 1D vector:

$$F^{[l+1]} = \text{Flatten}(A^{[l+1]}) \tag{10}$$

Step-6: Fully Connected Layer

Connect the flattened features to a fully connected layer:

$$Z^{[l+1]} = W^{[l+1]}F^{[l+1]} + b^{[l+1]} \tag{11}$$

where $W^{[l+1]}$ is the weights matrix, $b^{[l+1]}$ is the bias term, and $Z^{[l+1]}$ is the pre-activation.

Step-7: Output Layer

Apply a softmax activation function to obtain class probabilities:

$$\hat{Y} = \text{Softmax}(Z^{[l+1]}) \tag{12}$$

3.3.6. Neural Search Architecture Network

The Neural Search Architecture Network (NASNet) Large is a robust framework designed to diagnose malaria using images of red blood cells [44]. By leveraging advanced deep learning techniques, NASNet can effectively extract and analyze the intricate features in the images, enabling accurate and efficient identification of malaria-infected cells. Through its convolutional and fully connected layers, NASNet learns to capture the distinctive patterns and characteristics associated with infected red blood cells, enabling precise classification and diagnosis. The architecture is analyzed in Table 3. The basic mathematical working of the NASNet for diagnosing malaria using images of red blood cells is as follows:

Step-1: Input Image

Let us denote the input image as X, and the output (malaria diagnosis) as Y.

Step-2: Convolutional Layers

The convolutional layers capture spatial features from the input image. We denote the output of the ith convolutional layer as C_i. The NASNet architecture typically has multiple convolutional layers, represented as $C_1, C_2, \ldots, C_n$.

Table 3
Architecture analysis of applied NASNet model.

Layer (type)	Output shape	Param #
NASNet (Functional)	(None,4,4,4032)	84916818
Dropout (Dropout)	(None,4,4,4032)	0
flatten (Flatten)	(None, 64512)	0
dense (Dense)	(None, 1)	64513
Total params	84,981,331	

Step-3: Pooling Layer

After the convolutional layers, a pooling layer is employed to reduce the dimensionality of the features. We denote the output of the pooling layer as P. This layer helps in extracting the most relevant features from the convolutional layers.

Step-4: Fully Connected Layers

The features obtained from the pooling layer are fed into fully connected layers for detection. These layers are responsible for acquiring the correlation between the extracted features and the resulting diagnosis. We denote the output of the ith fully connected layer as F_i, with F_1 being the input to the first fully connected layer.

Step-5: Softmax Layer

Ultimately, the utilization of a softmax layer aims to transform the results from the most recent fully connected layer into a set of probabilities. The output of the softmax layer represents the probability distribution over the different classes, indicating the likelihood of each class. We denote the output of the softmax layer as S.

Step-6: Forward Propagation

To obtain the output diagnosis Y for a given input image X, we perform forward propagation through the NASNet architecture.

$$
\begin{aligned}
C_1 &= \text{Convolution}(X)\\
C_2 &= \text{Convolution}(C_1)\\
&\cdots\\
C_n &= \text{Convolution}(C_{n-1})\\
P &= \text{Pooling}(C_n)\\
F_1 &= \text{FullyConnected}(P)\\
F_2 &= \text{FullyConnected}(F_1)\\
&\cdots\\
F_m &= \text{FullyConnected}(F_{m-1})\\
S &= \text{Softmax}(F_m)\\
Y &= \text{argmax}(S)
\end{aligned}
$$

In the forward propagation, we apply the convolution operation followed by pooling and then pass the result through fully connected layers and softmax activation to obtain the output diagnosis Y. The argmax function selects the class with the highest probability from the softmax output.

3.4. Hyperparameter setting

The optimal parameters for the deep and machine learning models used in this study are chosen through a dynamic testing and training procedure [45]. To ensure the most accurate predictions, we determined the best-fit hyperparameters using the recursive process of the k-fold cross-validation process, which splits the dataset into train, validation, and test. Table 4 presents the selected hyperparameters for our applied methods. The analysis results demonstrate that the optimal parameters we determined have been successfully employed to achieve excellent performance in malaria diagnosis.

Table 4
Hyperparameter settings analysis of applied methods.

Technique	Hyperparameter Description
RF	max_depth=100, random_state=0, n_estimators=100
LR	random_state=0, max_iter=1000, multi_class='auto', C=1.0
SVM	random_state=0, max_iter=10
KNC	n_neighbors=2
CNN	activation= 'sigmoid', optimizer='adam', loss='binary_crossentropy'
NASNet	weights = 'imagenet', include_top = False

Table 5
Performance results analysis with classical neural network approaches.

Technique	Accuracy	Target class	Precision	Recall	F1
CNN	81%	parasitized	0.82	0.79	0.80
		uninfected	0.80	0.83	0.81
		Average	0.81	0.81	0.81
NASNet	72%	parasitized	0.86	0.52	0.65
		uninfected	0.65	0.91	0.76
		Average	0.76	0.72	0.70

4. Results and discussion

The Results section of our proposed study presents the primary outcomes and findings regarding the diagnosis of malaria. We employed several neural network approaches, compared their performance, and evaluated the results. Each applied model's performance is assessed using various comparative analysis mechanisms. This section provides a comprehensive analysis of the results we obtained during the diagnosis of malaria.

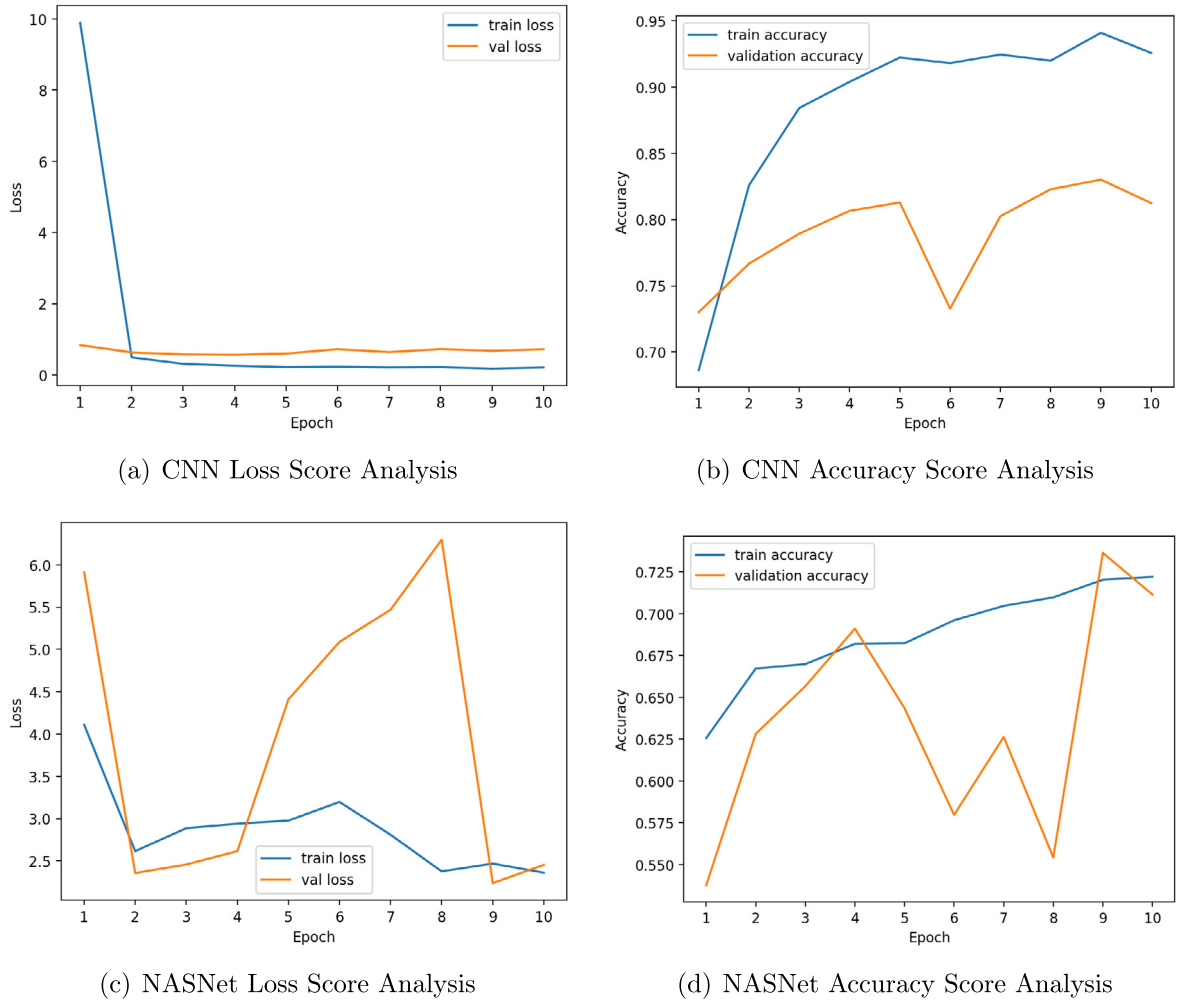
4.1. Experimental setup

We used Python programming (version 3.0) to implement the applied neural network techniques for building the experimental setup. The research experiments are carried out within the Google Colab platform, making use of a GPU backend that had 90 GB of disk space and 13 GB of RAM. The performance metrics employed in evaluating the results are precision, accuracy, recall, and F1 scores.

4.2. Results with classical approaches

The comparative performance analysis of the classical neural network approaches applied is shown in Table 5. We estimated the parameters of our applied classical approach, including precision, accuracy, recall, and F1 score. In our research study, we compared the classical neural network approaches of CNN and NASNetL. The performance results in the table show that the NASNetL model has the lowest accuracy score of 72%, while the CNN model achieves an average score of 81%. This analysis demonstrates that the applied classical approaches are not sufficient for diagnosing Malaria disease. Therefore, it is concluded that advanced techniques are needed to enhance the performance scores for malaria diagnosis.

The time series performance comparison analysis of classical neural network techniques applied during training is illustrated in Figs. 5(a) and 5(b). When malaria images are input to the CNN method, the training loss is initially high in the first epoch. However, after the second epoch, the CNN model updates its weights by finding the optimal values and reducing the loss. As the CNN training progresses, both the training accuracy and validation accuracy scores gradually increase. The analysis demonstrates that the CNN model achieves a training accuracy ranging from 80% to 90%. Although the classical CNN achieves an acceptable score for malaria image classification, it does not achieve the highest accuracy in this analysis.



(a) CNN Loss Score Analysis

(b) CNN Accuracy Score Analysis

(c) NASNet Loss Score Analysis

(d) NASNet Accuracy Score Analysis

Fig. 5. Time series-based performance comparison analysis of applied neural network approaches.

The time series-based performance comparison analysis of the classical neural network technique NASNet applied during training is illustrated in Figs. 5(c) and 5(d). When malaria images are input to the NASNet method, the training loss is initially high in the first epoch. However, after the second epoch, the NASNet model updates its weights by finding the optimal values and reducing the loss. The analysis shows that the training loss remains low from epochs 5 to 9. However, the validation loss scores are comparatively high. As the NASNet training progresses, both the training accuracy and validation accuracy scores gradually increase. Only the validation accuracy fluctuates during epochs 6 and 8 before improving to an optimal level. The analysis demonstrates that the NASNet model achieves a training accuracy ranging from 70% to 80%. Although the classical NASNet achieves an acceptable score for malaria image classification, it does not achieve the highest accuracy in this analysis.

4.3. Results with proposed feature extraction method

The performance results of each applied machine learning technique are evaluated using both CNN and NASNet transfer features in this section. For fair comparisons, spatial features are first extracted from CNN and evaluated. Then, spatial features are extracted from NASNet and evaluated.

4.3.1. CNN transfer features

Table 6 displays the evaluation of machine learning methods using CNN-based spatial features. The analysis reveals that the utilization of CNN features results in low-performance scores. The KNC technique achieves the highest precision score of 0.72; however, there is a need for further performance enhancement in malaria diagnosis. Based on this analysis, it can be concluded that CNN-based spatial features are not conducive to achieving high-performance scores.

Table 6
Performance results analysis with CNN transfer features.

Technique	Accuracy	Target class	Precision	Recall	F1
RF	62%	parasitized	0.57	0.94	0.71
		uninfected	0.84	0.31	0.45
		Average	0.71	0.62	0.58
LR	62%	parasitized	0.63	0.62	0.62
		uninfected	0.62	0.63	0.63
		Average	0.62	0.62	0.62
SVM	61%	parasitized	0.57	0.86	0.69
		uninfected	0.72	0.35	0.47
		Average	0.64	0.61	0.58
KNC	61%	parasitized	0.56	0.96	0.71
		uninfected	0.87	0.25	0.39
		Average	0.72	0.61	0.55

4.3.2. NASNet transfer features

The comparative results analysis of machine learning techniques with novel transfer learning features on unseen data is shown in Table 7. Our research study used advanced machine learning approaches

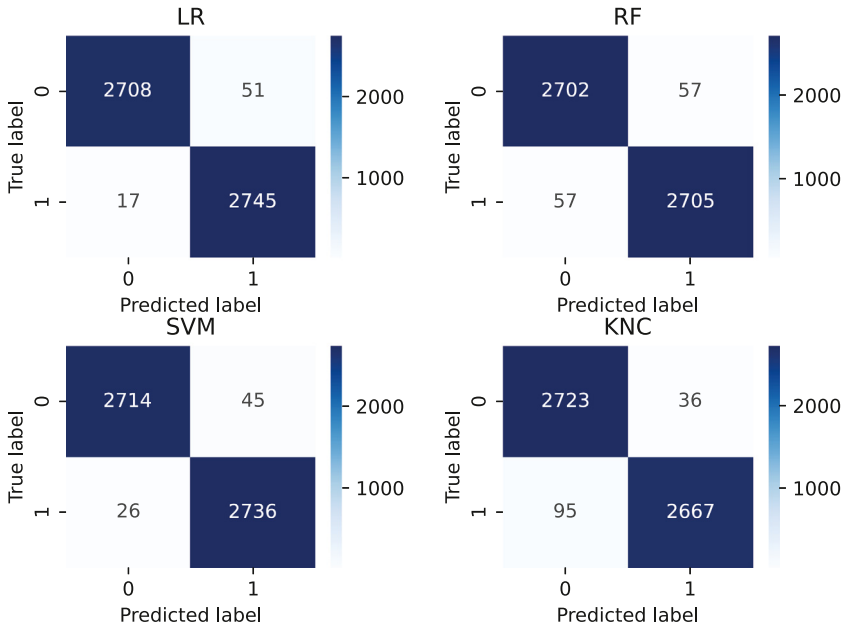


Fig. 6. Confusion matrix of the applied machine learning methods based on the proposed NNR feature extraction method.

Table 7
Performance results analysis with NNR transfer features.

Technique	Accuracy	Target class	Precision	Recall	F1
RF	98%	parasitized	0.98	0.98	0.98
		uninfected	0.98	0.98	0.98
		Average	0.98	0.98	0.98
LR	99%	parasitized	0.99	0.98	0.99
		uninfected	0.98	0.99	0.99
		Average	0.99	0.99	0.99
SVM	99%	parasitized	0.99	0.98	0.99
		uninfected	0.98	0.99	0.99
		Average	0.99	0.99	0.99
KNC	98%	parasitized	0.97	0.99	0.98
		uninfected	0.99	0.97	0.98
		Average	0.98	0.98	0.98

such as RF, LR, KNC, and SVM techniques to evaluate the performance with novel transfer features extracted by the NASNetL model. The analysis shows that the RF and KNC models achieve a maximum accuracy of 98%, as indicated by the classification reports. The SVM and LR models achieve an immense accuracy score of 99% for both models. This analysis demonstrates that both LR and SVM achieved high-performance scores with the proposed feature engineering approach. Consequently, this analysis concludes that transfer features extracted by the NASNet model from malaria images contribute to achieving high-performance scores.

The confusion matrix analysis of the applied machine learning approaches using the proposed NNR transfer features is illustrated in Fig. 6. The analysis shows that all the applied methods achieved a minimum error rate for unseen testing data when using the proposed features. The analysis validates the applied technique's high-performance scores with the proposed malaria diagnosis features.

The performance comparison based on histogram bar charts is illustrated in Fig. 7. The research investigates the effectiveness of various machine-learning techniques applied to CNN and NASNet spatial features. The results reveal that the performance scores of the machine learning approaches are relatively low, ranging from 61% to 62%, when utilizing the CNN spatial features. Conversely, the study concludes that significantly higher performance scores are achieved when employing the NASNet spatial features.

Table 8
Performance validation analysis of applied techniques with proposed NNR transfer features.

Technique	K-fold	K-fold accuracy	Standard deviation (+/−)
RF	10	98.0%	0.0018
LR	10	97.7%	0.0018
SVM	10	98.6%	0.0018
KNC	10	98.6%	0.0019

4.4. K-fold cross validations

The 10-fold cross-validation analysis is applied to machine learning models to validate their performance scores in this study. Table 8 demonstrates the outcomes of the applied k-fold validation analysis. The results show that RF achieves a cross-validation accuracy of 98.0%, while LR achieves 97.7%. Both models exhibit good performance with a standard deviation of 0.0018. SVM and KNC also achieve a cross-validation score of 98.6%, but the standard deviation is 0.0018 for SVM and 0.0019 for KNC. Based on this analysis, it can be concluded that the applied machine learning approaches provide generalized performance analysis for the diagnosis of malaria.

4.5. Computational complexity measurement

The computational complexity analysis of the applied machine learning method with the proposed transfer features is shown in Table 9. The analysis reveals that the KNC model requires a minimum time of 0.019 s, followed by SVM, LR, and RF for building on transfer feature data. The SVM model takes 0.025 s, while the LR model takes 0.209 s. The RF model exhibits the longest training time, requiring 1.161 s for estimation. This analysis demonstrates that the KNC model has good time complexity, as it takes less time when training data. However, KNC also achieved less-performance scores in comparisons.

4.6. Comparison with state-of-the-art approaches

The performance comparisons with state-of-the-art studies are presented in Table 10. The comparison analysis reveals that previous studies on malaria detection predominantly utilized classical deep-learning techniques. In contrast, our proposed approach is based on

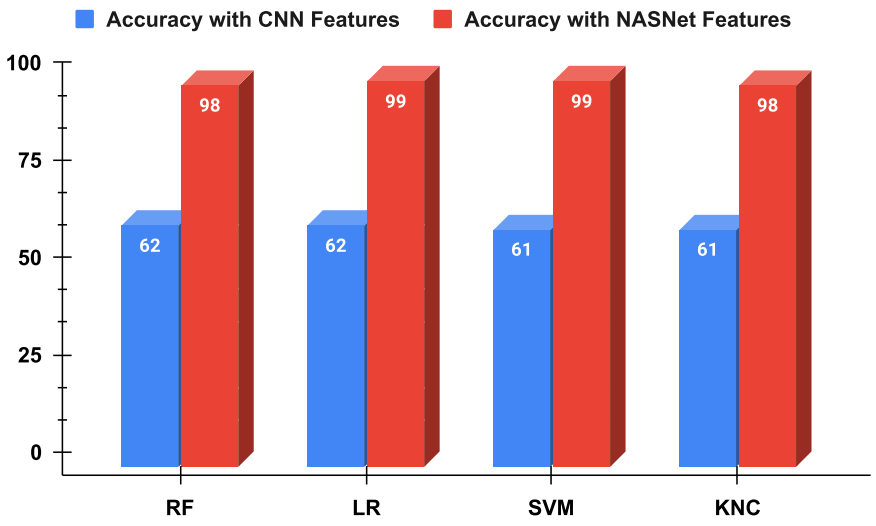


Fig. 7. Performance comparisons with CNN and NASNet transfer features.

Table 9
Computational complexity analysis of applied machine learning method with proposed NNR transfer features.

Technique	Runtime computations (seconds)
RF	1.161
SVM	0.025
KNC	0.019

Table 10
Comparison with related state-of-the-art studies.

Ref.	Learning type	Proposed technique	Performance accuracy
[30]	Deep Learning	DL-DAGNN	94%
[31]	Deep Learning	VGG-19-CNN	96%
[33]	Deep Learning	IDTL-MPDC	95%
[46]	Deep Learning	DenseNet-201	95%
Proposed	Transfer Learning	NNR+SVM	**99%**

transfer learning, demonstrating high-performance scores of 99% for malaria diagnosis. This analysis concludes that our proposed approach surpasses state-of-the-art studies with exceptional performance.

5. Conclusions and future work

The study proposes an efficient model for early malaria diagnosis and uses malaria images based on parasitized and uninfected red blood cells for the experiments. We applied classical neural network approaches and numerous machine learning techniques for comparison. The applied neural network approaches include NASNet and CNN. The applied machine learning methods for diagnosis are RF, LR, SVM, and KNC. We proposed a novel NNR method for transfer feature engineering. The proposed NNR approach first extracts spatial features from input malaria images, and then class prediction probability features are obtained from these spatial features. The newly created feature set is utilized to construct the machine learning methods. Our research experiments show that the SVM method outperformed state-of-the-art studies, achieving a high-performance score of 99% and a runtime computational complexity of only 0.025 s. We validated the performance of each applied method using k-fold cross-validation. We optimized the hyperparameters of the applied models through a tuning process to achieve high-performance scores for the early diagnosis of malaria.

For future work, we plan to develop a web-based tool that enables real-time monitoring and assists specialists in diagnosing malaria based on red blood cell images. Additionally, we aim to enhance the image dataset by collecting more data on red blood cell images.

In addition, we suggest implementing a more advanced pre-trained neural network architecture to extract high-level features from malaria images. This would enhance the effectiveness of malaria diagnosis using red blood cells.

CRediT authorship contribution statement

Azam Mehmood Qadri: Supervision, Conceptualization, Methodology, Software, Investigation, Validation, Writing – original draft. **Ali Raza:** Writing – original draft, Visualization, Investigation. **Fatma Eid:** Writing – original draft, Visualization, Investigation. **Laith Abualigah:** Writing – original draft, Visualization, Investigation.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

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