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Leveraging the Effectiveness of Interpretability in Malaria Cell Image Classification using Depthwise Inception Residual Model

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ABSTRACT

Malaria, caused by Plasmodium parasites, remains a critical global health issue, particularly in tropical regions. Traditional microscopic diagnosis is time-consuming and reliant on expert skills. This study proposes DepthResInceptNet, an innovative deep learning model that integrates depthwise convolution, inception, and residual learning for malaria detection in red blood cell images. The dataset comprised 27,557 images, split into training, validation, and testing subsets and pre-processed to standardize and augment data. The model's architecture leverages parallel convolutional filters and residual connections to enhance feature extraction and mitigate degradation, reducing computational costs and parameters. Evaluation metrics indicated high performance with an accuracy of 94.2% and recall of 97.0%. Comparative analysis with state-of-the-art models demonstrated the proposed model's superior reliability and efficiency. The application of Grad-CAM for model interpretability highlighted the decision-making regions, enhancing trustworthiness. DepthResInceptNet offers a robust and precise tool for automated malaria diagnosis, outperforming existing methods.

Keywords: Malaria blood cells, interpretability, residual learning, depthwise, deep learning.

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1. INTRODUCTION

Malaria is a debilitating disease caused by the Plasmodium parasite. The primary mode of transmission is through the bite of female Anopheles mosquitoes that are infected [1]. The disease is attributed to different species of Plasmodium, including Plasmodium falciparum and vivax. The parasites infiltrate and replicate within the human red blood cells. This disease continues to be a significant global ailment issue, particularly in certain nations, impacting millions of people each year and inflicting severe economic harm [2]. Common symptoms of malaria include high body temperature, tremors, headache, nausea, vomiting, muscle pain, fatigue, and chest pain. Untreated individuals can experience severe consequences and even mortality as a result of malaria. A delayed diagnosis of malaria might pose grave dangers, potentially resulting in the patient's demise. World Health Organization (WHO) recorded a global incidence of over 213 million cases of malaria in 2016 and still on a high increase of 15% at present [3]. The estimated yearly rate of fatality attributed to malaria is 409 thousand [4]. Nevertheless, conventional microscopic investigations take longer time to achieve precise diagnosis. The accurate and effective diagnosis of malaria relies on various aspects, including the clinical examination, cost and duration of the procedure, sensitivity, the rapid of attention to patient, and the need for an expertise [3]. Hence, there is a need for a sophisticated automated system that can promptly and precisely identify malaria from human red blood cells.

Recent researches have explored using automated image analysis tools for malaria diagnosis, using machine learning and deep learning models to differentiate between infected and healthy blood cells using staining traits. A study in [4] proposed a strategy for detecting malaria using dataset from Gadjah Mada University's Parasitology laboratory. Another study uses a technique of histogram to extract features of malaria parasite in images [5]. The obtained features were used to train an Artificial Neural Network (ANN) model. A multilayer perceptron with backpropagation algorithm as a training strategy was employed by the authors in [6] for identifying malaria parasite. The findings showed that the suggested artificial neural network (ANN) attained about 88% accuracy with 0.55 seconds computation time. Nevertheless, the performance was comparatively low, suggesting the necessity for more precise method. Suraksha et al. [7] used a CNN model for classifying blood smear images with promising outcome, indicating the need for further improvement. Advancements in AI have shown promising outcomes in the field of malaria detection. Bhansali et al. [8] suggested MalariaNet, a computationally efficient CNN for automated malaria detection, emphasizing the potential of CNN algorithm in this field. Similarly, Maqsood et al. [9] utilized deep learning for detecting malaria parasites in thin blood smear images, obtaining significant performance. Jiang et al. [10] also discussed the broader implications of AI in healthcare, further establishing the foundation for AI-driven diagnostic tools. The main significance of this paper are; implementing unique deep convolutional model of depthwise convolutional network, incorporating wider receptive fields of parallel convolutional filters with skip connections of residual learning to reduce computational parameters and costs as well as addressing vanishing gradient problem, and finally employing Grad-CAM to enhance model interpretability. The following sections of this study are as follows: Section 2 gives detailed explanation of the proposed framework. Section 3 provides the experimental findings, and the paper conclusion and future work are written in Section 4.

2. METHODOLOGY

This section provides detailed explanation of data collection and pre-processing, innovative approach, and the evaluation metrics for the classification of malaria.

2.1. Data Collection and Preprocessing

The image dataset used in this study was originally sourced from the National Institute of Health (NIH) and downloaded via Kaggle dataset repository available at (https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria). The dataset collection consists of micrographs of erythrocytes obtained from Giemsa-stained thin blood smear slides. The dataset contains a total of 27,557 images, of which 13,778 are infected and 13,779 are uninfected, as depicted in Table 1 and later renamed categorize them as either healthy or infected.

The RGB color mode, which includes three channels, presents resolutions spanning around 48 x 48 pixels to 386 x 396 pixels. To expedite the convergence of the proposed model, we standardize the input image size by resizing all images to 224 x 224 pixels. Figure 1 displays the sample images from both the infected and uninfected groups. The infected cells exhibits red globular forms, which are absent in the healthy.

The dataset is subdivided into three sets of train, validation, and test, with the ratio of 70:15:15. Standardization is applied to all the images to maintain consistency by performing rescaling, which is an essential pre-processing step before training the proposed model. The original images are adjusted to within the range of 0 to 1. Subsequently, data augmentation is employed to enhance the number of training instances and to ensure these instances are entirely dissimilar from the test dataset. The different augmentation techniques employed include rotation, flipping, shifting, and zooming.

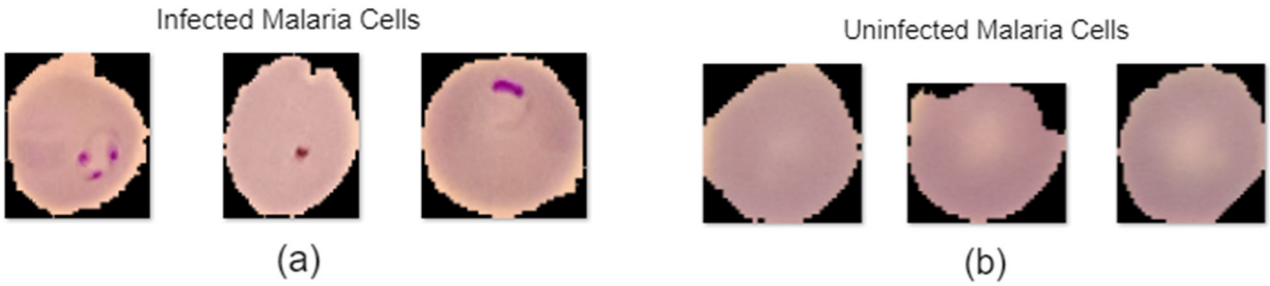


Figure 1. Illustration of the dataset for (a) infected (b) uninfected red blood malaria cells

Table 1. Malaria Dataset Description

Category	Number of images
Infected Cells	13,778
Uninfected Cells	13,779

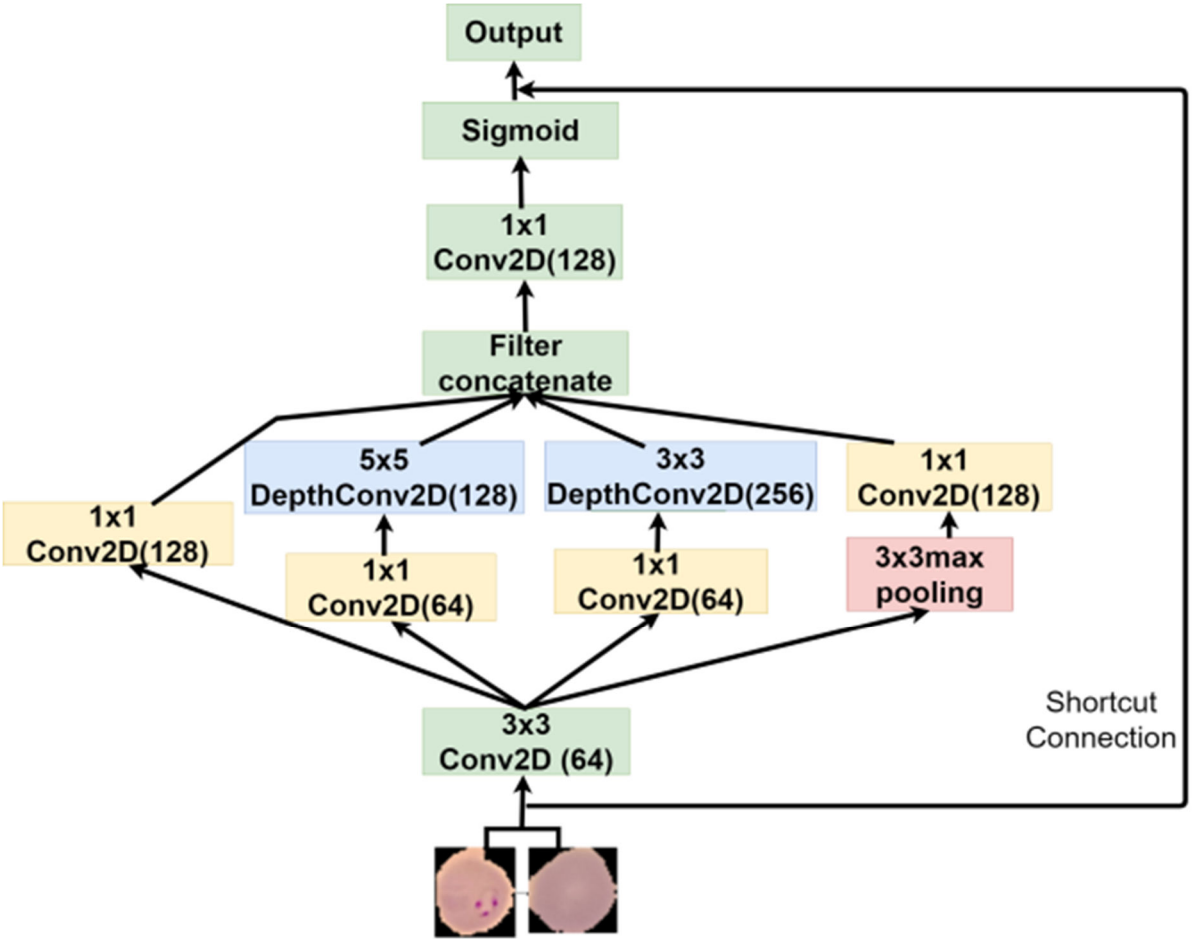


Figure 2. The architectural structure of the proposed DepthResInceptNet.

2.2. Proposed Model

This paper proposes a custom model that combines Depthwise Convolution, Inception, and Residual learning for the classification of malaria cells. The combination uses the convolution operation of Depthwise convolution within inception structure with skip connections of residual learning as illustrated in Figure 2. The DepthResInceptNet model combines the advantages of the three concepts: Depthwise separable convolution, Inception, and ResNet. This proposed innovative framework reduces computational parameters and costs using the bottleneck techniques and kernel factorization. It extracts more features by expanding the network's depth and width through parallel kernel network structure. Additionally, it addresses the problem of degradation using the skip connection of residual learning structure. The two DepthConv2D layers in Figure 2 have dimensions of 5x5 and 3x3 kernel sizes and 128 and 256 channels, respectively, crucial for the proposed DepthResInceptNet and offers more advantages compared to the standalone inception and ResNet networks.

2.3. Evaluation Metrics

The evaluation metrics used in this study are accuracy (ACC), precision (PREC), recall (REC), f1-score (F1), receiver operating characteristic-area under the curve (ROC-AUC), and confusion matrix.

$$(1)\ Confusion\ Matrix = \begin{bmatrix} TN & FP \\ FN & TP \end{bmatrix}$$

$$(2)\ \ Accuracy\ = \frac{TP + TN}{TP + FP + TN + FN}$$

$$(3)\ Precision\ = \frac{TP}{TP+FP}$$

$$(4)\ Recall = \frac{TP}{TP+FN}$$

$$(5)\ \ F1 - score\ = 2 * \frac{recision * Recall}{Precision + Recall}$$

$$(6)\ ROC - AUC = \frac{TP}{TP+FN}, \frac{FP}{FP+TN}$$

$$Where\ TP: True\ Positive, FN: False\ Negative, TN: True\ Negative, FP: False\ Positive$$

3. RESULT ANALYSIS AND DISCUSSION

This section will elucidate the proposed model hyperparameter tweaking, the results gotten from the proposed model and other fair analysis carried out.

3.1. Hyperparameter Optimization

To improve the performance of the proposed model, some hyperparameters adjustments were considered as shown in Table 2. The selected hyperparameters are learning rate, optimizer, filter sizes, dropout, activation function, and the number of convolutional layers which are used to control the model's learning. In this study, ReLU activation is used on every layer to add non-linearity for hierarchical feature learning while Adam optimizer is used due to its quick convergence performance and low memory cost. Learning rate is set to start at 0.001 and dynamically reduce for every 5 rounds without changes in the training results.

Table 2. Hyperparameter information

Batch size	Optimizer	Activation function	Dropout	Learning rate	Patience
32	Adam	ReLU	0.3	0.001	10

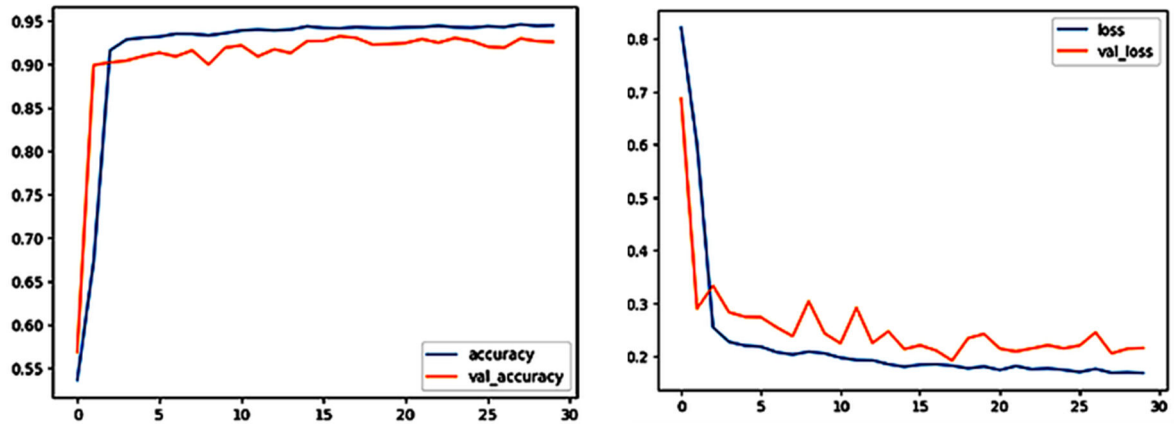
3.2. Discussion

The experimental analysis presented in this study adopted different evaluation metrics to validate the high performance of the proposed DepthResInceptNet in classifying malaria blood cells. The model achieved a high accuracy and low loss, indicated it strong classification ability and suitability, as further supported by its confusion matrix results.

Table 3. Statistical analysis of the proposed DepthResInceptNet

	ACC (%)	PREC (%)	REC (%)	AUC (%)	F1 (%)	SPE (%)
Training	95.0	97.3	97.4	98.2	97.2	98.1
Validation	94.2	96.3	97.0	97.4	96.6	97.0

Table 3 provides a statistical overview of the proposed DepthResInceptNet, which achieved an accuracy of 94.2% and recall of 97.0%. To further evaluate the capacity of the proposed model, a fair comparison with some pre-existing pre-trained models is presented in Table 4. For fairness, the same computational resource is used to train all the models on the same dataset, and batch size of 32. To accommodate the limitations of the computational resources, the pre-trained models' top layers were replaced with only a global average pooling layer followed by a sigmoid layer.

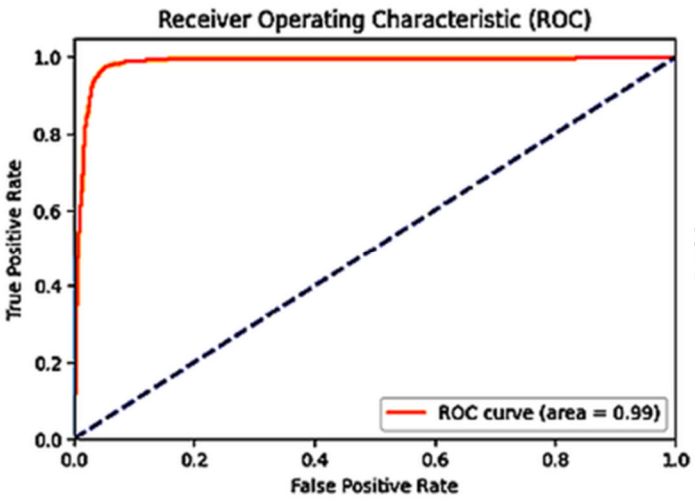


(a) Accuracy plot (b) Loss plot

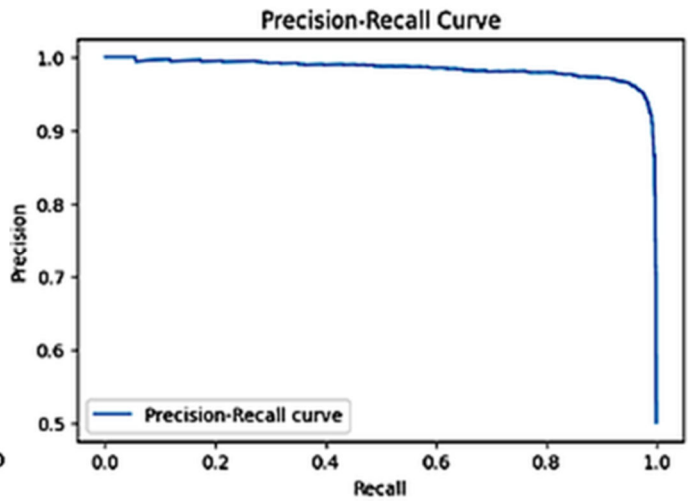
Figure 3. Performance curves of the proposed DepthResInceptNet (a) Accuracy plot, (b) Loss plot

Figure 3 displays both the rapid increase in both training and validation accuracy over 30 epochs, with the training accuracy starts at approximately 0.55 and quickly rising to stabilize around 0.95 as presented in Figure 3(a). The validation accuracy follows a similar trend, stabilizing around 0.92. This rapid convergence to high accuracy levels within the first few epochs indicates the model's efficiency in learning from the training data. In parallel, the loss curve in Figure 3(b) depicts a significant reduction in both training and validation loss, starting from approximately 0.8 and decreasing to around 0.1 for training loss, and from 0.8 to approximately 0.2 validation loss. The training loss decreases swiftly, indicating that the model is successfully minimizing the error on the training while the fluctuations of validation loss remains close to the training loss throughout the epochs, this further indicate the model's robustness.

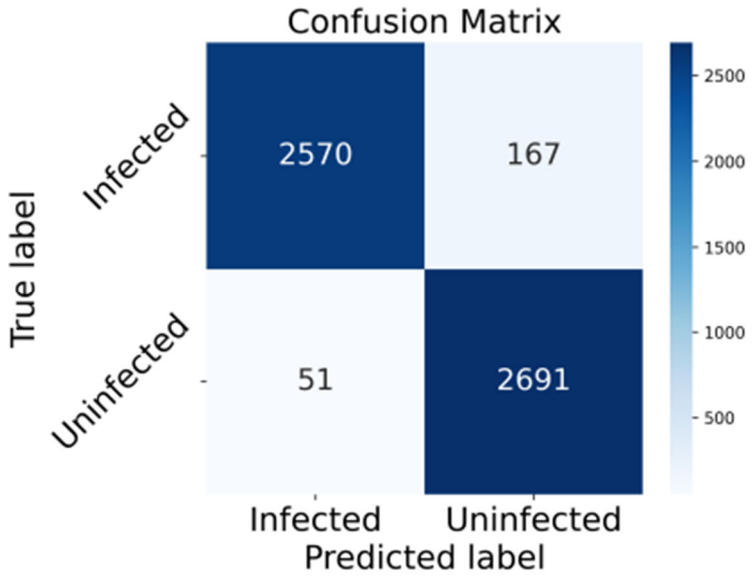
Figure 4(a) displays the ROC curve with an AUC of 0.98, which indicates near-perfect sensitivity and specificity, signifying the model's exceptional capability in distinguishing between two classes across various threshold settings. The Precision-Recall curve in Figure 4(b) further underscores this point by maintaining high precision nearly consistently across all recall levels, a critical feature for applications where the cost of false positives is high.



(a) ROC-AUC curve



(b) Precision-recall curve



(c) Confusion matrix

Figure 4. Evaluation result plots of the proposed DepthResInceptNet (a) ROC-AUC curve, (b) Precision-Recall curve, (C) Confusion Matrix

The confusion matrix in Figure 4(c) details the model's predictive accuracy, showing 2691 true positives and 2570 true negatives, with 167 false positives and 51 false negatives. This indicates the model's strong predictive power and effectiveness in minimizing both false positive and negative error rates, demonstrating DepthResInceptNet's robustness in classification tasks, making it highly suitable for practical applications needing high precision and recall. Table 4 and Table 5 demonstrate the efficacy of our proposed compared to pre-trained models and other research studies. It is evident that although more complex models have been proposed, our model exhibits commendable reliability and capability in accurately classifying malaria with high performance.

Table 4. Fair comparison analysis of DepthResInceptNet model with pre-trained models

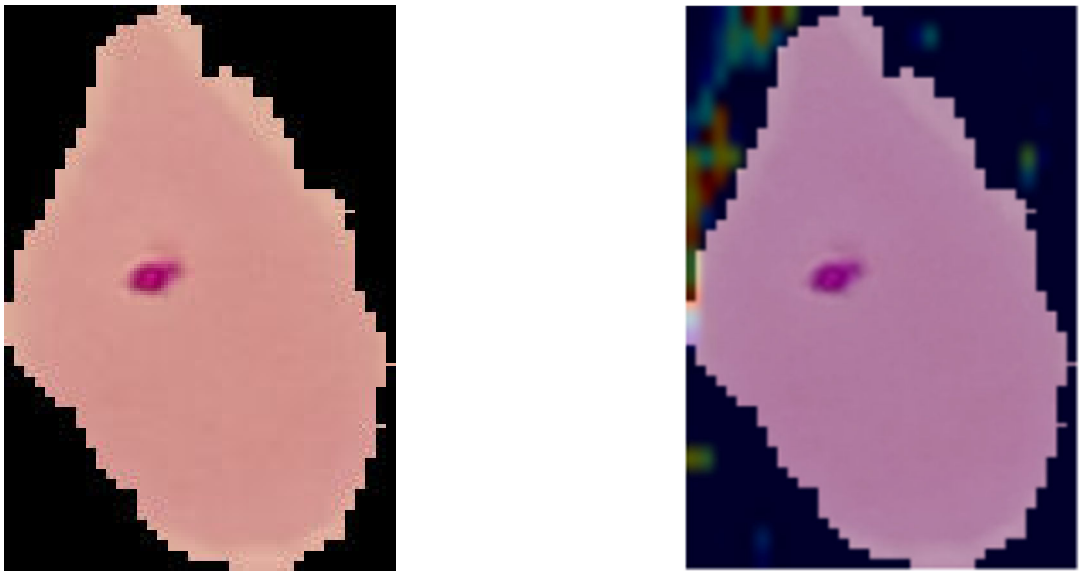
Model	Batch size	ACC (%)	REC (%)	SPEC (%)	Parameters
VGG16	32	90	87	86	14,360,714
ResNet-50	32	92	90	91	23,552,450
InceptionV3	32	93	91	92	21,850,849
Proposed	32	94.2	97.0	97.0	873,852

Table 5. Comparison analysis of DepthResInceptNet model with existing literature

Authors	ACC (%)	F1-s(%)	REC (%)	SPEC (%)	PREC (%)	AUC (%)
Oyewola et al. [1]	94.0	-	96.00	90.50	-	-
Suraksha et al. [2]	96.3	76.7	90.6%	78.7%	-	-
Qadir et al. [6]	95.4	77.8	81.2	-	74.6	-
Proposed	94.2	96.6	97.0	97.0	96.3	97.4

3.3. Model Interpretability

Figure 5 showcases the interpretability of the proposed DepthResInceptNet using Grad-CAM. The left side of the figure displays the original image, which serves as the input to the model. The right side illustrates the GRAD-CAM heat map superimposed on the same image. Grad-CAM pinpoints the intricate area in the image that contributes most vital to the decision-making process. In this example, the area around the center, marked by intense coloration, indicates the most influential regions detected by the model. Figure 5 helps in understanding the model's focus areas, enhancing the interpretability and trustworthiness of DepthResInceptNet in it decision-making process.



(a) Original Image (b) Grad-CAM image

Figure 5. Grad-CAM interpretability of Proposed DepthResInceptNet (a) Original image, (b) Grad-CAM image

4. CONCLUSIONS

This paper presents DepthResInceptNet, a robust and efficient model for the automatic detection of malaria in red blood cell images. By incorporating depthwise convolution, inception, and residual learning, the model achieves high accuracy of 94.2% and recall of 97.0%, outperforming existing models. The utilization of Grad-CAM improves the model's interpretability, providing valuable insights in the decision-making process. This study illustrates vital potential for improving malaria diagnosis, offering a reliable and cost-effective alternative system to traditional methods. Future work will focus on refining the model to handle larger and more diverse dataset, ensuring its applicability in different medical scenarios as well as its adaptability to other parasitic and infectious diseases.

References

[1] D.O. Oyewola, E.G. Dada, S. Misra, R. Damaševičius, A novel data augmentation convolutional neural network for detecting malaria parasite in blood smear images, Appl. Artif. Intell. 36 (1) (2022) 2033473.

[2] S. Suraksha, C. Santhosh, B. Vishwa, Classification of malaria cell images using deep learning approach, in: 2023 Third International Conference on Advances in Electrical, Computing, Communication and Sustainable Technologies(ICAECT),2023,pp. 1–5, http://dx.doi.org/10.1109/ICAECT57570.2023.10117649.

[3] B. Kakkar, M. goyal, P. Johri, Y. Kumar, Artificial intelligence-based approaches for detection and classification of different classes of malaria parasites using microscopic images: A systematic review, Arch. Comput. Methods Eng. (2023) 1–20.

[4] S.N. Mahmood, S.S. Mohammed, A.G. Ismaeel, H.G. Clarke, I.N. Mahmood, D.A. Aziz, S. Alani, Improved malaria cells detection using deep convolutional neural network, in: 2023 5th International Congress on Human-Computer Interaction, Optimization and Robotic Applications (HORA), 2023, pp. 1–4, http://dx.doi. org/10.1109/HORA58378.2023.10156747.

[5] Diker, A. (2022). An efficient model of residual based convolutional neural network with Bayesian optimization for the classification of malarial cell images. Computers in Biology and Medicine, 148, 105635.

[6] A.M. Qadir, P.A. Abdalla, M.I. Ghareb, Malaria parasite identification from red blood cell images using transfer learning models, Passer J. Basic Appl. Sci. 4 (Special issue) (2022) 63–79.

[7] Yang, F., Poostchi, M., Yu, H., Zhou, Z., Silamut, K., Yu, J., Maude, R.J., Jaeger, S., Antani, S., 2019. Deep learning for smartphone-based malaria parasite detection in thick blood smears. IEEE J. Biomed. Health Informatics 24 (5), 1427–1438.

[8] Rohan Bhansali, MalariaNet, A computationally efficient convolutional neural network architecture for automated malaria detection, Int. J. Eng. Res. V9 (12) (2020).

[9] A. Maqsood, M.S. Farid, M.H. Khan, M. Grzegorzek, Deep malaria parasite detection in thin blood smear microscopic images, Appl. Sci. 11 (5) (2021) 1–19.

[10] Jiang, Y., Li, X., Luo, H., Yin, S. and Kaynak, O., 2022. Quo vadis artificial intelligence? *Discover Artificial Intelligence*, *2*(1), p.4.