Predictive Deep Learning Models for Malaria Using Cell Images Dataset

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Abstract

Malaria, which is an endemic disease in most nations around the world, is also one of the most lethal diseases to children in Africa, particularly Nigeria, where twenty-nine countries account for 95% of malaria cases globally, with Nigeria accounting for 27%. Malaria prevention and treatment are also major difficulties in most African countries, and the disease is frequently diagnosed by health workers, particularly microbiologists, using microscopic blood smear samples. As a result, it has put a significant strain on the few medical facilities and health personnel available in most African nations, particularly Nigeria, the Democratic Republic of the Congo, Uganda, Mozambique, and Niger. Hence, artificial intelligence techniques, particularly deep learning, are increasingly widely employed for disease classification, diagnosis, and prediction. Deep learning predictive models for malaria were developed in this study utilizing a dataset of cell images. The convolutional neural network and ResNet-50 algorithms were used to create malaria models with cell image datasets, and the random rotational image augmentation technique was employed to maintain and optimize the models' performance. The predictive models' performance was evaluated, and the results show that ResNet-50 predictive models outperformed convolutional neural network predictive models in terms of being able to classify and predict infected and uninfected malaria cells with 95% accuracy, as well as correctly predicting negative cases of malaria with 95% accuracy. However, in terms of successfully predicting positive cases of malaria, the convolutional neural network predictive model surpassed the ResNet-50 predictive model with 95% accuracy.

Keywords:
Malaria; Deep Learning; Convolutional Neural Network; Residual Network; ResNet-50;

1. Introduction

Malaria is caused by protozoan parasites of the genus Plasmodium, which is spread via the bite of female anopheles' mosquitos, which infect red blood cells [27] [12]. Malaria is responsible for the majority of child mortality in Africa, and virtually every minute someone dies as a result of malaria in Africa. Malaria is also one of the primary causes of impairment among African children [31]. According to the World Health Organization (WHO), there will be an estimated 229 million cases of malaria in 87 countries by 2019 [31]. Nigeria accounts for 27% of malaria cases worldwide, the Democratic Republic of the Congo accounts for 12%, Uganda accounts for 5%, Mozambique accounts for 4%, and Niger accounts for 3% [31]. Malaria symptoms include fever, fever, headache, and, in many cases, life-threatening symptoms such as fainting and convulsions [31]. Millions of blood films are examined for malaria each year, with health workers or skilled microscopists manually counting parasites and infected red blood cells, which is prone to errors and false examinations [22].

The accuracy of malaria microscopic examination is greatly dependent on the expertise and capabilities of the health worker or microscopist [30]. As a result, not all examinations are found to be proper and accurate, and false negative cases of examination result in the use of unneeded antibiotics, lost days of work, a second consultation, and, in some cases, progression into severe malaria [27]. False positive cases of malaria testing result in the inappropriate use of anti-malaria medications, abdominal pain, diarrhea, and, in some cases, severe sequelae [12, 22, 27]. Consequently, artificial intelligence (AI) techniques such as machine learning, deep learning, data mining, expert systems, and others are being utilized to automate the inspection, prediction, and diagnosis of numerous diseases such as diabetes, SARS-Cov2, heart attack, and typhoid [3, 14-15].

Artificial intelligence-assisted diagnostic and predictive tools based on data-driven deep learning algorithms and techniques such as convolutional neural networks and residual networks, among others, had already become the architecture of choice for image preprocessing, analysis, and recognition tasks [16-18]. Furthermore, new applications of deep learning algorithms on picture datasets have greatly reduced the enormous clinical burden by assisting in disease triage and interpretation [20]. Deep Learning is one of the applied artificial intelligence approaches that is being employed for prediction and diagnosis of numerous diseases, making it popular among other AI techniques [5 -6, 19]. Convolutional neural network and residual network deep learning techniques are utilized in this study to construct predictive deep learning models for malaria using cell imaging datasets.

Manuscript received September 5, 2022
Manuscript revised September 20, 2022
https://doi.org/10.22937/IJCSNS.2022.22.9.89

2. Deep Learning

Deep learning is one of the one of machine leaning approaches that enables a system to learn from experience and observe the world through the realm of thought or hierarchy of approaches [24,34,36]. Because the computer system learns from experience, even computer users cannot officially describe all of the information necessary by the system [23]. The idea hierarchy allows computer systems to acquire complicated concepts by building them up from simple to sophisticated deeper layers [23, 37]. Unlike traditional machine-learning techniques, which are limited in their ability to process raw natural data, deep learning represents a diverse range of presentations obtained by designing simple but non-compliant modules for each to transform representation at a higher, often less understandable or abstract level [10 - 11]. As a result of the building of this appropriate adaptation, more difficult tasks or concepts can be learned from previous experience [25, 39].

Deep learning's theoretical roots are deeply established in classical neural networks, however unlike neural networks, deep learning employs numerous hidden neurons and layers, as well as new training procedures [23]. Deep learning is now making significant advancements and improvements in solving complex and difficult problems that have withstood the best efforts of the AI community for many years [6]. It has now been discovered to be very promising AI approaches that are very good at detecting intricate structure in high dimensional data, and it is thus applied in various fields such as business, research, medical, and government, among others. Deep learning is also breaking records in image identification and speech recognition. Deep learning has resulted in a slew of breakthroughs in picture categorization and recognition [1-3]. As a result, in this study, convolutional neural network and residual network learning algorithms are utilized to create prediction models for malaria using cell image datasets, respectively.

A. Convolutional Neural Network

The Convolutional Neural Network (CNN) is one of the most effective discriminatory algorithms, with layers composed of convolutional and pooling layers [1, 34-35]. Layers are piled on top of one another. The convolutional layer bears a significant amount of weight, however the composite layers soften the convolutional layer release and minimize the quantity of data rate from the lower layer [1, 24]. Weight sharing in the convolutional layer, together with carefully designed pooling techniques, endows the CNN with some invariance qualities [24]. CNN has been identified as one of the most successful deep learning vision algorithms for image recognition and computer vision [28]. In CNN's convolutional layer, Convolutional features mapping from the preceding layer are convolved with learnable kernels with non-linear or linear activation functions such hyperbolic tangent, sigmoid, softmax, and others to produce feature maps in CNN's convolutional layer [10]. As a result, each feature map output is mixed with several feature map inputs. As shown in equation (1) below, :-

$$x_j^i = f\left(\sum_{i\in M_j} x_i^{I-1} * k_{ij}^I + b_j^I\right), \tag{1}$$

Where x_j^i is the output of the current layer, x_i^{I-1} is the previous layer output, k_{ij}^I is the kernel for the present layer and b_j^I are the biases for the current layer. M_j is selection input maps while an addictive bias b is each output map.

At pooling layer of CNN the number of input and output features maps cannot change because if there are n input maps, then there must be n output map exactly. But the size of the each dimension of the output map will be reduced due to the down sampling operation. The operation can be formulated with the equation below:-

$$x_j^i = down\left(x_j^{I-1}\right), \tag{2}$$

In this study, a convolutional neural network technique was utilized to construct a Malaria predictive model using a dataset of cell images.

B. Residual Network

Residual Network (ResNet) was developed to address the vanishing gradient drawback with different number of layers which include 34, 50, 101, 152, 1202 among others [10 -11, 13]. The algorithm is a feed forward CNN with residual connections, with layers set by the output of $(I-1)^{th}$ which drives from residual layer defines as $x_{i-1}.F(x_{i-1})$ is the output after performing various operations. The final output of residual, the unit is x_I which can be defined with the equation below:-

$$x_I = F(x_{i-1}) + x_{i-1}\,. \tag{3}$$

ResNet-50 was employed in this work, which had 49 convolutional layers and 1 completely filled layer. ResNet-50 is a typical deep convolutional neural network with image, auto-encoding, and classification capabilities. [3].

3. Related Work

Using the Visual Geometry Group Network and Support Vector Machine methods, novel deep learning network models for recognizing infected falciparum malaria parasites were presented in [2]. In [32], researchers developed a new and robust CNN algorithm to classify malaria single cells in thin blood smears on standard microscope slides as infected or uninfected. The algorithm achieved 96.99% accuracy, 97.75% specificity, 97.73% precision, 97.36% F1 score, and 94.75% Matthews correlation coefficient. The work of [26] assessed the performance of pre-trained and custom CNNs and created an ideal model ensemble for classifying normal and parasitized cells in malaria thin blood smear images. A novel technique for pre-processing and analysis of thin microscopic images of blood infected with malaria parasite was proposed in the work of [29]. Deep learning techniques were used for detection of thin microscopic images of blood infected with malaria parasite in the work of [8] and learning techniques were found to be promising and efficient.

The study of [9] developed an automated diagnosis approach for malaria diagnosis utilizing microscopic images, and the approach quantifies and classifies red blood cells infected with Plasmodium falciparum or Plasmodium malaria in a thin blood smear. Kernel dilation and robust CNN were introduced in the study of [1] three various kernel techniques were utilized among which Fibonacci series wises CNN model performed best in all ramifications with 96.05% accuracy, 96.06% F1 score, and 96.33% recall. In the work of [4,] a dependable and rapid mobile phone android-based application platform for blood image processing for malaria detection using Giemsa strained thin blood film images was built. The application was designed, tested, and verified in MATLAB, and the system was capable of detecting blood components such as red blood cells, white blood cells, and infected red blood cells, as well as recognizing the different life phases of the parasite and calculating the level of infection (parasitemia). Deep learning approach for diagnosis of malaria with smart phone using thick blood smear was proposed in the work of [8]. The customized CCN algorithm was used in the work and result was found to be very promising. In work of [28] CCN based diagnostic model for malaria was implemented and the model optimized against overfitting and it has scored an F1 of over 94%. The model also used Thin Microscopic Blood Smear Samples. The overview of how machine learning techniques were used for analysis and detection of malaria was discussed in the study of [21]. The study acknowledged that, deep learning has wider acceptance and recognition among researchers in medical filed especially for image processing and recognition.

4. Materials and Methods

This section handles dataset collecting, preparation, augmentation, and splitting, and Figure 1 depicts the materials and procedures used to create predictive deep learning models for malaria utilizing cell pictures dataset.

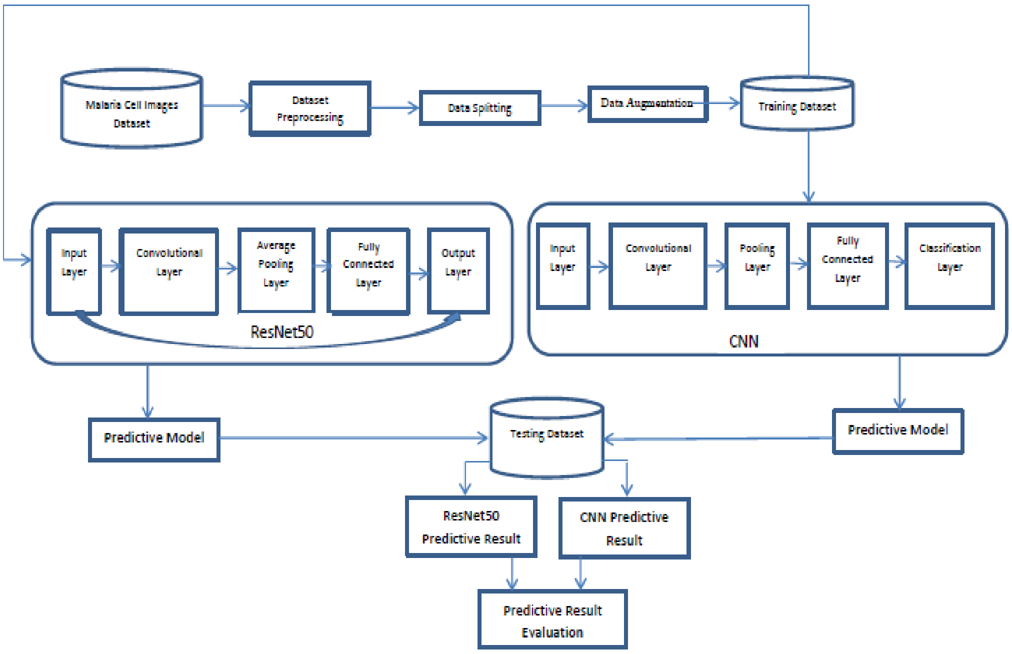

Figure 1: Material and Methods

C. *Dataset Collection, Preparation And Splitting*

This study made use of a public dataset for malaria cell pictures, which may be found at https://www.kaggle.com/iarunava/cell-images-for-detecting-malaria. The dataset contains 27,558 cell images, of which 22,046 are training photos and 5,512 are testing images. The dataset's cell picture can be parasitized (infected) or uninfected, and the dataset contains an equal number of cell images for both classifications. Figure 2 depicts a sampling of the dataset. The dataset was divided into 80% training and 20% testing sets. There are a total of 22046 training images and 5512 testing images.

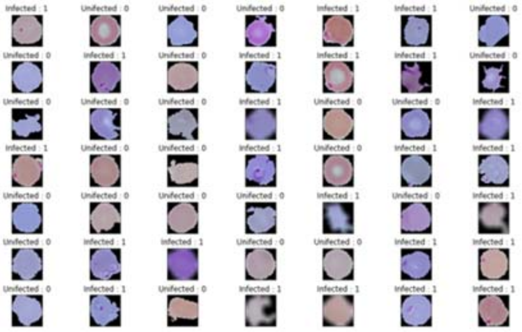

Figure 2: Sample of the dataset

D. *Data Augmentation*

In order to perform very effectively and accurately in terms of classifications and predictions, high-quality deep learning models rely substantially on high-quality training samples from the dataset. The random rotational image augmentation technique was employed in this work to maintain and optimize the model performance. The dataset was enhanced using a random rotational approach with a 90-degree range, width shift range=0.15, height shift range=0.15, horizontal flip=True, zoom range=[0.9, 1.25], and brightness range=[0.5, 1.5]. All of the networks were fed resized chest x-ray images of 279 × 280 pixels, which were done automatically, so order to obtain and keep much important information about the images' region of interest. As demonstrated in Equation 3, the sigmoid function (f) was utilized as the activation function for networks.

$$f\ (x) = Sigmoid\ (x)\frac{1}{1+e^{-x}} \tag{4}$$

For all networks, random numbers were assigned to the number of neurons, weights, and bias in the classification process (CNN and ResNet-50). Figure 2 depicts the cells formed using the random rotational image augmentation technique, both infected and uninfected.

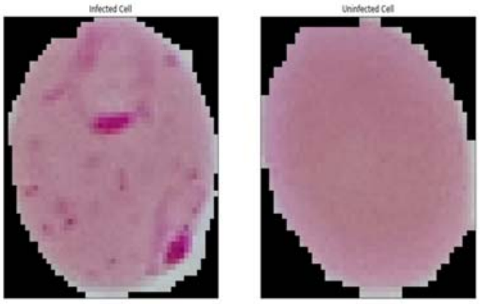

Figure 3: generated both infected and uninfected cells using random rotational image augmentation technique.

5. Results and Discussion

CNN and RetNet-50 deep learning techniques were used to create predictive models for Malaria using cell images dataset. The dataset contains a total of 27,558 cell images, of which 22,046 are training photos and 5,512 are testing images. The dataset's cell image can be parasitized (infected) or uninfected, and the dataset contains an equal number of cell images for both classifications. The dataset was trained on each deep learning technique, with 80% used for training and the remaining 20 percent used as testing sets. The models were validated using the dataset's test set after being trained for 10 epochs on the dataset's training set. The prediction models were checked to ensure that they were not overfitting to the training datasets, but rather fit equally to both the training and testing sets of the dataset. Figure 4 depicts the training and validation accuracy of a CNN-based predictive model, whereas Figure 5 depicts the model's training and validation loss, respectively.

Figure 4: Training and Validation Accuracy of CNN Based Predictive Model

Figure 5: Training and Validation Loss of CNN Based Predictive Model

As shown in Figures 6 and 7, the CNN Based Predictive Model's training and validation accuracy and training and validation loss are practically in the same trend towards the end, indicating that there was no overfitting to the training dataset. Figure depicts the training and validation accuracy of a ResNet-50-based predictive model, whereas Figure depicts the model's training and validation loss, respectively.

Figure 6: Training and Validation Accuracy of ResNet-50 Based Predictive Model

Figure 7: Training and Validation Loss of ResNet-50 Based Predictive Model

As shows in Figure the training and validation accuracy of the ResNet-50 Based Predictive Model is almost in the same trend towards the end, therefore, there was no overfitting to the training dataset. But however, as shown in Figure training and validation loss of the ResNet-50 Based Predictive Model are not in the same trend towards the end, therefore, there was overfitting to the training dataset.

The predictive models that were examined were evaluated using the following deep learning evaluation techniques: -

i. Accuracy: is defined as the ratio of correctly predicted cases by the model against the total number of instances, and it is defined using formula below: -

$$\frac{TP + TN}{TP + TN + FP + FN}$$

ii. Precision: is defined as the ratio of correctly predicted positive cases by the model against the total number of positive cases of the instances and it is defined using formula below: -

$$\frac{TP}{TP + FP}$$

iii. Recall: is defined as the ratio of correctly predicted negative cases by the model against the total number of negative cases of the instances and it is defined using formula below:-

$$\frac{TP}{TP + FN}$$

iv. F1-Support: is defined as the harmonic mean of precision and recall and it is defined using formula below:-

$$\frac{2 * (precision * recall)}{(precisio + recall)}$$

Note: TF stands for True Positive, FP stands for False Positive, TN stands for True Negative, FN stands for False Negative.

Table 1 displays the results of the prediction models' performance evaluations. Based on accuracy, the ResNet-50 predictive model was the best model with 94%, while the Precision CNN predictive model was the best model with 95%, the recall ResNet-50 predictive model was the best model with 95%, and the F1-score the bode models, ResNet-50 and CNN predictive models both had 94%. As a result, ResNet-50 predictive models outperformed CNN predictive models, properly classifying and predicting infected and uninfected malaria cells with 95% accuracy and correctly predicting negative cases of malaria with 95% accuracy. However, in terms of correctly predicting positive cases of malaria, the CNN predictive model surpassed the ResNet-50 predictive model with 95% accuracy.

Table 1: Performance Evaluation Results of Predictive Models.

Model	Accuracy	Precision	Recall	F1-score
CNN	0.94	0.95	0.93	0.94
ResNet-50	0. 95	0.94	0.95	0.94

6. Conclusion

Malaria, which is an endemic disease in most nations around the world, is also one of the most lethal diseases to children in Africa, particularly Nigeria, where twenty-nine countries account for 95% of malaria cases globally, with Nigeria accounting for 27%. Malaria prevention and treatment are also major difficulties in most African countries, and the disease is frequently diagnosed by health workers, particularly microbiologists, using microscopic blood smear samples. As a result, it has put a significant strain on the few medical facilities and health personnel available in most African nations, particularly Nigeria, the Democratic Republic of the Congo, Uganda, Mozambique, and Niger.

Deep learning is making significant advances and improvements in solving complex and difficult problems that have resisted the best efforts of the artificial intelligence community for many years, and it has been used in many domains such as medical, business, marketing, defense, labor, and production, among others, to solve complex problems and provide optimal results. As a result, utilizing deep learning, the convolutional neural network and ResNet50 algorithms were used to construct predictive models for malaria using cell image datasets in this study. The public dataset for malaria cell imagery was used, and it was divided into 80 percent training and 20% testing sets. The random rotating image augmentation technique was utilized to maintain and optimize the models' performance. The CNN Based Predictive Model's training and validation accuracy and loss were practically in the same trend towards the end, indicating that there was no overfitting to the training dataset. Furthermore, the ResNet-50 Based Predictive Model's training and validation accuracy are practically identical towards the end, and there was no overfitting to the training dataset.

However, there was overfitting for the ResNet-50 Based Predictive Model's training and validation loss. The performance evaluation of the predictive models performed in the study shows that ResNet-50 predictive models outperformed CNN predictive models in classifying and predicting infected and uninfected malaria cells with 95% accuracy and correctly predicting negative cases of malaria with 95% accuracy. However, in terms of correctly predicting positive cases of malaria, the CNN predictive model surpassed the ResNet-50 predictive model with 95% accuracy. The models can be expanded to various fields like as engineering, business, and marketing.

Reference

[1] A. B. Abdul Qayyum, T. Islam and M. A. Haque, "Malaria Diagnosis with Dilated Convolutional Neural Network Based Image Analysis," 2019 IEEE International Conference on Biomedical Engineering, Computer and Information Technology for Health (BECITHCON), 2019, pp. 68-72.

[2] A. Vijayalakshmi, R. Kanna, “Deep learning approach to detect malaria from microscopic images”, Multimedia Tools and Applications, 2019, https://doi.org/10.1007/s11042-019-7162-y

[3] A. A. Haruna, L. J. Muhammad, B. Z. Yahaya et al. “An Improved C4.5 Data Mining Driven Algorithm for the Diagnosis of Coronary Artery Disease”. International Conference on Digitization (ICD), Sharjah, United Arab Emirates, 2019, pp. 48-52

[4] C. Dallet, S. Kareem and I. Kale, "Real time blood image processing application for malaria diagnosis using mobile phones," 2014 IEEE International Symposium on Circuits and Systems (ISCAS), 2014, pp. 2405-2408

[5] C. Tan, F. Sun, T. Kong (2018) A survey on deep transfer learning, in: International conference on artificial neural networks, Springer, 2018, pp. 270–279 .

[6] D. Ravì *et al.* Deep Learning for Health Informatics*," in IEEE Journal of Biomedical and Health Informatics,* 2017, vol. 21, no. 1, pp. 4-21.

[7] F. S. Ishaq, L. J. Muhammad, B. Z. Yahaya, Y. Atomsa, “Data Mining Driven Models for Diagnosis of Diabetes Mellitus: A Survey”, Indian Journal of Science and Technology, 2018, vol. 11, no. 4

[8] F. Yang *et al.*, "Deep Learning for Smartphone-Based Malaria Parasite Detection in Thick Blood Smears," in *IEEE Journal of Biomedical and Health Informatics*, 2020, vol. 24, no. 5, pp. 1427-1438.

[9] G. Karthik, S. Muttan, M. P. Saravanan, R. Seetharaman and V. Vignesh, "Automated Malaria Diagnosis Using Microscopic Images," 2019 Third International Conference on Inventive Systems and Control (ICISC), 2019, pp. 514-517

[10] G. E. Hinton, S. Osindero S, Y. W. Teh (2006) A fast learning algorithm for deep belief nets. Neural Comput. ,18, p 1527–1554.

[11] H. Choi, S. Ryu and H. Kim, "Short-Term Load Forecasting based on ResNet and LSTM," 2018 IEEE International Conference on Communications, Control, and Computing Technologies for Smart Grids (SmartGridComm), 2018, pp. 1-6

[12] H. A. Mohammed and I. A. M. Abdelrahman, "Detection and classification of Malaria in thin blood slide images," 2017 International Conference on Communication, Control, Computing and Electronics Engineering (ICCCCEE), 2017, pp. 1-5.

[13] L. Deng, D Yu , “Deep Learning: Methods and Applications”. Foundations and Trends in Signal Processing, 2013, Vol. 7, Nos. 3–4, pp.197–387

[14] L. J. Muhammad, E. J. Garba, N. D. Oye, G. M. Wajiga, A. B. Garko, “Fuzzy rule-driven data mining framework for knowledge acquisition for expert system”. In: Translational Bioinformatics in Healthcare and Medicine. Elsevier, Academic Press, 2021, pp. 201–214.

[15] L. J. Muhammad, A. H. Ahmad, A. M. Ibrahim, A. Mansir, B. Bature, M. A. Jamila. “Performance Evaluation of Classification Data Mining Algorithms On Coronary Artery Disease Dataset”, IEEE 9th International Conference on Computer and Knowledge Engineering (ICCKE 2019), Ferdowsi University of Mashhad, October, 2019.

[16] S. Hussain, L. J. Muhammad, F. S. Ishaq, A. Yakubu, I. A. Mohammed. Performance Evaluation of Various Data Mining Algorithms on Road Traffic Accident Dataset. In: Satapathy S., Joshi A. (eds) Information and Communication Technology for Intelligent Systems. Smart Innovation, Systems and Technologies, 2019.

[17] L. J. Muhammad, E. A. Algehyne, S. S. Usman “Predictive Supervised Machine Learning Models for Diabetes Mellitus”. Springer Nature Computer Science, 2020.

[18] L. J. Muhammad, E. A. “Algehyne, Fuzzy based expert system for diagnosis of coronary artery disease in Nigeria” *Health Technol.* 2021, 11**,** pp. 319–329

[19] L. J. Muhammad, A. Garba A, G. Abba. “Security Challenges for Building Knowledge Based Economy in Nigeria”, International Journal of Security and Its Applications, 2015, pp. 13 -21.

[20] L. J. Muhammad, M. Besiru Jibrin, B. Z. Yahaya, I. A. Mohammed Besiru Jibrin, A. Ahmad and J. M. Amshi, "An Improved C4.5 Algorithm using Principle of Equivalent of Infinitesimal and Arithmetic Mean Best Selection Attribute for Large Dataset," 2020 10th International Conference on Computer and Knowledge Engineering (ICCKE), Mashhad, Iran, 2020, pp. 006-010

[21] M. Poostchi, K. Silamut, R. Maude, S. Jaeger, G. Thoma, “Image analysis and machine learning for detecting malaria”, *Translational Research,* 2018

[22] M. Elter, E. Haßlmeyer and T. Zerfaß, "Detection of malaria parasites in thick blood films," 2011 Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2011, pp. 5140-5144,

[23] M. Z. Alom,T. M. Taha, C Yakopcic at al. “A State-of-the-Art Survey on Deep Learning Theory and Architectures”. *Electronics*, 2019, *8*, 292.

[24] M. Islam, S. Mahmud, L. J. Muhammad . et al. Wearable Technology to Assist the Patients Infected with Novel Coronavirus (COVID-19). SN COMPUT. SCI. 2020, 1, 320.

[25] R. Yamashita, M. Nishio, R. K.G Do. *et al.* “Convolutional neural networks: an overview and application in radiology”. *Insights Imaging*, 2018, *9, pp***.** 611–629

[26] S. Rajaraman, S. Jaeger, S. K. Antani. “Performance evaluation of deep neural ensembles toward malaria parasite detection in thin-blood smear images", PeerJ, 2019, pp. 7:e6977

[27] S. F. Toha and U. K. Ngah, "Computer Aided Medical Diagnosis for the Identification of Malaria Parasites," 2007 International Conference on Signal Processing, Communications and Networking, 2007, pp. 521-522

[28] S. S. Prakash, B. C. Kovoor and K. Visakha, "Convolutional Neural Network Based Malaria Parasite Infection Detection Using Thin Microscopic Blood Smear Samples," 2020 Second International Conference on Inventive Research in Computing Applications (ICIRCA), 2020, pp. 308-313.

[29] S. K. Reni, I. Kale and R. Morling, "Analysis of thin blood images for automated malaria diagnosis," 2015 E-Health and Bioengineering Conference (EHB), 2015, pp. 1-4.

[30] S. Nayak, S. Kumar and M. Jangid, "Malaria Detection Using Multiple Deep Learning Approaches," 2019 2nd International Conference on Intelligent Communication and Computational Techniques (ICCT), 2019, pp. 292-297.

[31] World Health Organization. “Years of Global Progress and Challenges, World malaria report 2020”, (WHO), 2020, pp. 1-123.

[32] Z. Liang et al., "CNN-based image analysis for malaria diagnosis," 2016 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2016, pp. 493-496, doi: 10.1109/BIBM.2016.7822567.

[33] Y. LeCun, L. Bottou, Y. Bengio et all. “Gradient-based learning applied to document recognition”. *Proc. IEEE*, 1998, *86*, pp. 2278–2324.

[34] O. A. Sarumi, O. Aouedi, L. J. Muhammad. Potential of Deep Learning Algorithms in Mitigating the Spread of COVID-19. In: J. Nayak, B. Naik, A. Abraham (eds) Understanding COVID-19: The Role of Computational Intelligence. Studies in Computational Intelligence,. 2021, vol 963.

[35] Alsayed, O.; Rahim, M.S.M.; Bidewi, I.A. Selection of the Right Undergraduate Major by Students Using Supervised Learning Techniques. *Appl. Sci.* 2021, *11*, 10639. https://doi.org/10.3390/app112210639.

[36] L. J. Muhammad et al., "Deep Learning Models for Classification and Localization of COVID-19 Abnormalities on Chest Radiographs," 2021 4th International Conference on Computing & Information Sciences (ICCIS), 2021, pp. 1-6, doi: 10.1109/ICCIS54243.2021.9676401.

[37] Algehyne, E.A.; Jibril, M.L.;Algehainy, N.A.; Alamri, O.A.;Alzahrani, A.K. Fuzzy Neural Network Expert System with an Improved Gini Index Random Forest-Based Feature Importance Measure Algorithm for Early Diagnosis of Breast Cancer in Saudi Arabia. Big Data Cogn. Comput. 2022, 6, 13. https://doi.org/10.3390/bdcc6010013

[38] Muhammad, L.J.; Jibrin, M.B.; Yahaya, B.Z.; Jibrin, I.A.M.B.; Ahmad, A.; Amshi, J.M. An Improved C4.5 Algorithm using Principle of Equivalent of Infinitesimal and Arithmetic Mean Best Selection Attribute for Large Dataset. In Proceedings of the 2020 10th International Conference on Computer and Knowledge Engineering (ICCKE), Mashhad, Iran, 29 -30 Oct.; pp. 006–010.

[39] Muhammad, L.J. Deep Learning Models for Predicting COVID-19 Using Chest X-Ray Images. In *Trends and Advancements of Image Processing and Its Applications*; Johri, P., Diván, M.J., Khanam, R., Marciszack, M., Will, A., Eds.; EAI/Springer Innovations in Communication and Computing; Springer: Cham, Switzerland, 2022; https://doi.org/10.1007/978-3-030-75945-2_6.