



Paludism Diagnosis Using Deep Learning

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Abstract. Medical experts rely on various methods to detect diseases, aiming to identify the presence of parasites in blood samples. This research focuses on crafting a sophisticated deep-learning model tailored for paludism detection, leveraging microscopic images of blood smears. By surpassing the constraints of conventional diagnostic methods, our model seeks to enhance the precision of malaria detection. Our used approach is convolutional neural networks (CNNs). Evaluation is conducted on a publicly accessible dataset of malaria-infected blood smears, affirming the effectiveness of our approach over existing techniques with achieving results in accuracy, precision, F1-score, specificity, recall, sensitivity, and AUC, with values of 0.9975, 0.9893, 0.9975, 0.9892, 0.9994, 0.98, and 0.9985, respectively.

Keywords: Malaria · Paludism · Convolutional Neural Network · Artificial Intelligence · Deep Learning · Machine Learning · Image Processing

1 Introduction

Recent advancements in information technology and image processing have brought about a monumental transformation in the landscape of decision-making and diagnosis within the medical sector. These breakthroughs have ushered in a new era of innovation and efficiency, reshaping the way healthcare professionals operate and patients receive care. Technologies such as Medical IoT, Artificial Intelligence (AI), and Big Data have seamlessly integrated into the fabric of healthcare, marking the dawn of Health 4.0. This paradigm shift signifies a departure from traditional paper-based medical systems towards the adoption of intelligent electronic health records, laying the groundwork for a more interconnected and data-driven healthcare ecosystem.

The integration of AI into the realm of healthcare diagnosis represents a transformative milestone, where artificial intelligence algorithms emerge as indispensable allies to healthcare providers in navigating the complexities of disease detection and patient management. Leveraging the power of advanced machine learning and deep learning methodologies, these AI systems meticulously analyze vast and diverse datasets sourced from a myriad of channels. From examining

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intricate medical imagery such as X-rays, MRIs, and CT scans to delving into comprehensive patient electronic health records (EHRs) and genetic profiles, AI-driven diagnostics offer unparalleled insights and predictive capabilities. By facilitating early disease detection, refining diagnostic precision, and tailoring personalized treatment regimens, AI augments the efficacy and efficiency of clinical decision-making processes, ultimately charting a new course for the future of patient care and medical practice. AI can also recommend appropriate treatment plans like Pneumonia Detection in Pediatrics [15], Paediatric Bone Age Assessment from Hand X-ray Using [22], Diabetic Retinopathy Detection [6], Vital Sign Predictions Using Long-Short-Term Memory Networks [5], and the Detection of Fractures in Cervical Spine [16]. This technology has the potential to improve patient outcomes, reduce diagnostic errors, and enhance the efficiency of healthcare delivery.

In this research, we aim to realize a brand new Artificial Intelligence model brought several results from different DL models developed for malaria detection and compared their architectures, used methodologies and algorithms, and results to find a good starting point. We then further improved on the approach by using different loss functions and changing the hyper-parameters on them to see their effect on the results until we finally found the optimal model, while using a hybrid dataset created from images found on a public dataset and images collected from the south of Algeria by the help of biologist specialists. Finally, we showcased the innovation of this research by displaying the most important comparisons and results that we achieved, improving on existent approaches by exceeding their results and offering a work that is new on the regional level, while using data gathered from this region.

2 Background

the remaining subsections provides a definition about the paludism pathology, how it infect people and change the structure of blood cell, after that how can we diagnose this pathology. Then talking about the role of Artificial Intelligence(AI), Machine Learning(ML), and Deep Learning (DL) in medical diagnostics.

2.1 Paludism

Malaria, also known as Paludism, is a life-threatening mosquito-borne disease caused by parasites of the Plasmodium genus. It is transmitted to humans through the bite of infected female Anopheles mosquitoes (see Figure 1) [8]. Malaria remains a significant public health challenge, particularly in tropical and subtropical regions, affecting millions of people worldwide each year. Symptoms typically include fever, chills, and flu-like illness, which can progress to severe complications if left untreated. Effective prevention measures include the usage of insecticide-treated bed nets, indoor residual spraying, and antimalarial medications. Despite ongoing efforts to control and eliminate the disease, malaria

continues to pose a considerable burden on global health systems and economies. Figure. 1 shows the malaria infection by female mosquitoes [4] [10].

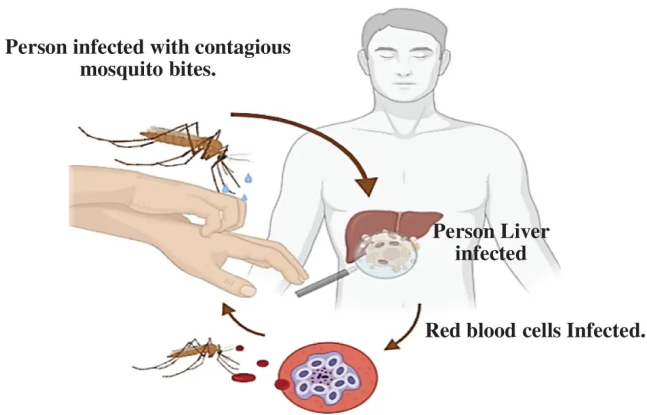


Fig. 1. The transmission of malaria by female mosquitoes [8].

2.2 Artificial Intelligence

Artificial Intelligence (AI) is a branch of computer science [20] that deals with the creation of intelligent machines that can perform tasks that typically require human intelligence. In the medical field, AI is utilized to analyze complex medical data, assist in diagnosis, personalized treatment plans, and improve patient outcomes. AI algorithms can process vast amounts of medical data quickly and accurately, aiding healthcare professionals in making informed decisions. From medical imaging interpretation to drug discovery and patient monitoring, AI has the potential to revolutionize healthcare by enhancing the efficiency, accuracy, and accessibility of medical services.

Machine Learning (ML) Artificial Intelligence (AI) encompasses a range of techniques and methodologies, with machine learning being a prominent subset. Machine Learning involves training algorithms to recognize patterns in data and make predictions or decisions without being explicitly programmed for each task [18]. Through exposure to large datasets, these algorithms learn to generalize from examples, improving their performance over time. It's akin to teaching a computer to learn from experience, enabling it to adapt and evolve in handling new situations. Machine learning powers many AI applications, from recommendation systems and natural language processing to image recognition and medical diagnostics.

Deep Learning (DL) Deep Learning is a subset of machine learning that uses neural networks with many layers (hence "deep") to learn from data [21].

Unlike traditional machine learning, which often requires manual feature extraction, deep learning algorithms can automatically discover intricate patterns and representations within the data. It's like teaching a machine to learn abstract concepts by building increasingly complex layers of understanding. So, while all deep learning is machine learning, not all machine learning is deep learning. Its ability to extract intricate patterns from large datasets has led to breakthroughs in Pneumonia Detection in Pediatrics [15], Paediatric Bone Age Assessment from Hand X-ray Using [22], Diabetic Retinopathy Detection [6], Vital Sign Predictions Using Long-Short-Term Memory Networks [5], and the Detection of Fractures in Cervical Spine [16].

3 Related Works

Prior research in the field of image detection using deep learning models provides valuable insights into the methodologies, challenges, and achievements in this area. Various studies have explored different approaches to malaria detection, leveraging diverse datasets, model architectures, and evaluation metrics as illustrated in Table ?? . This table shows the different and the most relevant works related to malaria detection using deep learning. R. Liu Et al. proposed An AI-based object detection system for malaria diagnosis from smartphone thin-blood-smear images using a classifier based on convolutional neural networks (CNN) to diagnose conditions using images of blood smears, effectively minimizing errors caused by false positive cells. The findings indicate that AIDMAN effectively manages interference, achieving a diagnostic accuracy rate of 98.44% [10]. T. Jameela Et al. collected images of infected and non-infected erythrocytes, then fed them into CNN models such as ResNet50, ResNet34, VGG-16, and VGG-19, all trained on the same dataset. Transfer learning and fine-tuning techniques were applied, and the results were compared. The VGG-19 model demonstrated the best overall performance among the evaluated parameters and dataset, and they got 0.97, 1.9341, 0.9641, 0.9796 of accuracy, F1-Score, Specificity, and Sensitivity respectively [9]. Then, the good study of E. Hassan Et al. The MCNN model proposed in this study utilizes transfer learning with three different pre-trained models to classify malaria cell images. The study introduces an effective model for feature extraction and classification from images. Results are compared across various loss functions, including Hinge, squared Hinge, binary cross-entropy, and categorical cross-entropy, to assess the overall performance of the model. Fine-tuning of weights and dataset augmentation techniques are employed to address overfitting issues. Performance evaluation of the proposed method is conducted using GPU for malaria detection. The proposed model achieves scores of 0.9929, 0.9848, 0.9859, 0.9924, 0.0152, 0.0141, 0.0071, 0.9890, 0.9894, and 0.9780 in terms of specificity, sensitivity, precision, accuracy, F1-score, and Matthews Correlation Coefficient (MCC), respectively [8]. Also, Maqsood et al. introduce a tailored CNN model that surpasses all examined deep learning models. Their approach utilizes bilateral filtering and image augmentation techniques to enhance the visibility of red blood cell fea-

tures before model training. By employing image augmentation techniques, their customized CNN model achieves generalization and mitigates overfitting. Experimental assessments are conducted on the widely-used NIH Malaria Dataset, demonstrating that their proposed algorithm achieves a 96.82% accuracy rate in detecting malaria from microscopic blood smears [11]. Nakasi Et al. assess and compare the performance of three pre-trained deep learning architectures, namely faster R-CNN, SSD, and RetinaNet, on a dataset of thick blood smear images using the Tensorflow object detection API. Employing data augmentation techniques to enhance the performance of the meta architectures, they achieve a peak accuracy of 93.03% with Faster R-CNN, which yields the best results among the evaluated models[13]. Puntonet Et al. [2] introduced traditional cell segmentation techniques relying on object detection algorithms. Meanwhile, Sarkar et al. [17] proposed a shallow CNN architecture designed for malaria diagnosis using thin blood smear RBC slide images. Despite achieving comparable classification accuracy to VGG-16 and ResNet-50 models, their approach significantly reduces computational runtime. Mehanian Et al. propose a Cnn model for Malaria Diagnosis and they got 95% of sensitivity [12]. Zamora Et al. work on Unsupervised online clustering and detection algorithms using crowdsourced data for malaria diagnosis [3]. Rajaraman Et al. used Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images [14]. and finally, Sedik El al. propose a CNN model for Efficient Data-Augmented Detection of COVID-19 Infections [19]. However, our proposed model stands on top, surpassing all preceding works in its unparalleled efficiency and exceptional performance metrics. Demonstrating remarkable prowess across various metrics including accuracy, precision, F1-score, specificity, recall, sensitivity, and AUC, our model shines with the values of 0.9975, 0.9893, 0.9975, 0.9892, 0.9994, 0.98, and 0.9985, respectively. These stellar results not only underscore the superiority of our approach but also promise a new era of advancement and excellence in the field. Such precision promises transformative impacts, offering confidence in the reliability and effectiveness of our model for its intended purposes.

| Author | Methodology | Accuracy | Precision | F1-Score | Specificity | Sensitivity | AUC | Year |
|------------|-------------|----------|-----------|----------|-------------|-------------|--------|------|
| R. liu | CNN | 0.9844 | N/A | N/A | N/A | N/A | N/A | 2023 |
| T. jameela | CNN | 0.9720 | N/A | 1.9399 | 0.9641 | 0.9796 | N/A | 2022 |
| E. Hassan | VGG19 | 0.9890 | 0.9859 | 0.9894 | 0.9929 | 0.9848 | N/A | 2022 |
| Maqsood | CNN | 0.9682 | N/A | N/A | 0.9778 | 0.9633 | N/A | 2021 |
| Nakasi | Faster-RCNN | 93.03% | N/A | N/A | N/A | N/A | N/A | 2020 |
| Sarkar | VGG19 | 96.15% | N/A | N/A | 97.53% | 94.82% | N/A | 2020 |
| Sedik | CNN | 97.99% | N/A | N/A | N/A | N/A | 2020 | |
| Cabrera | SVM | N/A | N/A | N/A | N/A | 94% | N/A | 2019 |
| Rajaraman | CNN | 98.60% | N/A | N/A | 99.2% | 98.10% | 99.90% | 2018 |
| Mehanian | CNN | N/A | N/A | N/A | N/A | 95% | 90% | 2017 |
| Puntonet | SVM | 86.11% | N/A | N/A | N/A | N/A | N/A | 2015 |

Table 1. Related works

4 Proposed System

The paludism detection proposed system visualized in Figure. 2 illustrates the sequential steps of our proposed system. Each of the included stage, in this architecture, will be more detailed and explained in the following paragraph in this section.

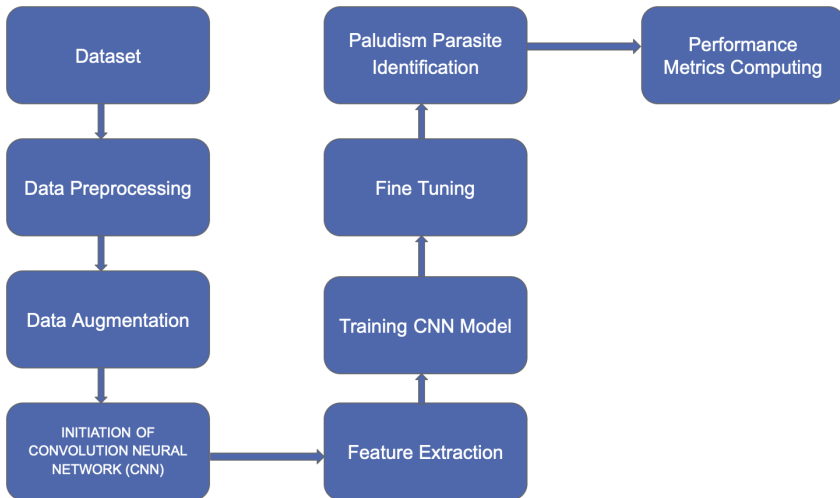


Fig. 2. Proposed System for Malaria Diagnosis

4.1 Dataset Description

In our study on malaria detection using a CNN model, our dataset is sourced from two distinct locations. The first part comprises 27,558 images obtained from online repositories [7], while the second part consists of 442 images collected from the facilities of the National Institute For Higher Paramedical Training Blida with the goal of addressing these limitations and eventually applying the model to local populations. These images are categorized into two classes: **uninfected** and **parasitized**. Figure. 3 shows an example of two images (thus, two classes) obtained from the Higher Paramedical Training Center, hence belonging to our local data set.

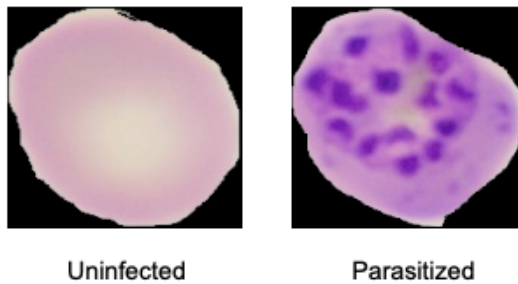


Fig. 3. Example of data set of classes

To summarize, our dataset contains an equal distribution of 14000 images for each class, ensuring a balanced representation of both uninfected and parasitized samples. This balanced class distribution is crucial for training our CNN model effectively and minimizing bias in our results.

4.2 Image Data Preprocessing

In preparing the dataset for training our Convolutional Neural Network (CNN) model for Paludism Diagnosis, we implemented several data preprocessing and augmentation techniques to enhance the quality and diversity of our data. Initially, we performed standard preprocessing steps, including resizing all images to a consistent size of 100x100 pixels and normalizing pixel values to a standardized range [0, 1]. Additionally, we carefully inspected the dataset for any corrupted or low-quality images and removed them to ensure data integrity. To address the class imbalance and increase the diversity of our training data, we employed data augmentation techniques such as rotation, flipping, zooming, and shifting. By randomly applying these transformations to our images, we generated new samples that simulate variations in image orientation, scale, and position. This

augmentation process not only increased the size of our dataset but also introduced robustness to our CNN model by exposing it to a wider range of image variations.

Furthermore, given the sensitive nature of medical image data, we paid special attention to maintaining the integrity and authenticity of our dataset throughout the preprocessing and augmentation process. We ensured that all data manipulations were performed transparently and ethically, with careful consideration of patient privacy and consent.

Overall, the combination of preprocessing and augmentation techniques employed in our dataset preparation phase played a crucial role in improving the performance and generalization ability of our CNN model for malaria detection.

4.3 Deep CNN Model

Our proposed convolutional neural network (CNN) architecture for malaria detection is designed to effectively capture and learn discriminative features from microscopic images of blood smears. The architecture consists of four Conv2D layers, each followed by a rectified linear unit (ReLU) activation function to introduce non-linearity. The number of filters in these convolutional layers is gradually increased from 50 to 90, then decreased to 10, and finally to 5, allowing the model to learn hierarchical representations of the input images. Following the convolutional layers, three dense layers are incorporated with ReLU activation functions, facilitating the aggregation and refinement of learned features. The final dense layer employs a sigmoid activation function to produce binary predictions indicating the likelihood of each class (infected or uninfected).

This architecture is tailored to the specific characteristics of malaria-infected blood smear images, aiming to achieve high accuracy and robustness in detecting the presence of malaria parasites. Additionally, the simplicity of the architecture makes it computationally efficient and suitable for deployment in resource-constrained environments. To compare the performance of our basic CNN model, we experiment with different loss functions during model compilation. We consider standard loss functions such as binary cross-entropy and sparse categorical cross-entropy, as well as more specialized loss functions like binary focal loss. The binary focal loss function is particularly suitable for imbalanced datasets, as it assigns higher weights to hard-to-classify samples, thereby focusing the model's attention on informative examples. By evaluating the performance of our model architectures across multiple loss functions, we aim to gain insights into their respective strengths and weaknesses in the context of malaria detection. Through empirical analysis and comparative experiments, we seek to identify the most effective combination of model architecture and loss function for accurate and reliable detection of malaria parasites in microscopic images of blood smears. Figure. 4 shows the Proposed CNN Architecture

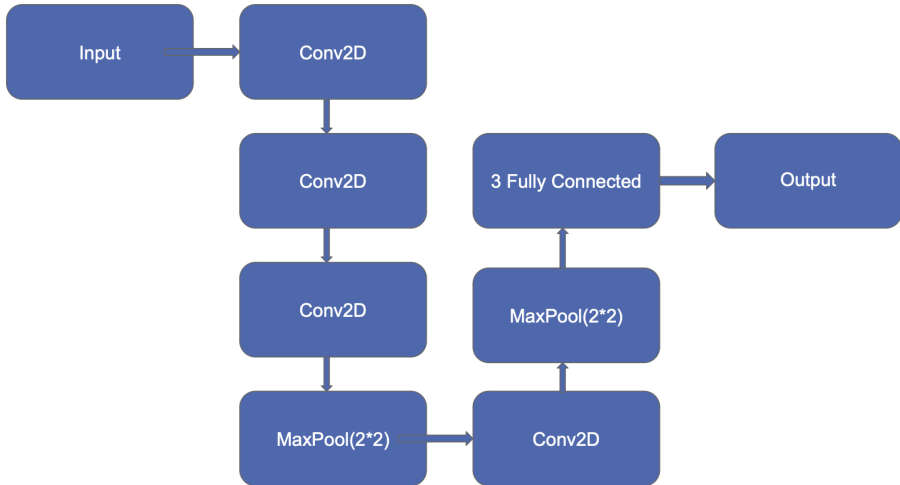


Fig. 4. Proposed CNN Architecture

4.4 Training and Experimentation

During the training phase, K-Fold cross-validation was utilized with $k=3$, following a methodology similar to that described in existing literature such as the research conducted by Nizar Ahmed Et al. on the classification of various subtypes of leukemia from microscopic blood cell images using Convolutional Neural Networks (CNN) [1]. This methodology enabled a systematic assessment of model performance while reducing the likelihood of overfitting. Throughout the experimental process, different hyperparameters were investigated, including batch size and number of epochs, and the optimizer in order to enhance model effectiveness. After multiple iterations, it was determined that a batch size of 16, 140 epochs and RMSProp optimizer produced the most favorable outcomes in terms of both accuracy and convergence. This outcome highlights the significance of hyperparameter optimization in achieving peak performance in tasks related to deep learning. By employing cross-validation techniques and refining hyperparameters, the objective was to establish the reliability and applicability of the models across various datasets and folds, thereby strengthening the credibility of the results and implications.

5 Results

– Binary Cross-Entropy Loss Function

This function records the number of errors and the accuracy of its estimations for every category. It accomplishes this by averaging the mistakes in the two

categories [8]. Equation 1 illustrates the formula of calculating binary cross entropy loss function. It is calculated as follows:

$$\text{loss} = - \frac{1}{\text{output size}} \sum_{i=1}^{\text{output size}} y_i \cdot \log \hat{y}_i + (1 - y_i) \cdot \log (1 - \hat{y}_i) \quad (1)$$

– **Categorical Cross entropy Loss Function**

The computation of the difference between two probability distributions is its main goal. This function is applied to a multi-class classification job that combines the Softmax activation function with categorical cross-entropy [8]. Equation 2 illustrates the formula of calculating category cross entropy loss function. It is calculated as follows:

$$\text{Loss} = - \sum_{i=1}^{\text{output size}} y_i \log \hat{y}_i \quad (2)$$

In the following charts, we present the results obtained from our various experiments comparing the performance of our CNN model with different loss functions and hyperparameters. These experiments were conducted to evaluate the effectiveness of different loss functions in optimizing the performance of our model for malaria detection. Through rigorous experimentation and analysis, we aim to identify the most suitable loss function for achieving accurate and reliable malaria detection using our CNN model. The results presented in these charts offer valuable insights into the impact of binary cross entropy loss function on the overall performance of our model. Figure 5 shows the obtained results in the training phase with Categorical Cross-entropy Loss Function. Figure 6 shows the obtained results in the training phase with Binary Cross-entropy Loss Function.

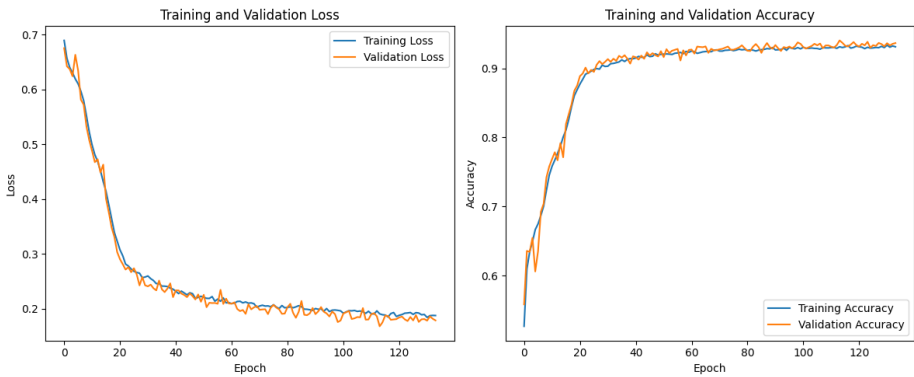


Fig. 5. Training Results with categorical cross entropy loss function

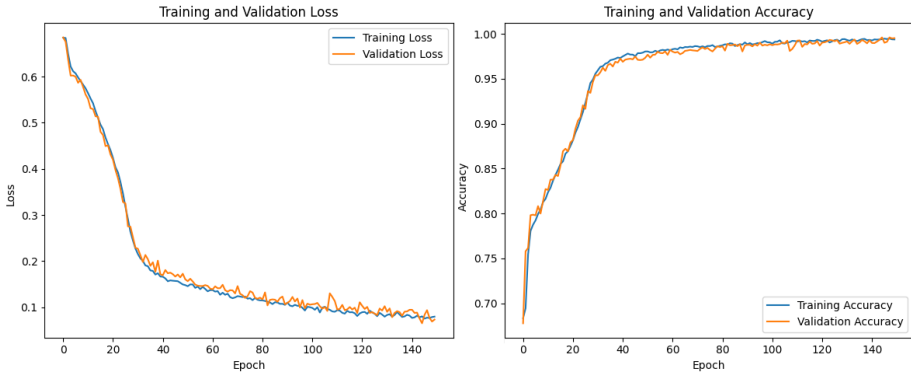


Fig. 6. Training Results with binary cross entropy loss function

Moreover, we evaluated the performance of our CNN model in predicting the presence of hard-to-detect malaria parasite cells in microscopic images of blood smears. The tables provide a comprehensive overview of key performance metrics, including accuracy, precision, specificity, F1-score recall, sensitivity, and AUC, obtained across different loss functions. Through meticulous analysis, we identified instances where our model successfully detected these challenging cells, resulting in true positive predictions. These accurate predictions demonstrate the robustness and efficacy of our model in identifying subtle and hard-to-detect malaria parasite cells, showcasing its potential for enhancing malaria diagnosis accuracy in real-world clinical settings. By highlighting these successful predictions, we underscore the practical utility and clinical relevance of our CNN model in improving malaria detection outcomes and ultimately advancing patient care. Table. 2 shows testing results with loss functions.

| Metric | Method | Results |
|-----------------------------|------------|--|
| Categorical Cross Entropy | CNN | Accuracy: 0.9372 Precision: 0.9358 F1-Score: 0.9394 Specificity: 0.9348 Recall: 0.9397 Sensitivity: 0.92 AUC: 0.91 |
| Binary Cross Entropy | CNN | Accuracy: 0.9975 Precision: 0.9893 F1-Score: 0.9975 Specificity: 0.9892 Recall: 1.000 Sensitivity: 0.98 AUC: 0.9985 |

Table 2. Testing Results across Loss Functions

Finally, this is a comparison between the best results obtained in our study with those of the best previous research over 2022-2024. Table. 3 shows a comparison of results between our work and related works

| CNN | Accuracy | Precision | F1-Score | Specificity | recall | sensitivity | AUC |
|-------------------------------|---------------|---------------|---------------|---------------|--------------|-------------|---------------|
| [10] | 0.9844 | N/A | N/A | N/A | N/A | N/A | N/A |
| [9] | 0.9720 | N/A | 1.9399 | 0.9641 | N/A | 0.9796 | N/A |
| [8] | 0.9890 | 0.9859 | 0.9894 | 0.9929 | N/A | 0.9848 | N/A |
| Our Proposed CNN Model | 0.9975 | 0.9893 | 0.9975 | 0.9892 | 1.000 | 0.98 | 0.9985 |

Table 3. Comparison between our results and best previous research over 2022-2024.

6 Conclusion

Developing a new model with high accuracy and gathering sufficient medical image data pose significant challenges. In this study, we have amassed a substantial dataset and proposed a Deep CNN model utilizing various techniques such as K-Fold cross-validation, adjusting epochs, implementing Early Stopping, and Model Checkpoint methods for malaria cell detection. We evaluated the model's performance using different loss functions (binary cross-entropy, categorical cross-entropy) and fine-tuned the obtained weights while augmenting the combined dataset to prevent overfitting. Our proposed model achieved outstanding results in accuracy, precision, F1-score, specificity, recall, sensitivity, and AUC, with values of 0.9975, 0.9893, 0.9975, 0.9892, 0.9994, 0.98, and 0.9985, respectively, using the binary cross-entropy loss function. Moving forward, our model holds promise for predicting parasitized and uninfected cells, offering valuable support to the E-health domain, and holds the potential for mitigating the impact of this disease by reducing mortality rates. This work opens several perspectives to be developed in our future researches, first we aim to offer an unprecedented work on the local level and keep improving on it with data collected locally, on another hand we will improve it for all the types of malaria and their multiple stages, and finally we are planning to make the model accessible for users (researchers as well as doctors) through the developed healthcare platform, that we are building in the TIASM project¹.

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