MALARIA CELL CLASSIFICATION USING CONVOLUTIONAL NEURAL NETWORK

PRESENTED BY

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CONTENTS

INTRODUCTION

- Malaria is a life threatening disease spread by Anopheles mosquitoes and caused by Plasmodium.

- A CNN is proposed for malaria cell classification.

WHAT IS A CONVOLUTIONAL NEURAL NETWORK?

A Convolutional Neural Network is a type of deep learning model particularly effective for image classification and feature extraction.


METHODOLOGY

CONVOLUTIONAL NEURAL NETWORK

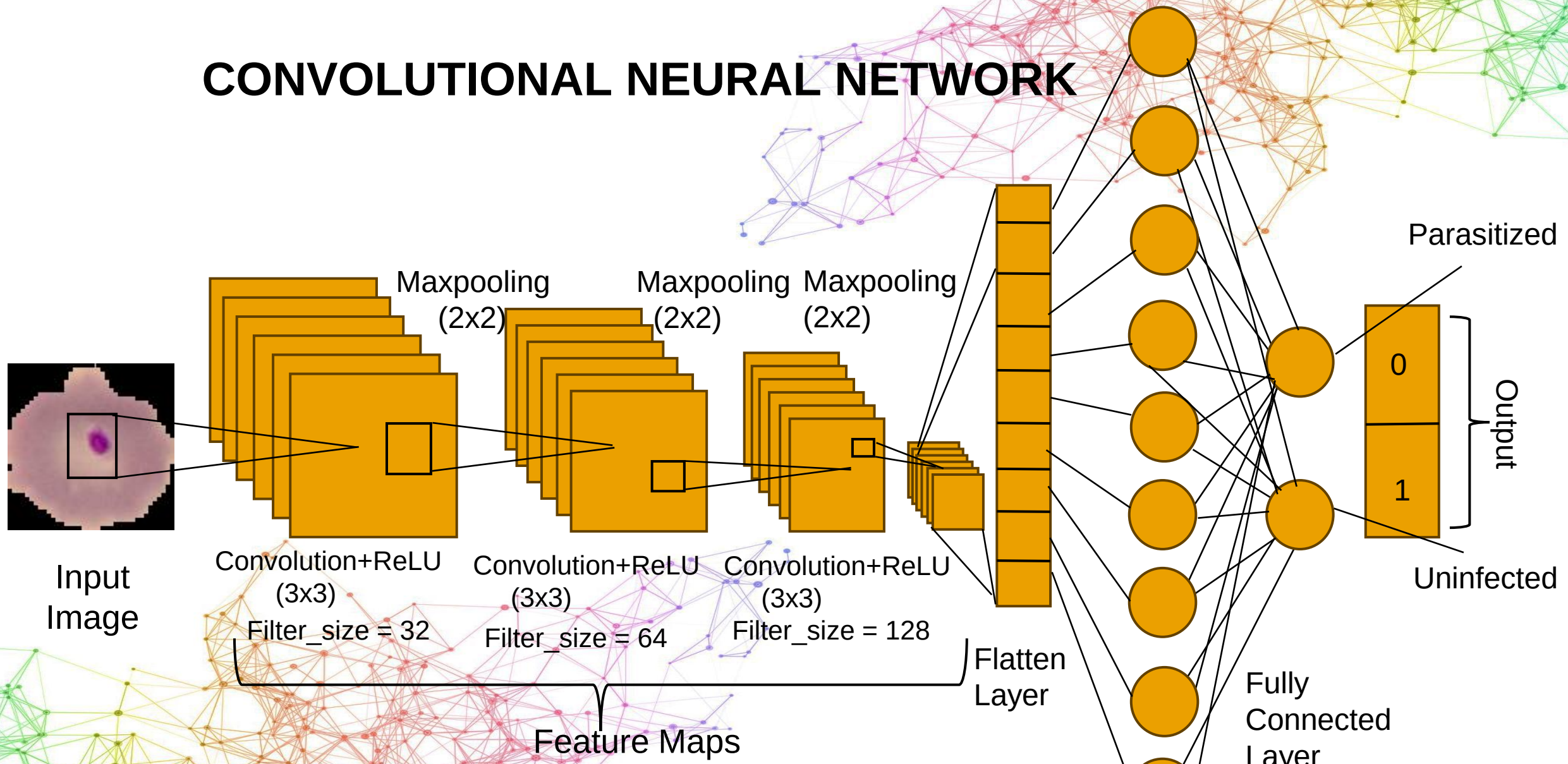


Fig.1. Model Architecture

The CNN architecture contains the following features:

- Three Convolutional layers with kernel dimension (3,3) and filter size 32, 64 and128 respectively.
- ReLU activation function is used to introduce non-linearity.
- Three maxpooling layers with pool size (2,2)
- Flatten layer after feature extraction
- Two dense fully connected layers
  - 128 fully connected neurons in hidden layer
  - 2 neurons in the output layer for the final classification outcome.
- The classification is finally calculated using softmax function.

MODEL BASIC BLOCKS

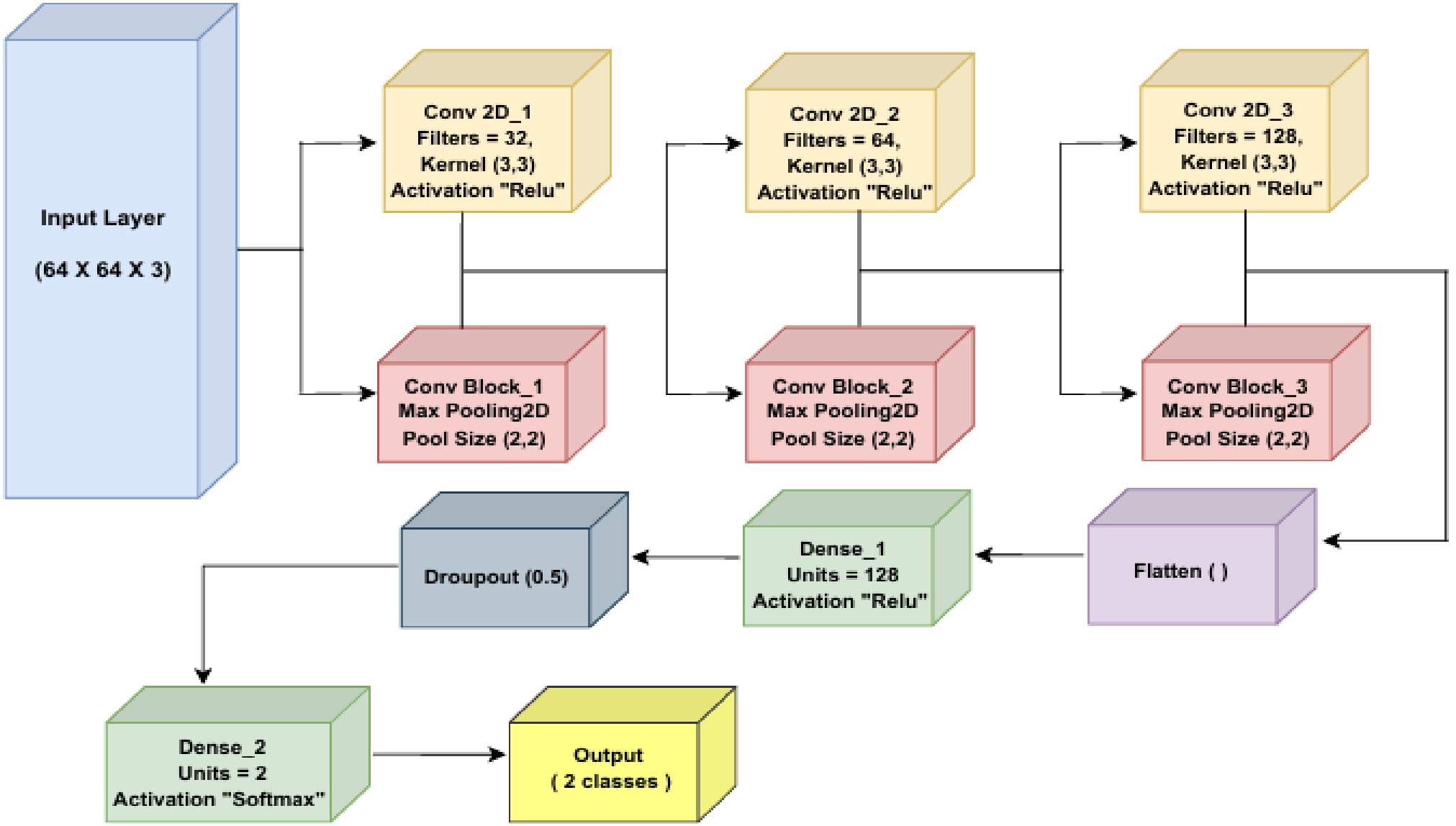


Fig.2. Model Basic Blocks

CNN ARCHITECTURE

CONVOLUTIONAL BLOCKS

- **Conv2D (The Feature Detector):** These layers use small filters to scan the image and detect features like edges, textures and patterns. We started with 32 filters, then 64 and finally 128, all employing a (3, 3) kernel size which got more complex with each layer. We used the ReLU activation function to introduce non-linearity.
- **MaxPooling2D (The Shrinker):** This layer reduces the size of the image data, keeping only the most important features. This makes the model faster and less prone to getting fixated on tiny details (overfitting).

CLASSIFICATION LAYER

- **Flatten:** The 3D feature maps were unwrapped into a single long list of numbers.
- **Dense Layer:** A standard neural network layer with 128 neurons processed this list. We added a Dropout layer (0.5), which randomly ignores half the neurons during training. This forces the remaining neurons to be more robust and is a powerful way to prevent overfitting.
- **Output Layer:** The final layer had 2 neurons (one for each class) with a Softmax activation function for class probability prediction.

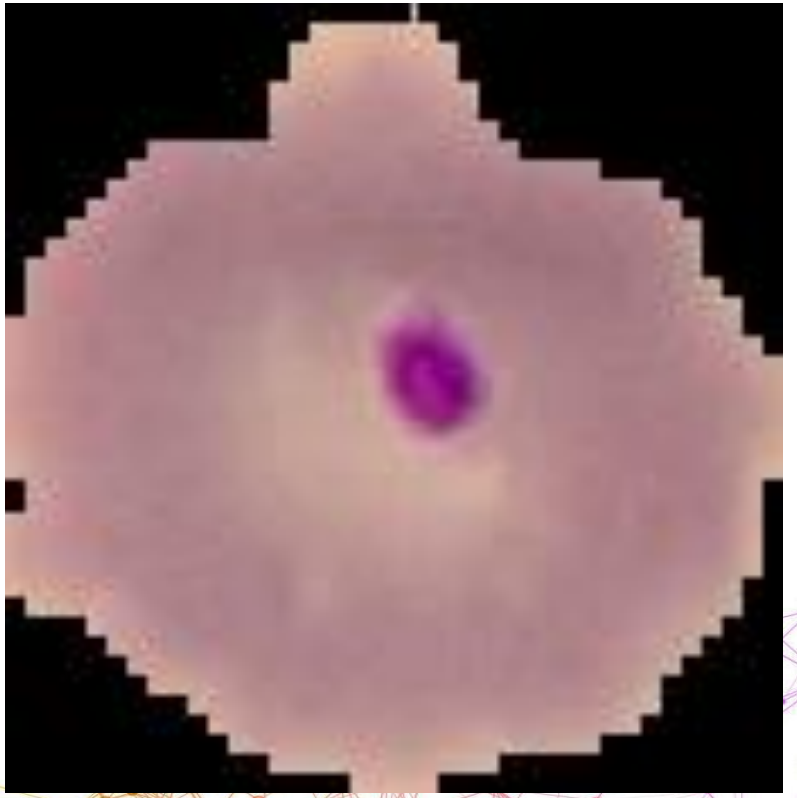

DATASET
COLLECTION

- The dataset consists of a large set of parasitized and uninfected cell images observed under microscope.

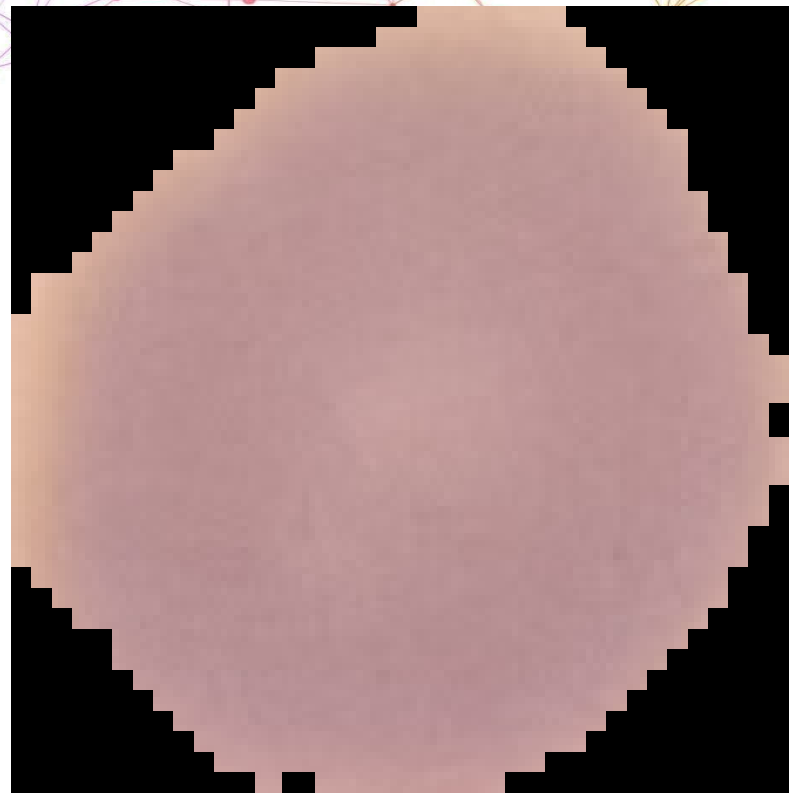
- The dataset has a total of 27,558 images.

- The dataset has been extracted from https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria

DATASET IMAGES



PARASITIZED CELL IMAGE



UNINFECTED CELL IMAGE

Fig.3. Cell Images


DATA PREPROCESSING

DATA TRANSFORMATION

The images are resized to 64 X 64 pixels for efficient deep learning analysis.

DATA LABELING

The parasitized cell images are assigned label '0' and uninfected cell images are assigned label '1'.

The images and their respective labels are stored in separate numpy arrays.

DATA PREPROCESSING

Normalization: Image pixels are represented by numbers, typically from 0 to 255. We divided all these numbers by 255.0 to scale them down to a small range between 0 and 1.

One-Hot Encoding: The labels were simple: 0 for Uninfected, 1 for Parasitized. These labels are converted into a "one-hot" format (e.g., 1 becomes [0, 1], 0 becomes [1, 0]).

Splitting the Data: The entire dataset is divided into two main parts: 70% for Training (the material the model learns from) and 30% for Testing (unseen material to check how well it learned).


MODEL TRAINING AND
VISUALIZATION

MODEL TRAINING

- The model is compiled using the Adam optimizer
- Then, the model is trained for 10 epochs using a batch_size of 32. (10 full passes through the training data).

```
Epoch 1/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 195s 371ms/step - accuracy: 0.8319 - loss: 0.3596 - val_accuracy: 0.9383 - val_loss: 0.1881
Epoch 2/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 203s 419ms/step - accuracy: 0.9512 - loss: 0.1560 - val_accuracy: 0.9552 - val_loss: 0.1417
Epoch 3/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 154s 320ms/step - accuracy: 0.9546 - loss: 0.1413 - val_accuracy: 0.9500 - val_loss: 0.1374
Epoch 4/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 249s 417ms/step - accuracy: 0.9574 - loss: 0.1287 - val_accuracy: 0.9585 - val_loss: 0.1288
Epoch 5/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 178s 366ms/step - accuracy: 0.9596 - loss: 0.1195 - val_accuracy: 0.9583 - val_loss: 0.1285
Epoch 6/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 175s 361ms/step - accuracy: 0.9600 - loss: 0.1135 - val_accuracy: 0.9590 - val_loss: 0.1278
Epoch 7/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 186s 386ms/step - accuracy: 0.9629 - loss: 0.1053 - val_accuracy: 0.9619 - val_loss: 0.1303
Epoch 8/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 234s 448ms/step - accuracy: 0.9650 - loss: 0.1004 - val_accuracy: 0.9611 - val_loss: 0.1356
Epoch 9/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 186s 384ms/step - accuracy: 0.9677 - loss: 0.0904 - val_accuracy: 0.9580 - val_loss: 0.1437
Epoch 10/10
483/483 ━━━━━━━━━━━━━━━━━━━━ 170s 351ms/step - accuracy: 0.9695 - loss: 0.0827 - val_accuracy: 0.9565 - val_loss: 0.1469
```

Fig.4. Epoch Visualization

VISUALIZATION

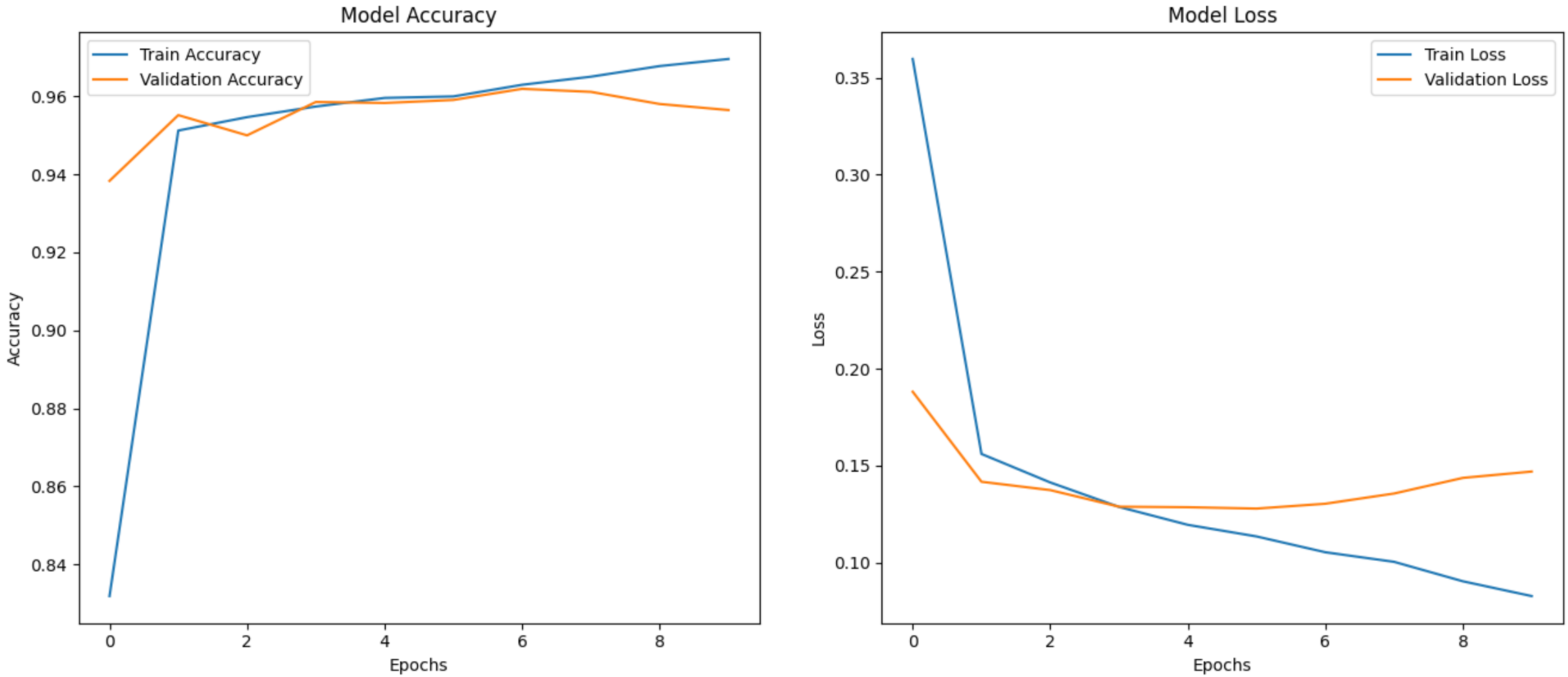


Fig.5. Training Accuracy and Loss Graph


MODEL TESTING

MODEL TESTING

Loading the model : The pre-trained CNN model (malaria_cnn_model.h5) is loaded using Keras. A quick check confirmed that the model was successfully loaded and ready for testing.

Preparing the data : The unseen datasets are normalized and encoded into one-hot encoding.

Testing and Visualization : The dataset is finally loaded into the model. The dataset is processed with 10 epochs and batch_size 32 in the model. To assess the model's performance on unseen datasets, the loss and accuracy graphs are plotted.

Assessing the Runtime: In this stage, the full evaluation process was timed using Python's time module.

OUTPUT PANEL VISUALIZATION

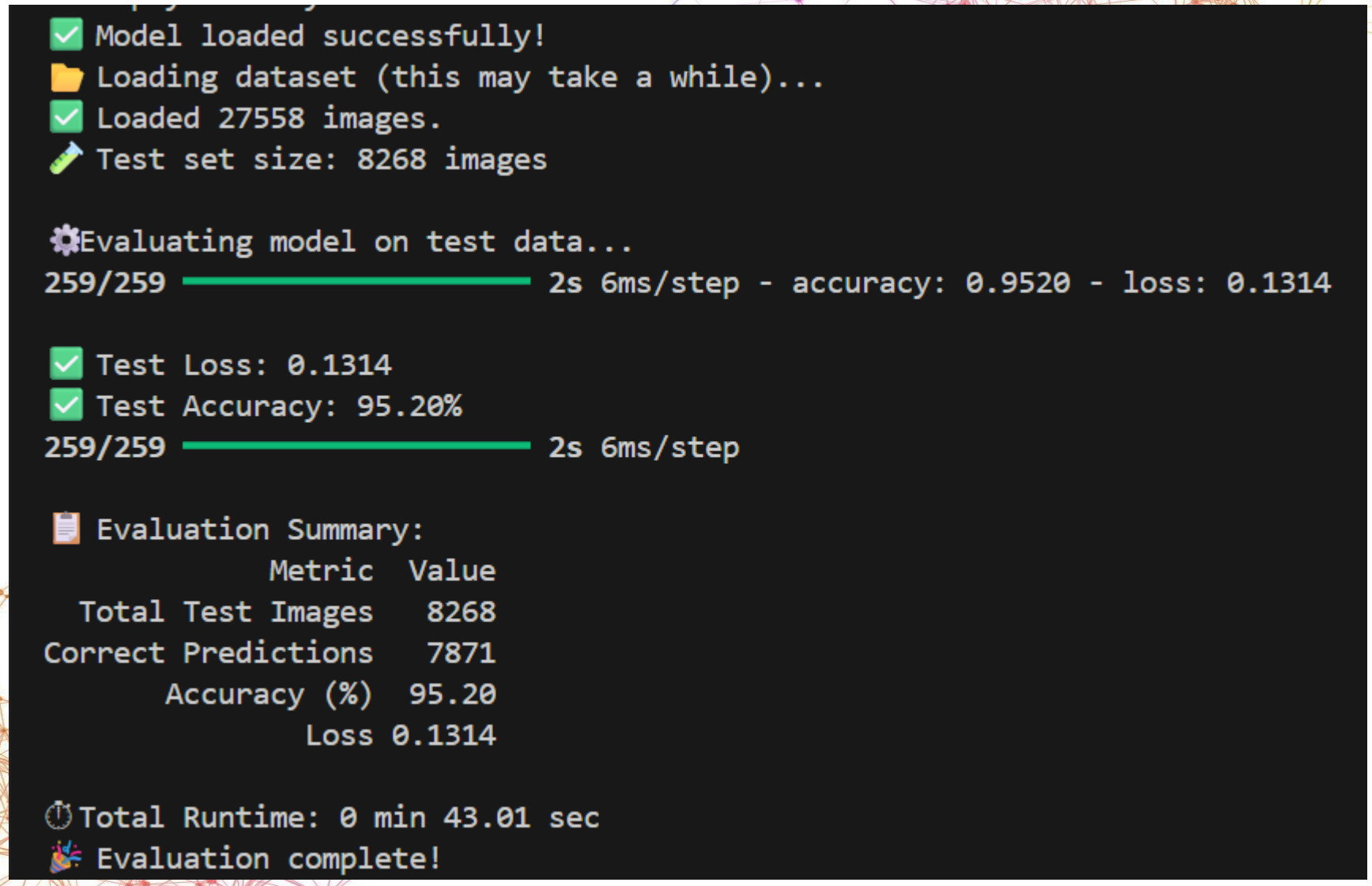


Fig.6. Output Panel

MODEL EVALUATION

- Model Evaluation assesses a model's overall performance, efficiency, and reliability.
- They provide standardized, quantitative measures to understand the model's performance.
- Through the Evaluation metrices, we can
  - ensure that the model meets the desired accuracy and robustness requirements.

CONFUSION MATRIX

The confusion matrix summarizes the model's performance by showing the number of correct and incorrect classifications for each category.

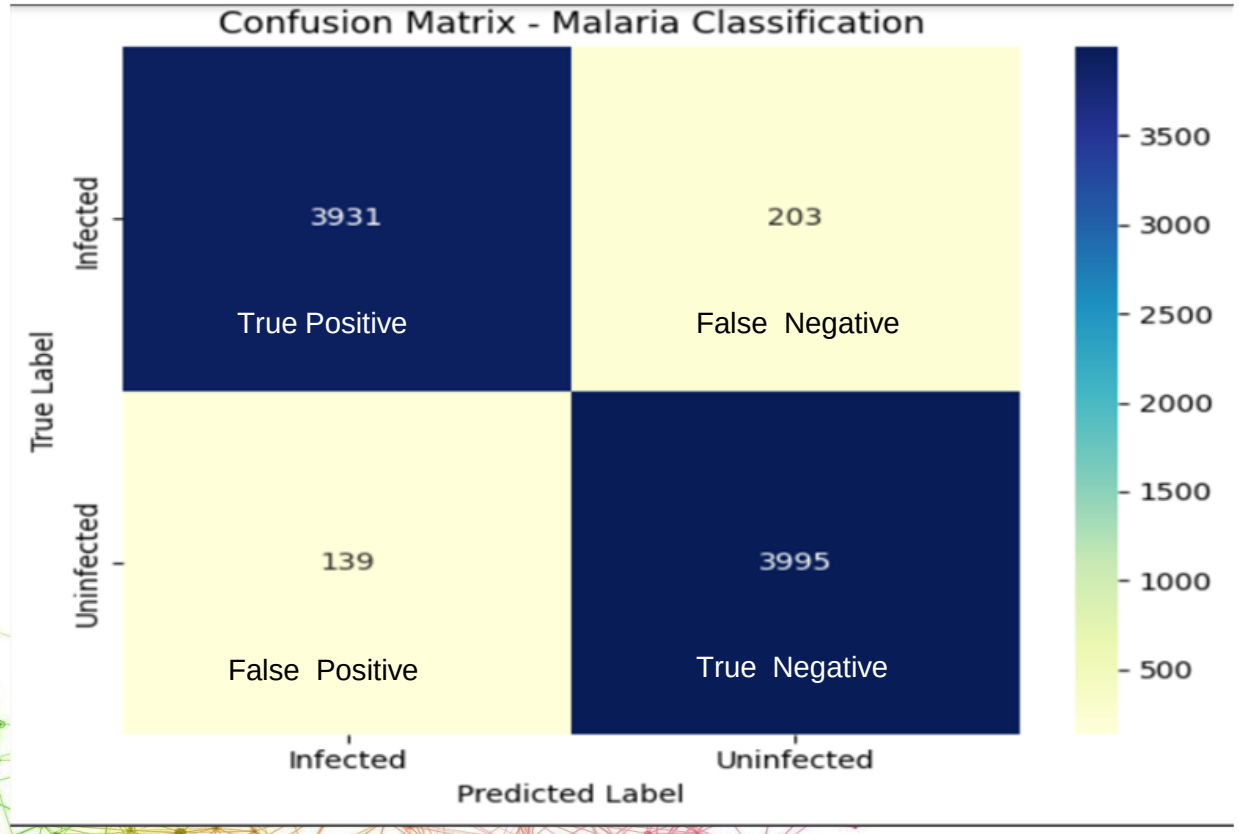


Fig.8. Confusion Matrix

- The model correctly identified 3931 infected and 3995 uninfected cells, with only minor misclassifications.
- This indicates strong classification ability and high predictive reliability.

FORMULAS

The important formulas to calculate the model's evaluation metrics are:

Note: True Positive (TP), True Negative (TN), False Positive (FP), False Negative (FN).

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

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

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

$$\text{F1 Score (F)} = \frac{2 \times P \times R}{P+R}$$

Evaluation Metrics

Table.1. Evaluation Metrics

Metric	Result (%)
Accuracy	95.86
Precision	95.16
Recall (Sensitivity)	96.64
F1 Score	95.90

CONCLUSION

- The CNN model developed for malaria cell classification has shown strong and balanced performance across all metrics.
- The high accuracy and F1 score validate its robustness and reliability.
- With minimal misclassifications, the model proves to be efficient for automated malaria detection and could serve as a supportive diagnostic tool in healthcare environments.

APPENDICES

[1]Github Link for the project: https://github.com/DebasmitaChatterjee/Malaria-Cell-Classification.git

[2]Dataset: https://www.kaggle.com/datasets/iarunava/cell-images-for-detecting-malaria

REFERENCES

[1] Chima, J. S., Shah, A., Shah, K., & Ramesh, R. (2020). Malaria cell image classification using deep learning. International Journal of Recent Technology and Engineering, 8(6), 5553-59.

[2] Sivaramakrishnan, R., Antani, S., & Jaeger, S. (2017, October). Visualizing deep learning activations for improved malaria cell classification. In Medical informatics and healthcare (pp. 40-47). PMLR.

[3]https://www.geeksforgeeks.org/machine-learning/introduction-convolution-neural-network/

[4]https://eranfeit.net/how-to-classify-malaria-cells-using-convolutional-neural-network/


THANK YOU