REPORT ON THE MALARIA CELL DETECTION APP USING STREAMLIT

To detect that whether a particular given cell is malaria infected or not there was a quite a number of steps that was followed.

First, I downloaded the Kaggle Malaria cell detection Dataset .
The dataset had 13779 Unifected and 13779 Infected coloured microscopic cell images of dimensions 128X128X3 . Then I bulit a simple tensorflow and keras based CNN model to train on the dataset to predict the microscopic picture is infected or unifected with Malaria.

The structure of the CNN modeldel that I used to train is as follows ->

1. A input layer which took images of size 128X128X3 as an input to the CNN

2. Then I used a same padded 2D Convolution Layer with 32 filters , each filter size was of 5X5 with ReLu Activation .

3. A 2D Max pooling layer of pool size 2X2

4. A same padded 2D Convolution layer with 64 filters , each filter size was 3X3 with ReLu Activation

5. A 2D Max pooling layer of pool size 2X2 and strides 2X2

6. A same padded 2D Cnvolution layer with 128 filters , each filter size was 3X3 with ReLu Activation

7. A 2D Max pooling layer of pool size 2X2 and strides 2X2

8. A same padded 2D Convolution layer with 128 filters , each filter size was 3X3 with ReLu Activation

9. A 2D Max pooling layer of pool size 2X 2 with strides 2X2

10. A Flatten Layer

11. A Dense Layer of size 512 and ReLu Activation

12. A Dense Output Layer of size 2 , because there were two classes to be predicted (Infected or Unifected) and Sigmoid Activation Function is used as for classification generally Sigmoid Activation Function is used.

To compile the whole model together I used Adam Optimizer.

For loss I used Binary Cross Entropy Loss .

For training the model the dataset was spilt into 80 % (train) and 20%(validation).

I used batch size 32 and epoch 50 to train the model .

After training the dataset till epoch 50 , the accuracy was determined till 95.12 %