

Malaria Infection Prediction.

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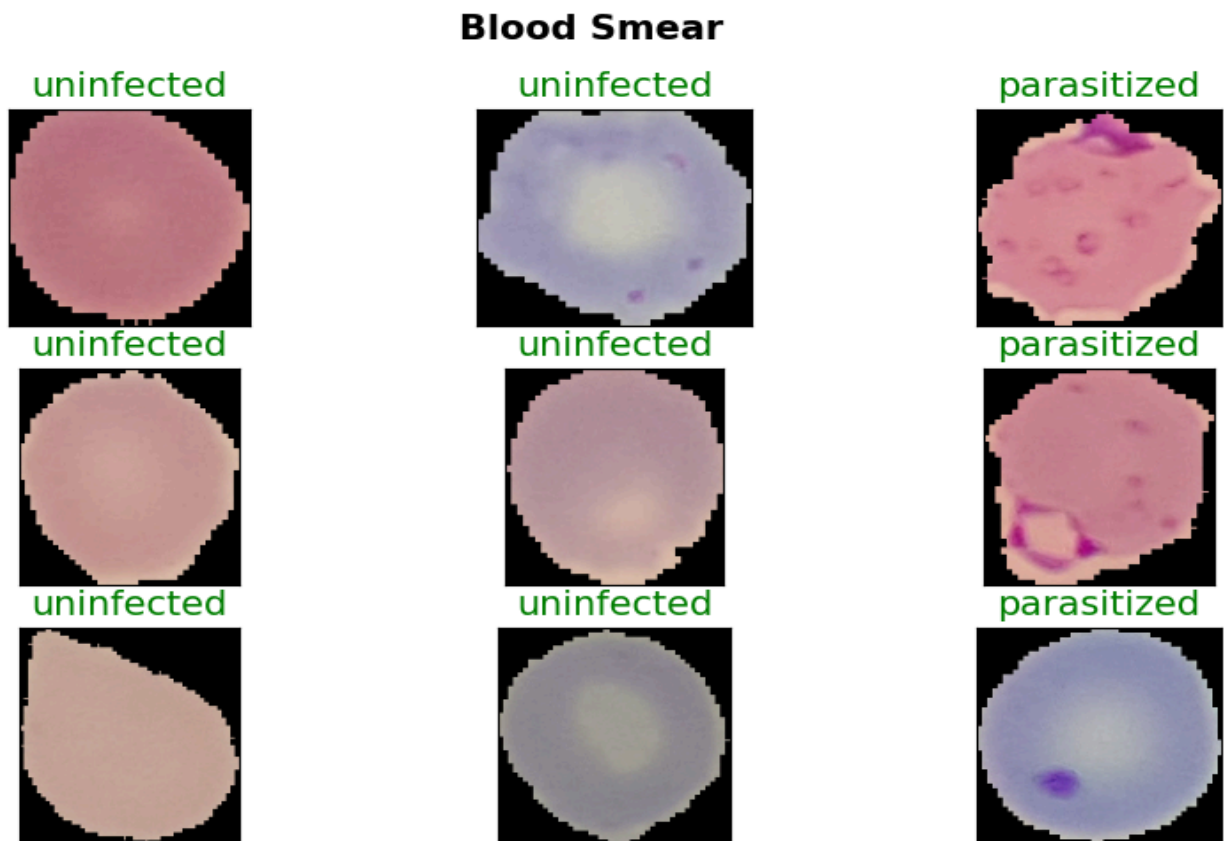
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Overview

- Three unique models are developed and evaluated for the task of classifying blood smear cells to differentiate between those infected with the malaria parasite and those that are not. These models are built on the malaria dataset from TensorFlow Datasets.
 1. A Multilayer Perceptron (MLP) model, serving as the baseline.
 2. A Convolutional Neural Network(CNN).
 3. A Fine-Tuned VGG16 model.
- The results are promising, particularly when it comes to the CNN and Fine-Tuned VGG16 models, which exhibit exceptional accuracy in identifying malaria-infected cells.

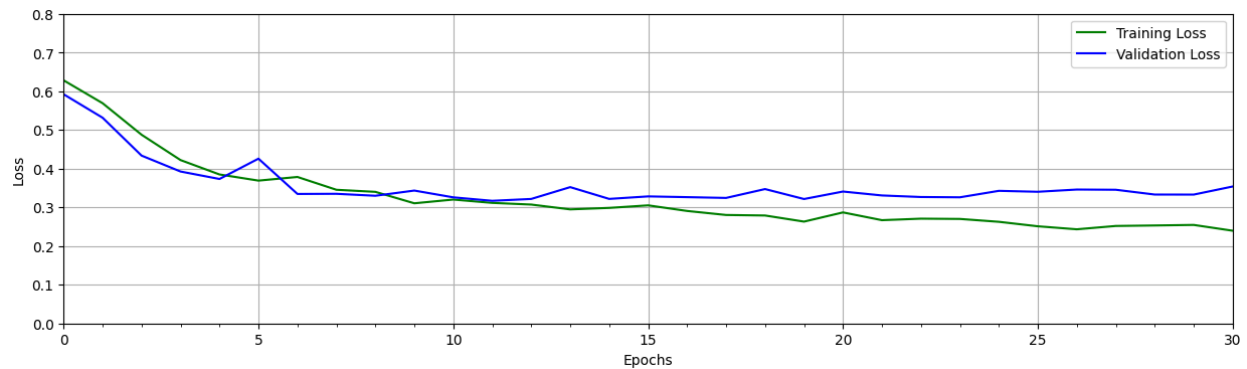
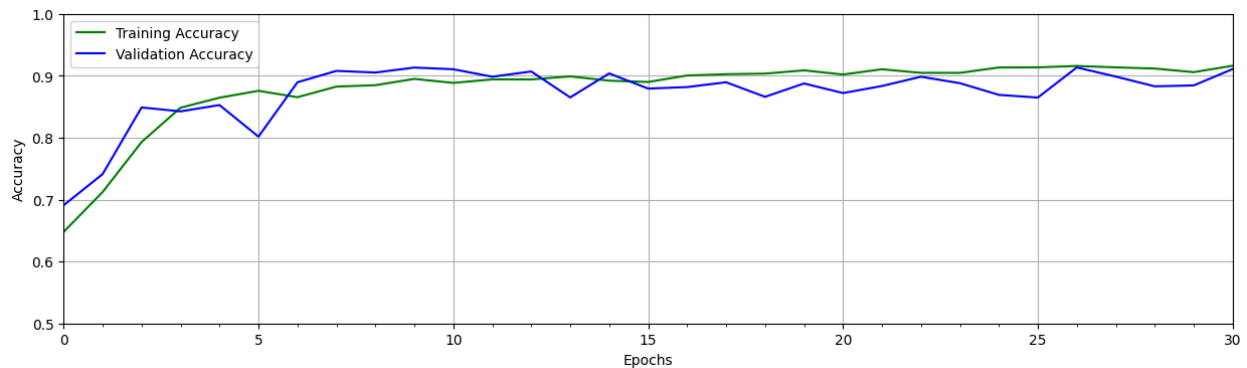
Sample Data.



- Sample blood smear images from the dataset.

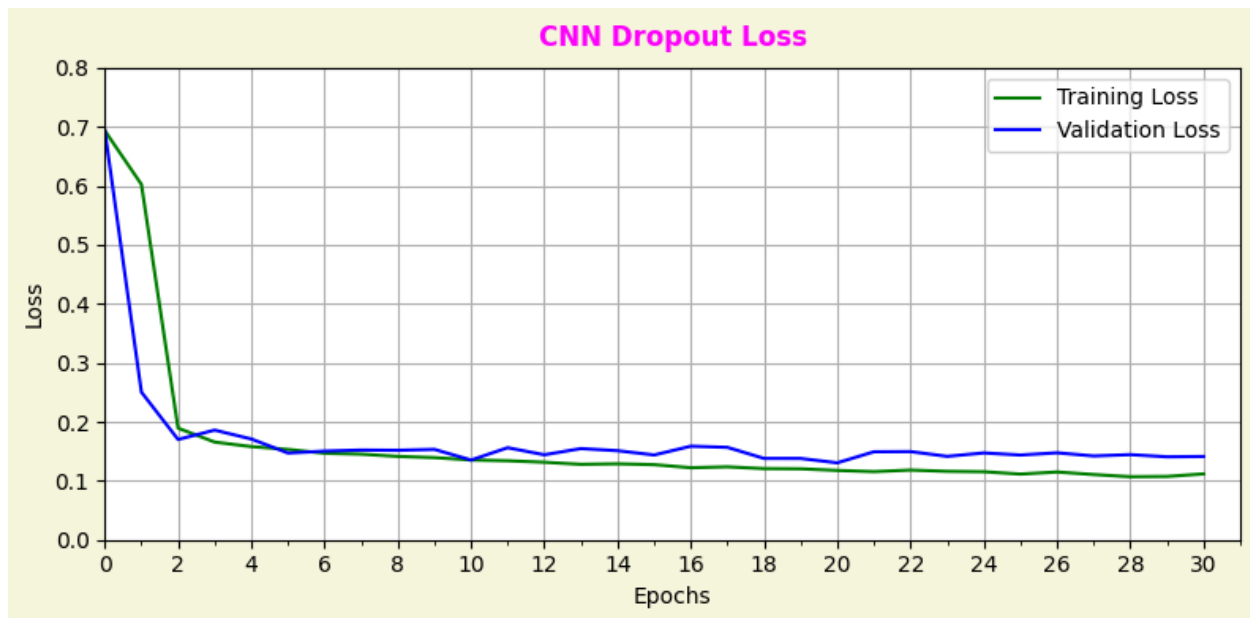
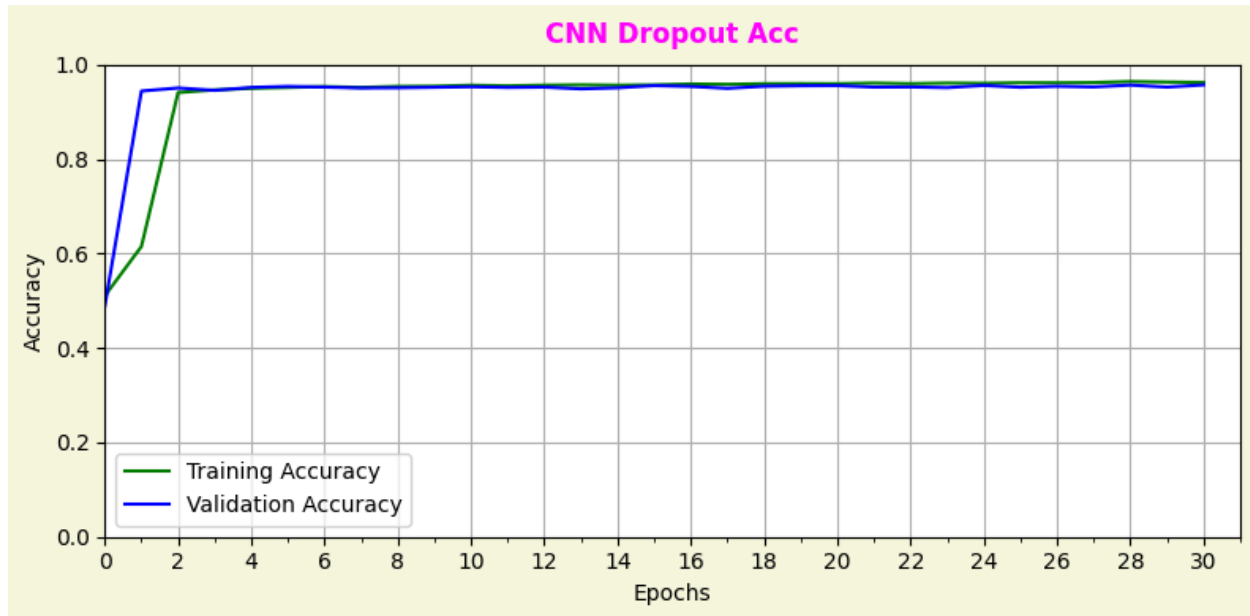
Training Results.

MLP Model.



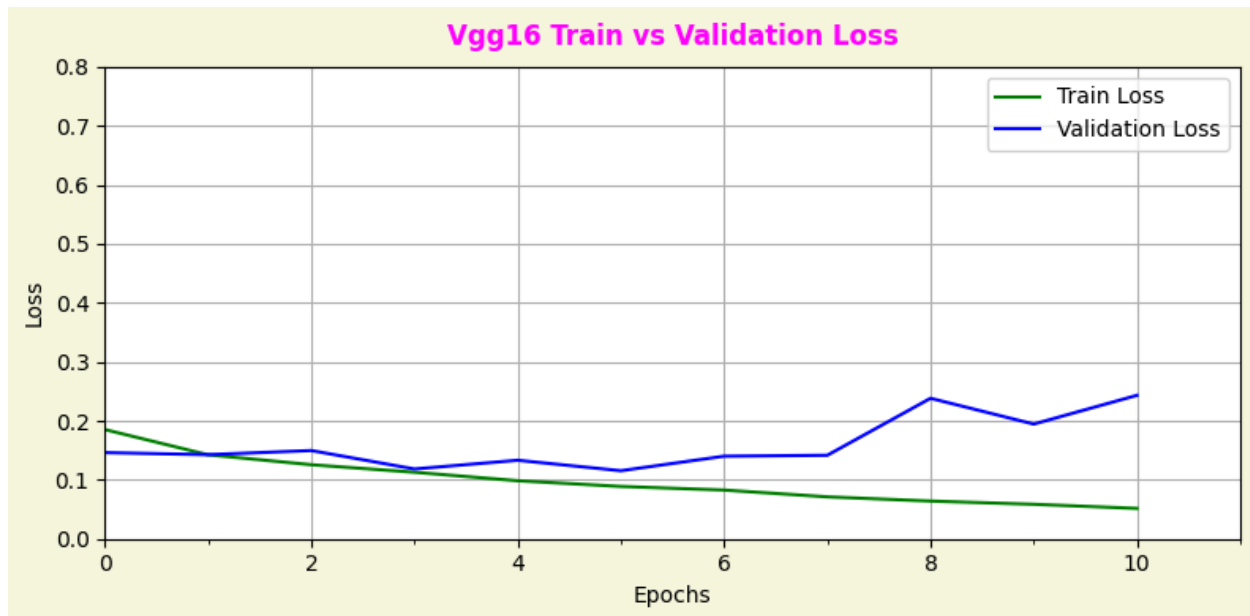
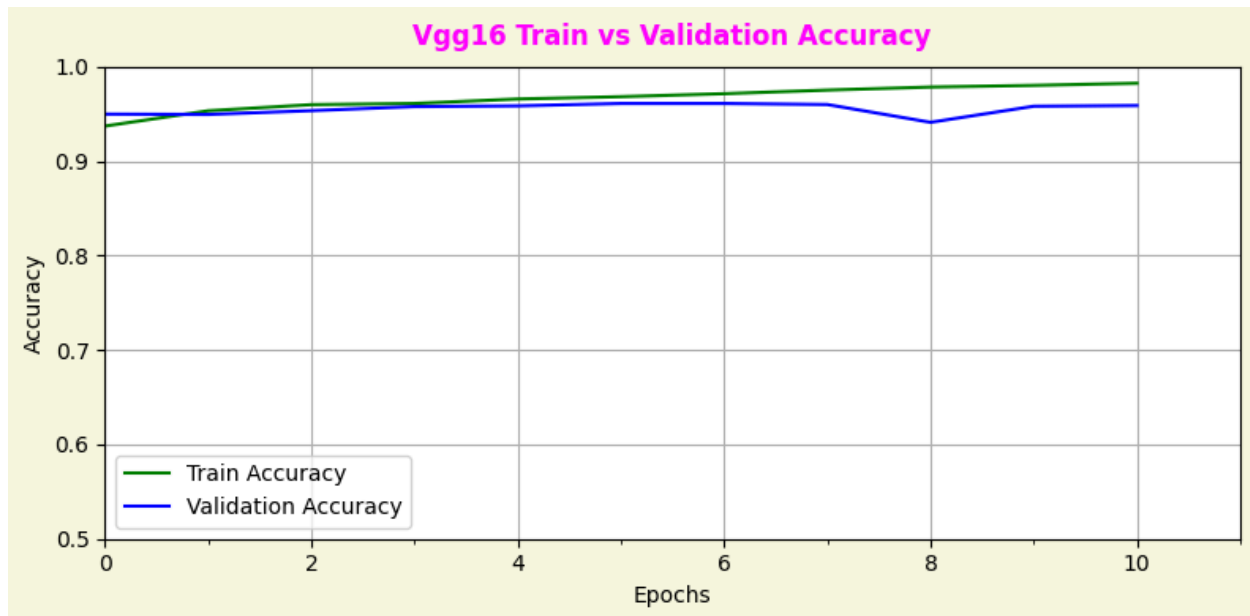
- The MLP model performed admirably in spite of its usual constraints in image classification tasks.
- By the end of training, both the validation and training accuracies had increased to slightly over 90%. At first, the training loss and the validation loss followed each other closely, but halfway through training, divergence started happening, suggesting overfitting.

Custom CNN Model.



- The training and validation accuracies improved steadily for the first two epochs, reaching a respectable 96% by the end of training.
- Notably, the early training stages of the CNN model showed a significant drop in both training and validation loss, indicating a solid performance. The CNN model exhibited significant robustness.

Fine-Tuned VGG16 Model.



- Utilising transfer learning and fine-tuning with VGG16, initial optimism surrounded its potential performance; however, the learning curve for training and validation loss post-5th epoch, revealed a concerning trend of rapid escalation, indicating overfitting.
- Early stopping was applied to avoid further overfitting. Despite these challenges, the model demonstrated resilience, maintaining consistent accuracy throughout training, with occasional epochs achieving up to 98% accuracy.

Model Evaluation.

Test and Validation Datasets.

- With validation dataset.

```
[19]: evaluation = model_vgg.evaluate(valid_ds)
      print(f"Prediction accuracy: {evaluation[1] * 100:.3f}")

87/87 ————— 11s 130ms/step - accuracy: 0.9656 - loss: 0.1062
Prediction accuracy: 96.118
```

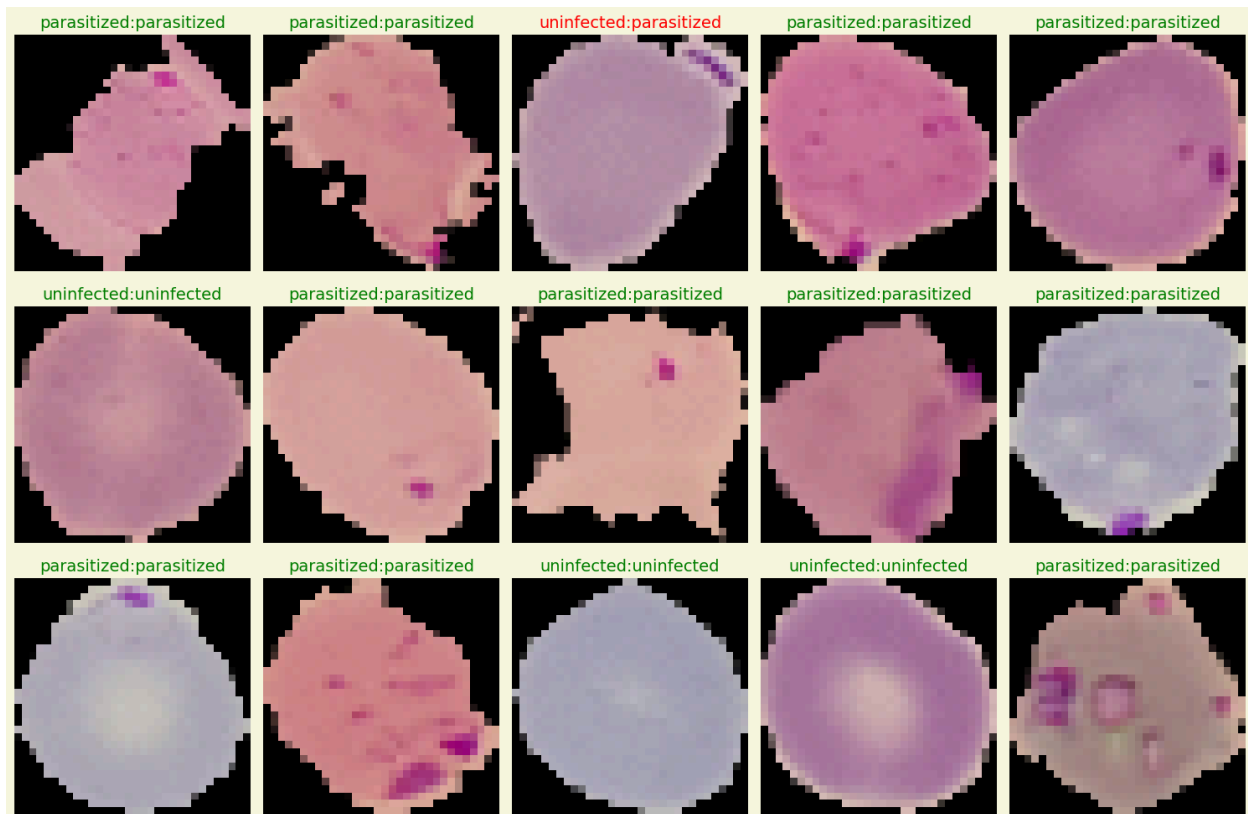
- With test dataset.

```
[20]: evaluation = model_vgg.evaluate(test_ds)
      print(f"Prediction accuracy: {evaluation[1] * 100:.3f}")

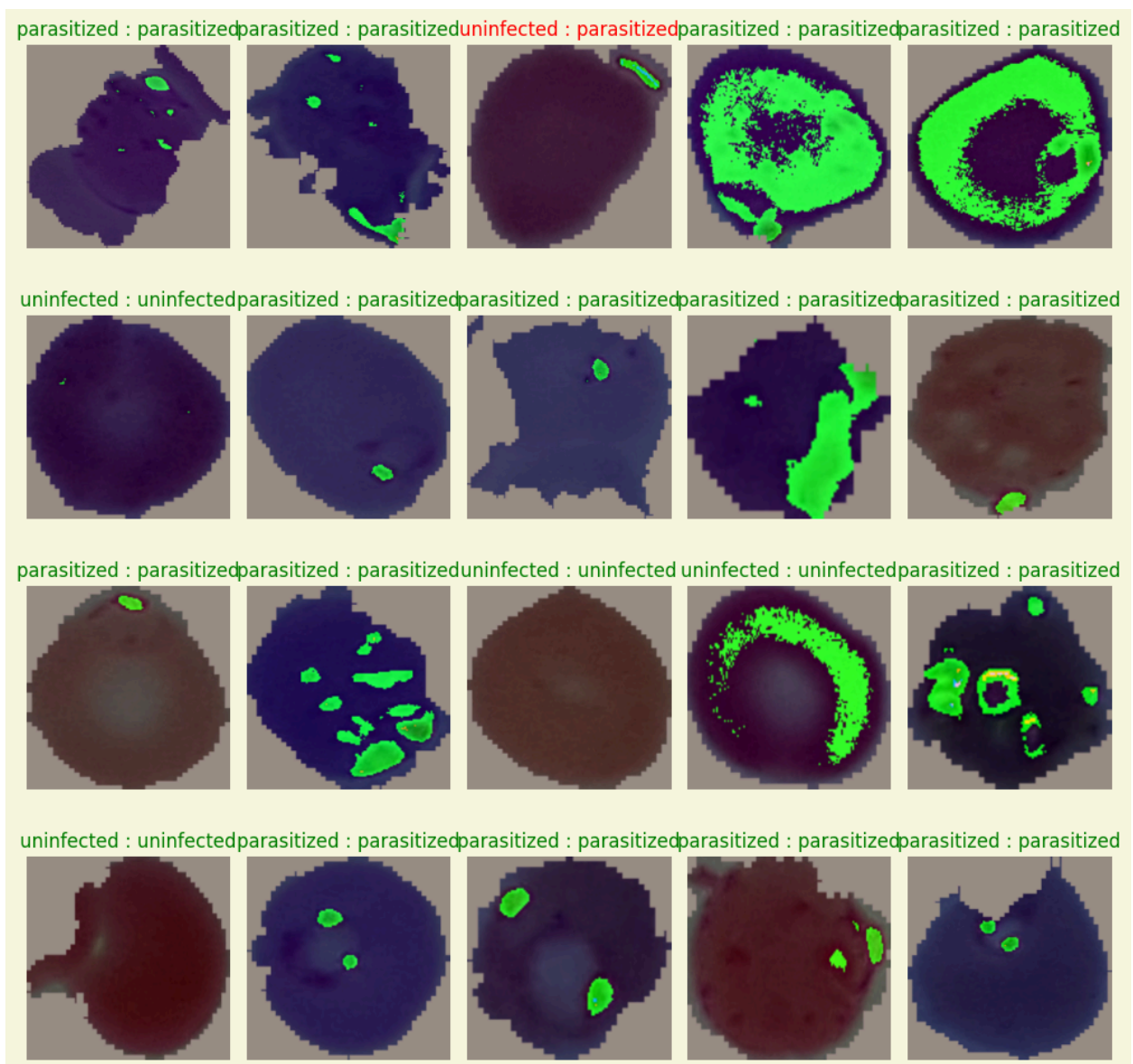
87/87 ————— 12s 134ms/step - accuracy: 0.9656 - loss: 0.1062
Prediction accuracy: 96.118
```

- The Fine-Tuned VGG16 model exhibits commendable performance on both the validation and test datasets, obtaining an accuracy score of 96.118% across both sets.

Sample Test Dataset.

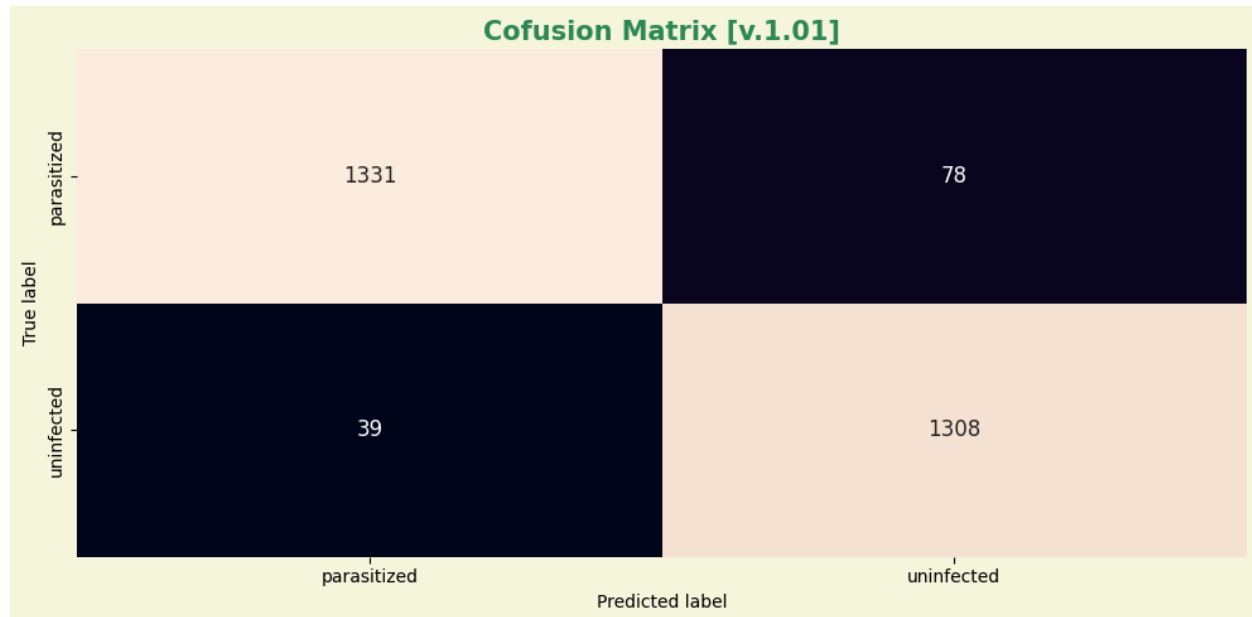


- The image displays a sample output from the Custom CNN Model prediction.
- The model did quite an exceptional job by correctly classifying all images except one.



- This updated output provides a better visualisation similar to the previous image, reflecting the prediction result produced by the Fine-Tuned VGG16 model.
- Notably, it becomes clear why the blood smear image in the first row and third column was categorised as "parasitized" by both the CNN and Fine-Tuned VGG models.
- Even with this one exception, both models perform admirably in correctly classifying most images.

Confusion Matrix.



- The image shows a confusion matrix created using the CNN Model's predictions and ground truth labels. The matrix confirms the convolutional network's robustness and generalizability, despite the existence of a few false positives and negatives.

Conclusion.

To sum up, the Fine-Tuned VGG16 model and the convolutional neural network showed great promise in automating the classification of malaria-infected blood smear cells. By utilising advanced modelling techniques, these models offer encouraging prospects for the creation of accurate diagnostic tools for the identification of malaria.