Malaria Detection Using Deep Learning Models

Submitted by:
Sheikh-Sedat Touray
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Introduction

Malaria remains one of the most serious and widespread infectious diseases globally. Rapid and accurate detection of malaria is crucial for effective treatment and management. In this project, we developed and compared deep learning models for the classification of cell images as either "Parasitized" or "Uninfected" using Convolutional Neural Networks (CNNs). We implemented two main approaches:

1. **Training a CNN from Scratch**
2. **Using Transfer Learning with the Pretrained VGG16 Model**

Review of Previous or Similar Results

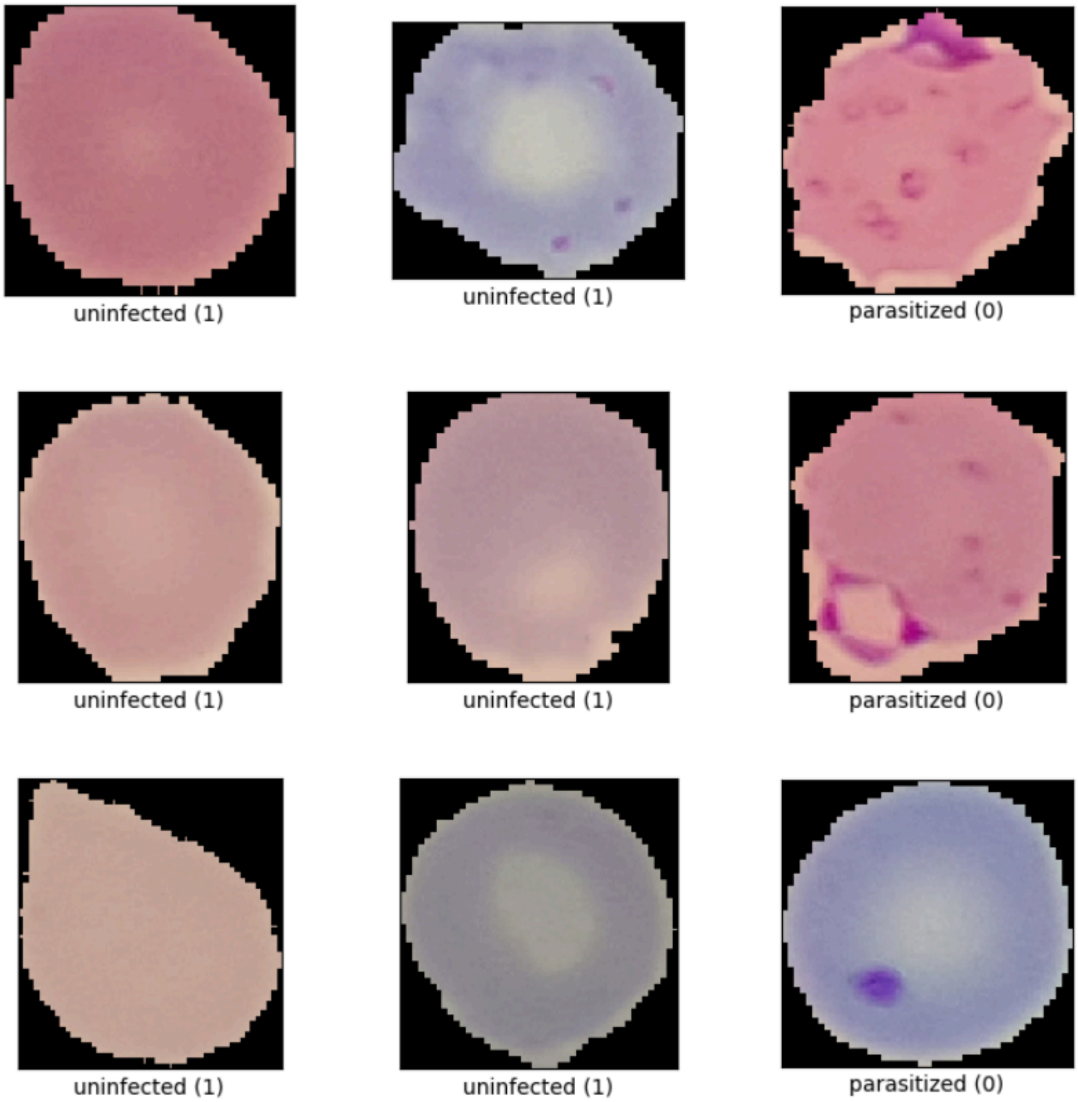
A similar study was conducted using Fastai and PyTorch on a different malaria detection dataset provided on ceb.nlm.nih.gov. Various architectures, such as ResNet34, ResNet50, and ResNet152, were employed. The ResNet34 model achieved over 97% accuracy. This study is still ongoing, with plans to publish further results soon.

Dataset

The dataset used in this project consists of 27,558 cell images, categorized into two classes:

- **Parasitized**: Cells infected with malaria parasites.
- **Uninfected**: Healthy cells without malaria parasites.

- **Image Examples in the Dataset and their Labels**



The dataset was split into training and validation sets with an 80-20 split.

Data Preprocessing

1. **Image Resizing**: All images were resized to a uniform size of 128x128 pixels for the model trained from scratch and 64x64 pixels for the VGG16 model.
2. **Normalization**: Pixel values were scaled to the range [0, 1] to facilitate faster and more stable training.
3. **Data Augmentation**: To improve generalization and model robustness, data augmentation techniques were applied, including rotation, width and height shifts, shear, zoom, and horizontal flips.

Model Architectures

1. CNN Model from Scratch

A CNN model was built from scratch with the following architecture:

- **Conv2D Layers**: Three convolutional layers with ReLU activation, followed by MaxPooling layers to reduce spatial dimensions.
- **Dense Layers**: A fully connected layer with 128 units and ReLU activation, followed by a Dropout layer for regularization.

- **Output Layer**: A single neuron with Sigmoid activation for binary classification.

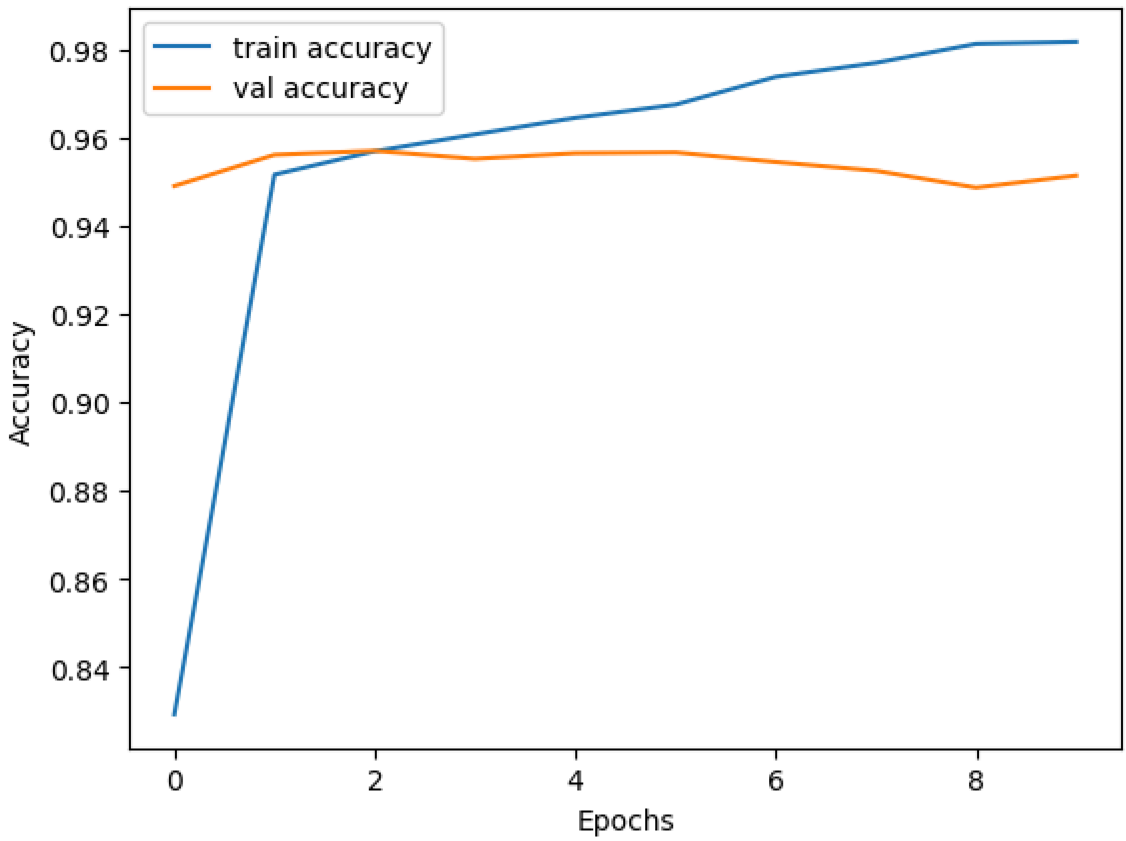
Model Summary:

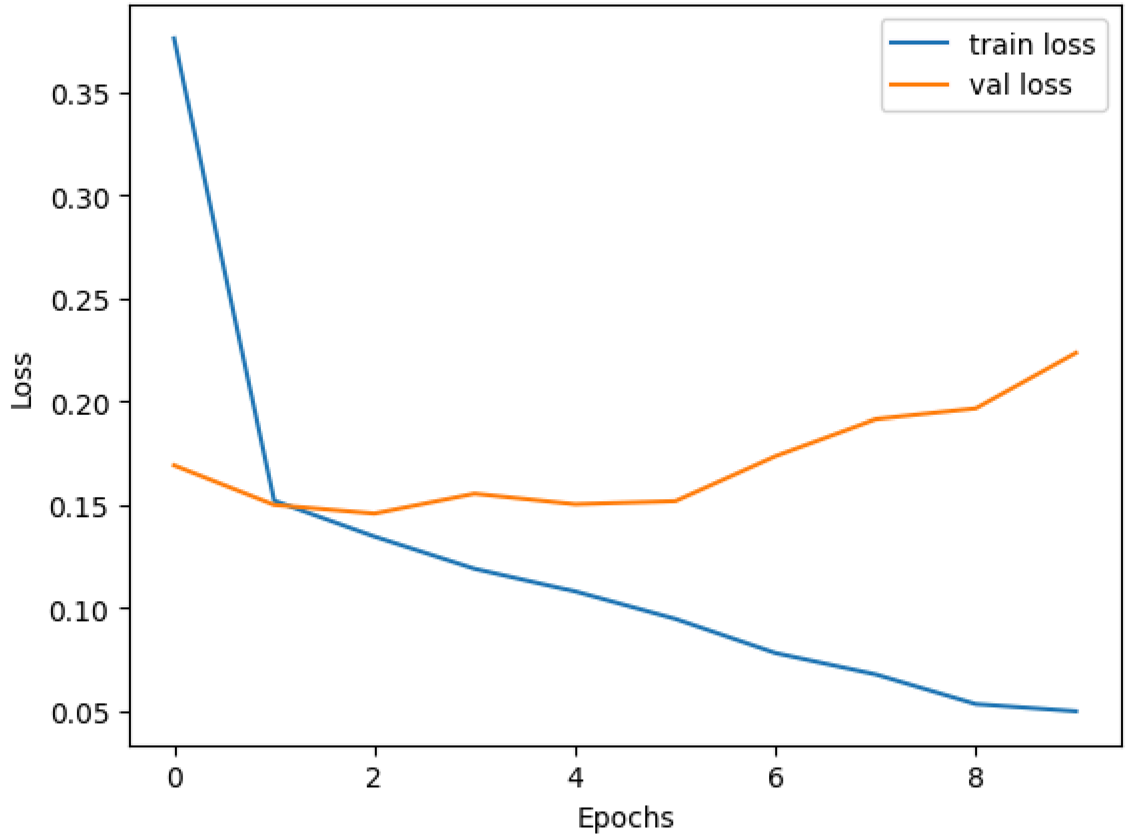
Layer (Type)	Output Shape	Param #
Conv2D (32 filters, 3x3)	(126, 126, 32)	896
MaxPooling2D (2x2)	(63, 63, 32)	0
Conv2D (64 filters, 3x3)	(61, 61, 64)	18,496
MaxPooling2D (2x2)	(30, 30, 64)	0
Conv2D (128 filters, 3x3)	(28, 28, 128)	73,856
MaxPooling2D (2x2)	(14, 14, 128)	0
Flatten	(25088)	0
Dense (128 units, ReLU)	(128)	3,211,392
Dropout (0.5)	(128)	0
Dense (1 unit, Sigmoid)	(1)	129

Results:

- **Validation Accuracy**: 95.16%
- **Validation Loss**: 0.2127

Analyzing the CNN from Scratch Results:





2. Transfer Learning with VGG16

The VGG16 model, pretrained on the ImageNet dataset, was used as the base model. We retained the convolutional layers and added custom dense layers on top for classification.

- **ConvBase**: Pretrained VGG16 layers, frozen to retain their weights.
- **Dense Layers**: Similar to the scratch model but adapted for 64x64 input size.

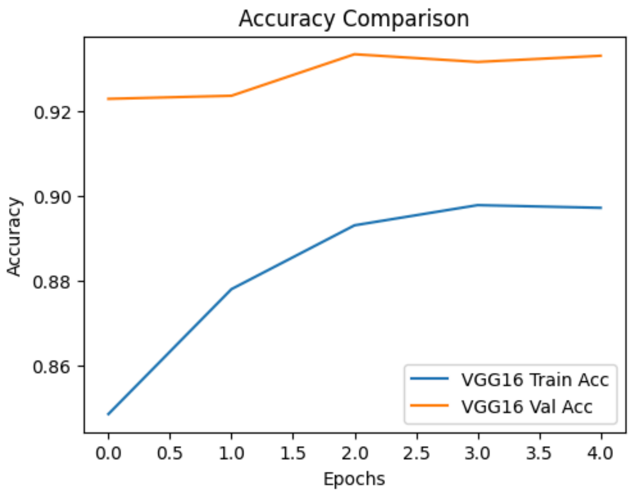
Model Summary:

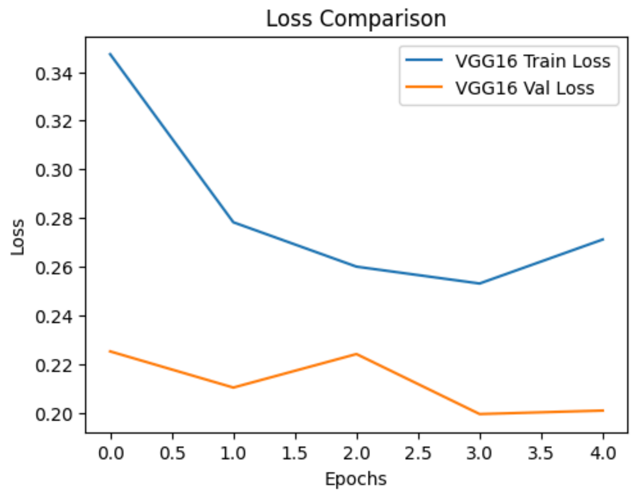
Layer (Type)	Output Shape	Param #
VGG16 (ConvBase)	(2, 2, 512)	14,714,688
Flatten	(2048)	0
Dense (128 units)	(128)	262,272
Dropout (0.5)	(128)	0
Dense (1 unit)	(1)	129

Results:

- **Validation Accuracy**: 92.36%
- **Validation Loss**: 0.2103

Analyzing the VGG16 Results:





Analysis and Discussion

1. **Training from Scratch**: The model trained from scratch achieved higher accuracy compared to the transfer learning approach, indicating that it effectively learned the features specific to malaria detection from the dataset.

Predictions of the Model Build from Scratch

The model build from Scratch was able to predict 5 out of 5 times the wether the patient had malaria or did not have malaria. The probabilities of 1 or closer to 1 show the patient is **Uninfected**, whereas the probabilities of 0 show that the patient is **Parasitized**.

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1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 157ms/step
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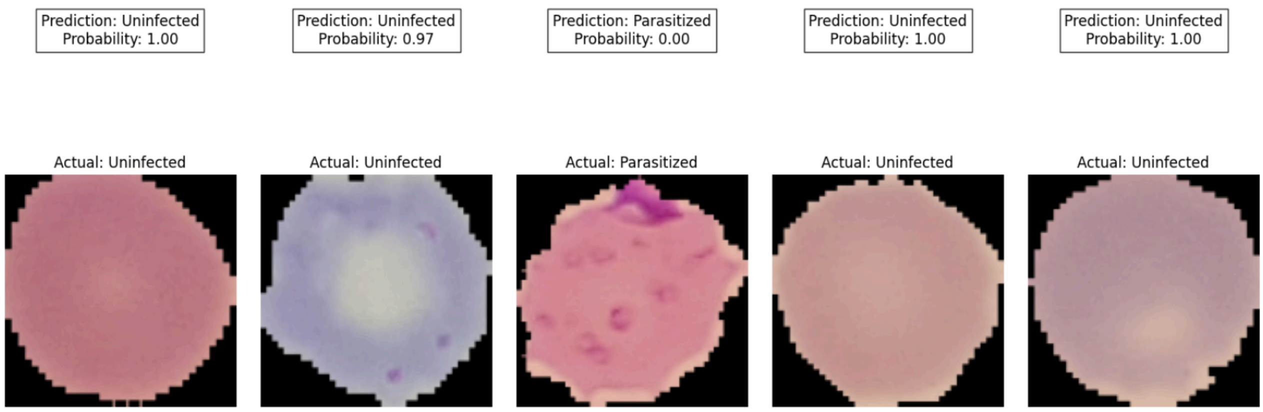

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1. **Transfer Learning with VGG16**: While the VGG16 model had a slightly lower accuracy, it still performed well, demonstrating the strength of transfer learning even with a smaller image size and fewer epochs.

Predictions of the VGG16 Model

The VGG16 (pre-trained) model was able to predict 5 out of 5 times the wether the patient had malaria or did not have malaria also even with less data and after we have significantly reduced the image size. However, we can see some signs of overfitting and noise in the predictions.

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1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 392ms/step
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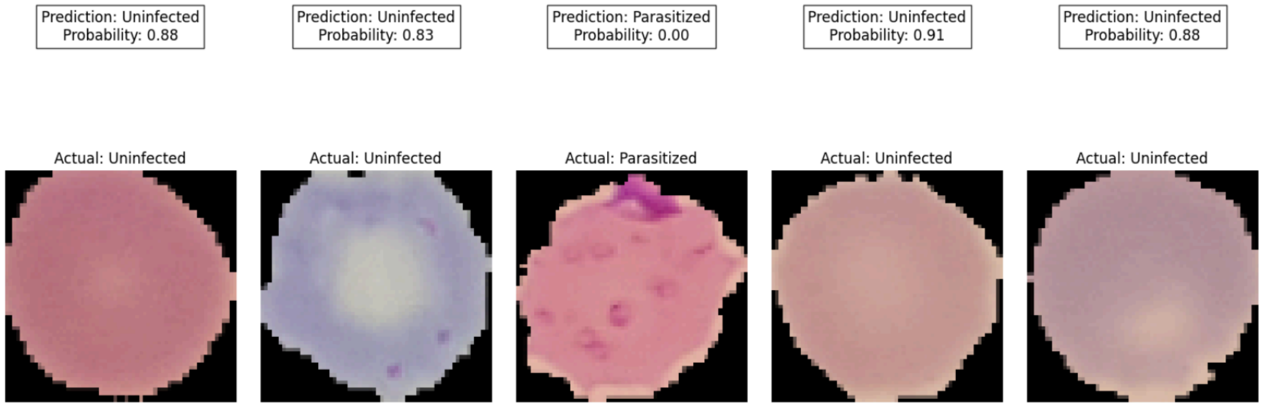

Challenges and Limitations:

- **Training Time**: The model trained from scratch required significantly more time per epoch compared to the VGG16 model due to the need to learn all features from the data.
- **Overfitting**: Both models showed signs of overfitting, as indicated by the increasing validation loss after several epochs. This could be mitigated by implementing more regularization techniques or using a more extensive dataset.

Conclusion

Both approaches provided valuable insights into the strengths and weaknesses of training models from scratch versus using transfer learning. The CNN model trained from scratch slightly outperformed the VGG16 model, suggesting that it could be more tailored to this specific task. However, transfer learning remains a powerful tool, especially when computational resources or data are limited.

Future Work

To further enhance the model's performance, the following steps could be explored:

- **Hyperparameter Tuning**: Experimenting with different optimizers, learning rates, and batch sizes.
- **Advanced Data Augmentation**: Including techniques such as CutMix or Mixup.
- **Ensemble Methods**: Combining predictions from multiple models to improve accuracy and robustness.

References

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- Chollet, F. (2018). *Deep Learning with Python*. Manning Publications.
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- https://www.news-medical.net/health/Mosquito-borne-Diseases.aspx
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