Capstone Report

Capstone Project 2

Detecting Malaria using Image classification

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Problem Statement

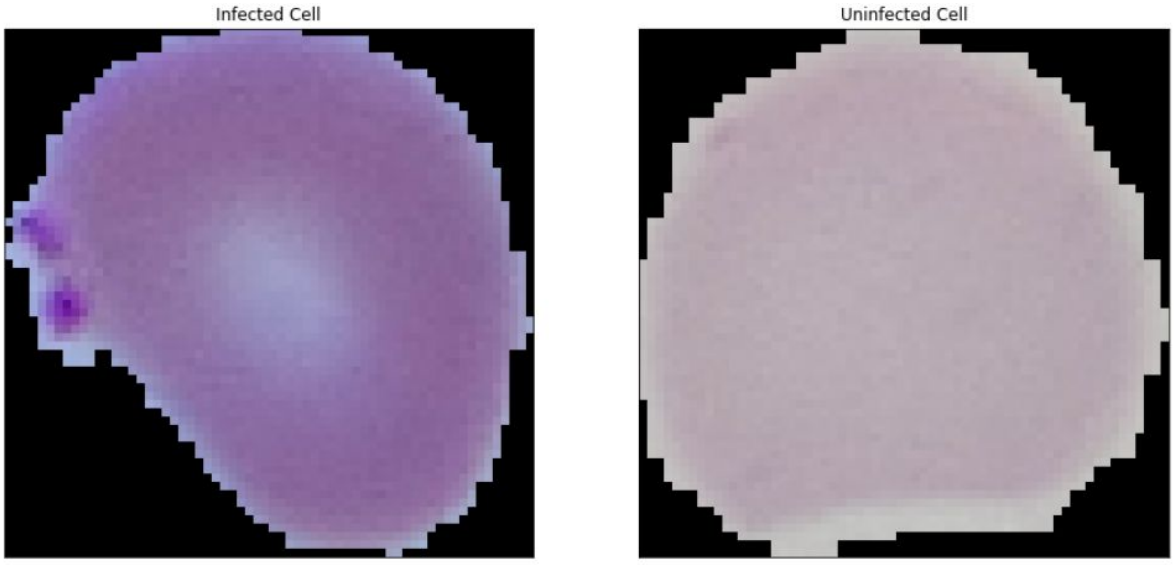
To solve with the best accuracy by detecting and deploying Image Cells that contain Malaria or not.

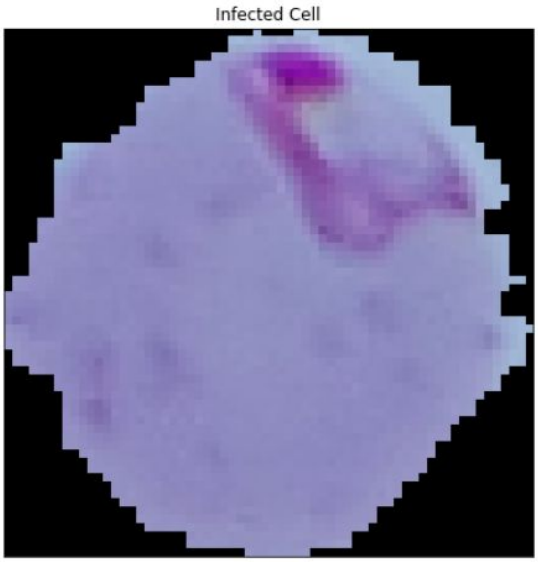
Introduction

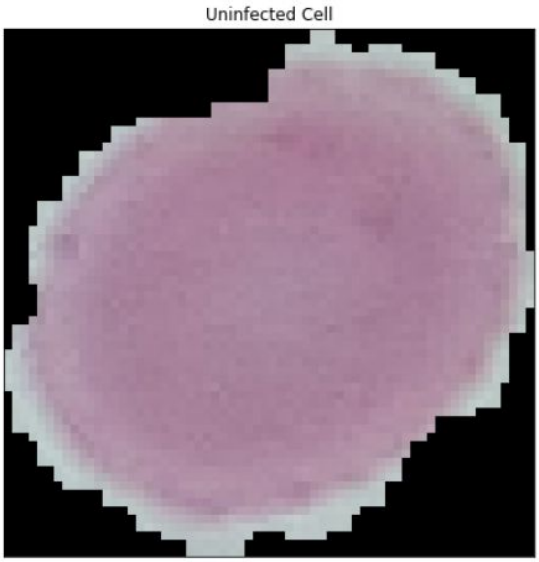
Malaria is a life-threatening disease caused by parasites that are transmitted to people through the bites of infected female Anopheles mosquitoes. It is preventable and curable.
Here I am trying to solve with the best accuracy by detecting and deploying Image Cells that contain Malaria or not!
The client for this project is Healthcare Industries. This project will help them as a Healthcare company will be able to classify the malaria-infected and uninfected cells. They will be able to deploy this predictive system even in remote corners of the world.
The data used in this project is taken from kaggle. The dataset is divided into two parts, one containing infected cells images and the other containing uninfected cell images.
The kaggle link for data is: https://www.kaggle.com/iarunava/cell-images-for-detecting-malaria

Methodology

The data is in the form of images, this means in the form of 3d array. The images are provided in two folders i.e. infected and uninfected. We have to append the data into a list of arrays while labelling another list of categorical values (0,1). We are reducing the size of images to (64, 64) to make it easier for processing, and to keep the uniformity.
The infected and uninfected cell images can be seen side by side below.







After reading the images, the shape of the data is (27558, 64, 64, 3). The number means:

- 27558: the length of the list is the number of images
- (64, 64): is the pixel size of image
- 3: contains the values of RGB of the image.

And the shape of the labels is (27558, 2). Here the number means:

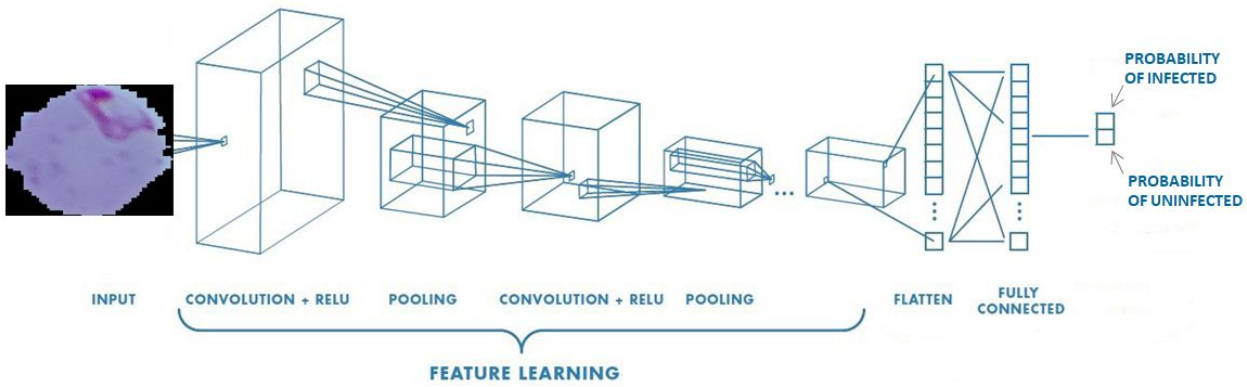
- 27558: the length of the list corresponding to the images data
- 2: labels categorical values of 0 or 1

Following are the data processing steps:

1. The data and labels are converted into numpy array. It can be numpy array before but just to be sure.
2. An array is generated containing numbers zero to the length of data. The array is then randomly shuffled.
3. The array is used to shuffle the data and labels. As they were containing first infected then uninfected images.
4. The data is converted to float data type. This is done so when scaling is done, the numbers after decimal remains.
5. The data is scaled by dividing it by 255, the largest number in representing colors.
6. The data is then split in 70-30 ratio. With 70% of data in train and 30% of data in test.
7. The model was run in google colab due to its high requirement of computing process.

Now the images has been represented as the list of array(numbers). We can proceed with the model building.

Architecture



Deep Learning Model

We have used the CNN method of neural network for the model. The following parameters are finalized after multiple values were iterated.

These are the model parameters used in training the model. We are using four layers of image processing steps in this scenario. The activation function used is relu middle layers and sigmoid in the final layer. The details of the model are as follows:

- Input shape = (64,64,3) #the shape of an image as array
- Layers = 4
- Method = SeparableConv2D
- Each layer method
    - Conv2D
    - Filters = 64, 128, 256, 64
    - Kernel size = (3,3)
    - Activation = relu
    - BatchNormalization
    - Max Pooling = (2,2)
    - Dropout = 0.2
- Flatten = Yes
- Pre-final layer = Dense: 256 nodes, activation: relu
- Dropout = 0.2
- Final Layer = 2 output nodes, activation: sigmoid

Data Augmentation Parameters

We have done data augmentation to create similar images with a bit of distortions like zooming, flipping the image. This makes the model more robust against the new images.

Train:

- rescale=1./255,
- shear_range=0.2,
- zoom_range=0.2,
- horizontal_flip=True,
- vertical_flip=True

Validation/Test:

- rescale=1./255

Note: Because the shuffle parameter in data augmentation is True by default the recall was low initially. We have to put False in Shuffle so we can get the proper labels when we are testing against prediction.

Callbacks

We put a few callback functions to keep the model running smooth. The earlystopping function is to stop the training when the validation loss is not improving and model checkpoint is the save the model at the lowest validation loss.

Earlystopping:

- Monitor: val_loss
- Min_delta = 0.001
- Patience = 7
- Verbose = 2
- Mode = ‘min’

ModelCheckpoint:

- Monitor = 'val_loss'
- Verbose = 1,
- Save_best_only = True
- Mode = 'min'
- Save_weights_only = False

Compile

- Loss = binary_crossentropy
- Optimizer = adam (The learning rate is set to be default.)
- Metrics = accuracy

Fit

- steps_per_epoch = 1000
- verbose = 1
- validation_steps = 200
- epochs = 10
- use_multiprocessing=True

Note: We have loaded the model weights for the lowest validation loss while training.

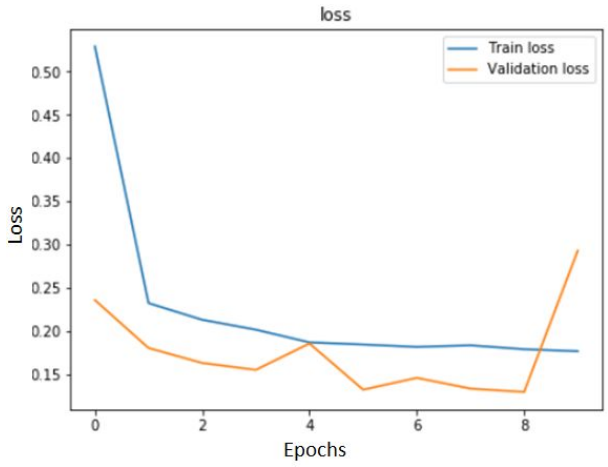
Observations:

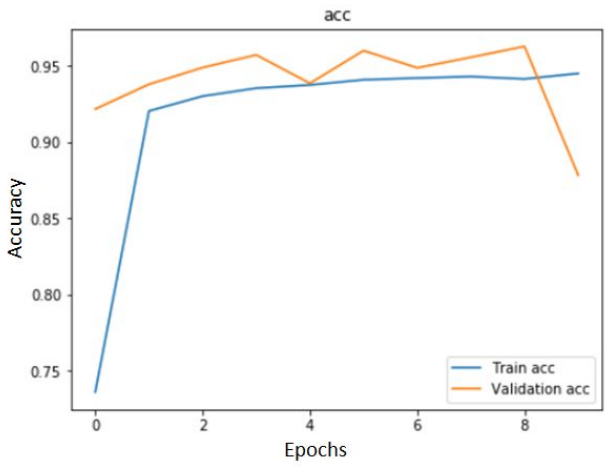
The results are:

- Training Accuracy = 0.9416
- Training Loss = 0.1792
- Validation Accuracy = 0.9630
- Validation Loss = 0.1298
- Testing Accuracy = 0.9506
- Testing Loss = 0.1489

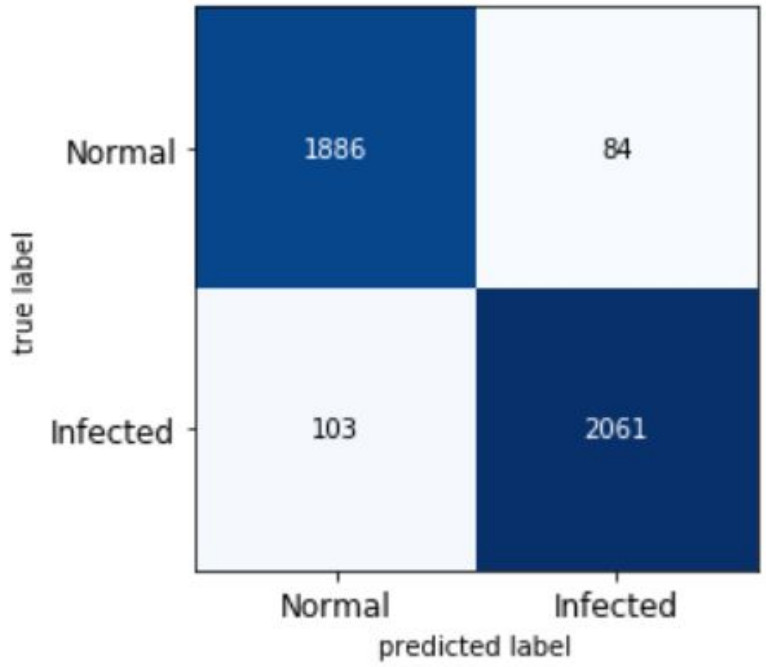
Model Training:

The point of best accuracy and minimum loss was loaded for predictions.





Confusion Matrix



The False positives(84) and False negatives(103) are very low compared to Tp and Tn. But we have to be very careful in Fp and Fn cases as a Fp case will suggest to start treatment when the disease is not present and Fn case will suggest that the patient doesn't have the disease when in reality the patient is infected.

Classification Report

	precision	recall	f1-score	support
0	0.95	0.96	0.95	1970
1	0.96	0.95	0.96	2164
accuracy			0.95	4134
macro avg	0.95	0.95	0.95	4134
weighted avg	0.95	0.95	0.95	4134

The high precision and recall is a good sign that this method can be used in real scenarios.

Conclusion

We have got a good test accuracy of 0.95. The model is with good precision able to successfully predict from the blood cell image if it is infected or not. The f1-score of 0.95 shows the capability of model in having a good recall and precision.

The only assumption we took here is that the infected cells are only infected by malaria, no other disease is affecting the cells. We have trained malaria infected cells against healthy cells only.

The model needs to be updated regularly with new images. This model can be used in integration with other models when other diseases might be present.