

## **Project Summary**

### **Executive Summary:**

In this project, we explored a number of ways for building a deep learning model that can accurately detect infected red blood cells from a set of images. These techniques ranged from image pre-processing techniques, model alterations and hyperparameter tuning, as well as the use of a pre-trained model. After trialing these techniques, we were able to identify a model that provides a balanced performance, meaning that the accuracy metrics were all relatively high. Despite obtaining a strong model, we did not exhaust all the available options available to maximize performance even further. Thus, for future improvement it would be worth exploring options such as trying other pre-trained models and using transfer learning. Finding models that have already been carefully crafted for a dataset similar to ours can be highly beneficial because we could simply alter some of its features to fit our problem. Additionally, we can actually display the cells that are being misclassified and try to understand why, and then consult with medical experts to obtain a better understanding or even have them correct any potential misclassified labels of the dataset. After these improvements, our next step would be to begin deployment of our model, so that we can use its capabilities in real time and reach our overall goal of detecting malaria as soon as possible to help eradicate its consequences. This would involve communication with the engineering team to create a pipeline which would grant us greater control and flexibility for our model, as well as scalability. This is important because we were only dealing with a single dataset for our current model whereas we will want it to be able

to process much more data and in real time, so if there are issues then we want to be able to quickly fix it and a pipeline will help greatly with that.

## **Problem and Solution Summary**

Our main challenge was being able to distinguish between red blood cells that are infected, and those that are not. Different features such as color, opacity, and other types of noise can make it difficult for our automated model to make this distinction. Thus, our main objective was to utilize different techniques to both equip our model to be more effective at this task and also alter the images in a way to make this goal less challenging. We tried various techniques such as HSV conversion and augmentation for our images, as well as adding features to our model such as batch normalization. Our final proposed solution design involves grayscale images being fed into a keras-tuned model. The grayscale conversion helped eliminate some of the noise of the images that may have contributed to the misclassification of some of our images, while the keras tuner helped us obtain the best hyperparameters needed for our model to work optimally with the data.

## **Recommendations for Implementation**

Our grayscale technique helped make the images easier to classify for our model, however one thing to consider is that the removal of colour may pose a potential limitation with future data. If for example, a red blood cell has a characteristic that appears similar to that of an infected cell but can only be distinguished by its colour, then our model might fail to make that distinction. Thus, communication with medical experts on this topic might help us better explore

this potential limitation and thus create contingencies that will help prevent it from being a problem. Another key challenge involves the keras tuner. Firstly, the keras tuner runs a combination of random values for the hyperparameters which may not exactly cover the most optimal possible values, and secondly it can be very slow to run. Thus, other tuning techniques such as Bayesian optimization may produce better results because it allows us to jointly tune more parameters with fewer experiments and find better values, all at a potentially quicker speed. The slow speeds of our tuning might also mean that we should consult with the engineering team to make sure an appropriate environment can be established so that when further potential tuning happens down the line, we won't be limited by slow processing speeds. This is especially important considering we will be working with live data and in high amounts. Thus, consultation with both medical experts for further intuition on image distinction as well as with the engineering team to establish an appropriate environment for deployment should be of priority importance. Following that, we can explore different tuning methods such as bayesian or grid search to find even better hyperparameters than what we found with our Keras tuner.