Artificial Intelligence Offers a Better Way to Diagnose Malaria

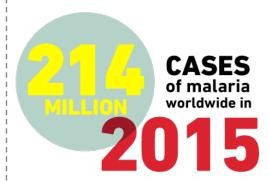
Adwoa Twumwaa ANSAH

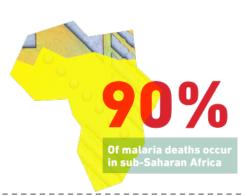
James Shao Hwee CHUA

Zhiqing XIAO

Malaria is a widespread and life-threatening disease, especially in rural areas

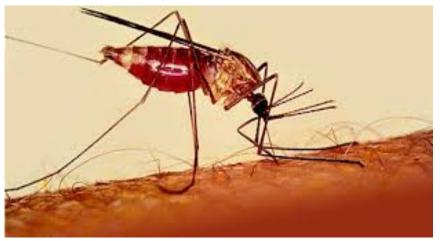






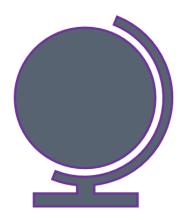








Malaria: An increasing threat to everyone



Global

Malaria thrives wherever the vector can survive, which is usually in tropical regions. However, with increasing global temperatures, it is suspected that the vector would soon be able to survive in Europe



Business

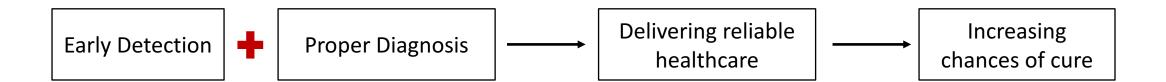
Many western businesses are expanding their activities to include Africa. Although many locals have developed just enough immunity to protect them from malaria, foreigners might not be so fortunate.



Travel

For example, in the United States, the Centers for Disease Control and Prevention (CDC) report 1,700 cases of malaria annually, majority of which are people who travel to countries where malaria is more common [can also be transmitted through blood transfusions & organ transplants]

The need for an automated malaria diagnosis process



Microscopic inspection

Inefficient

Low Accuracy

Specialized infrastructure

Specialized human resources

Lack of standardization

- Manual counting methods are very long, tedious
- False-negative: progression into severe malaria
- False-positive: unnecessary use of drugs and suffering from side effects
- Inadequate and frequently unavailable in rural areas where malaria has a marked predominance
- Important for testing for drugresistance, measuring drugeffectiveness, and classifying disease severity
- Depends heavily on the experience and skill of the microscopist

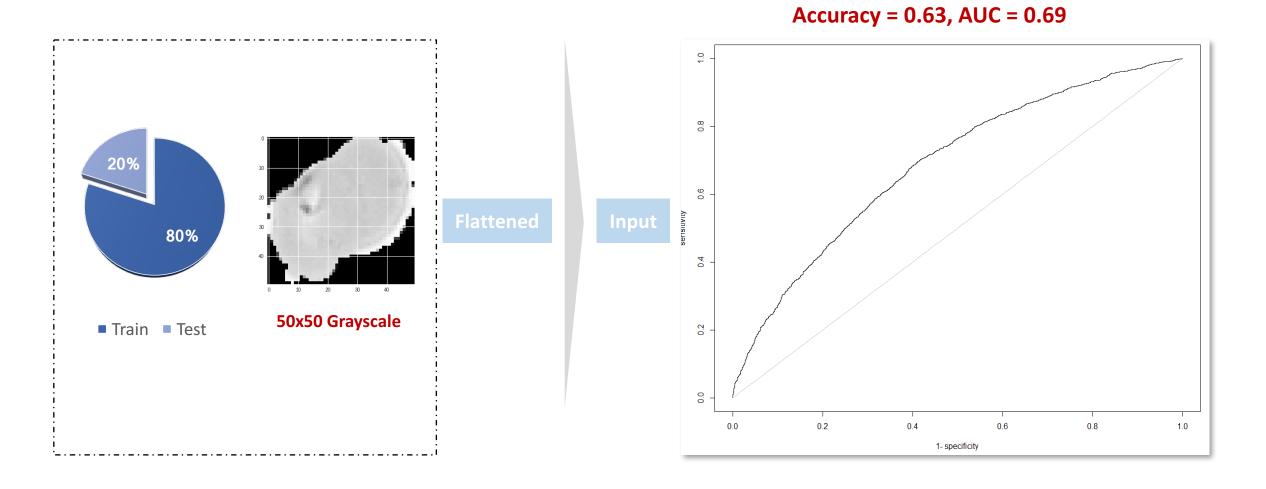
Dataset

CREATE A CLASSIFIER TO DIFFERENTIATE BETWEEN INFECTED AND UNINFECTED CELL 50% uninfected cells 50% infected cells

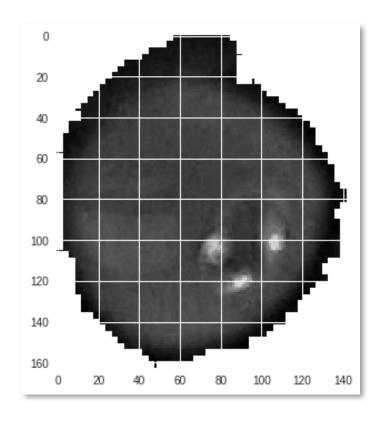
Source: U.S. National Library of Medicine



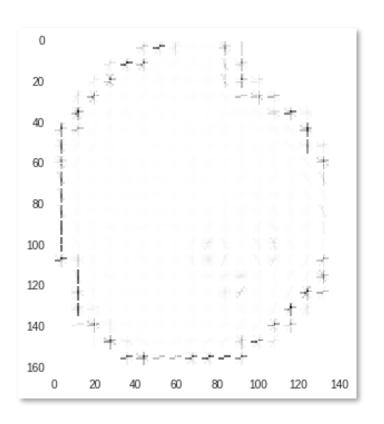
Base Model - Logistic Regression



Base Model - Feature Engineering: Histogram Of Gradients







Shape detection

Reduce images from 2500 pixels to 800 features-> Faster model training

Base Model - Logistic Regression with HOG feature engineering



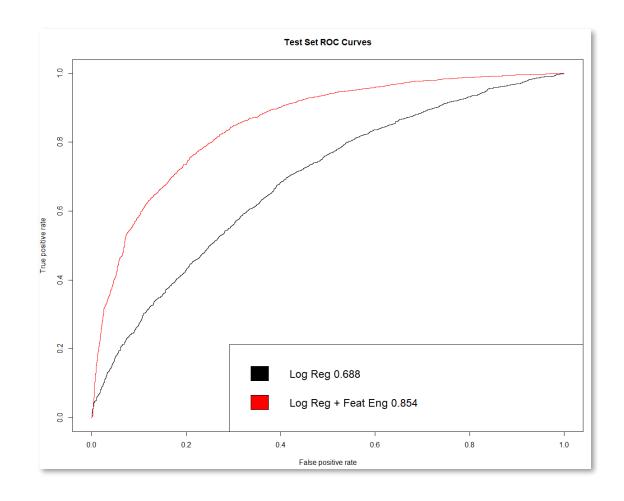
AUC: From 0.69 to **0.85**

Accuracy: From 63% to 77%

95% CI: (0.7621, 0.7844)

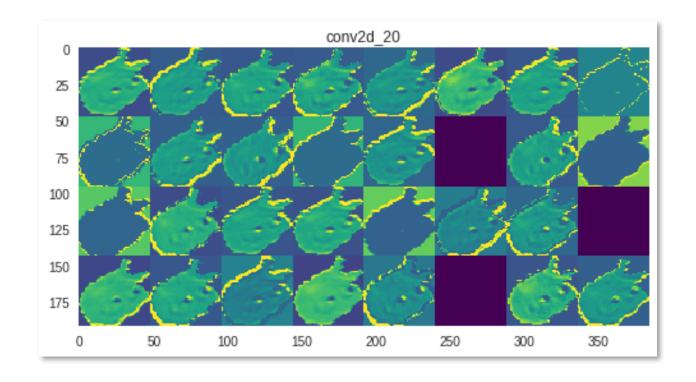


Feature engineering worked!



Convolutional Neural Network (CNN)

- CNNs allow us to build a classifier without doing the feature engineering ourselves.
- We can see edge detection working in the first layer of our CNN



Convolutional Neural Network (CNN)

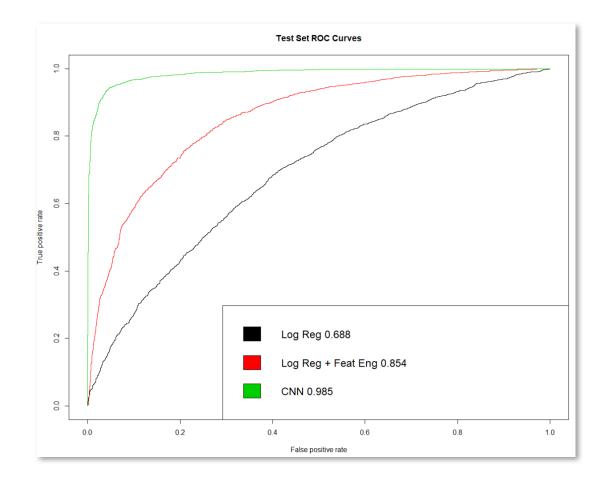
 Due to hardware limits, we trained a relatively simple Convolutional Neural Net

• Accuracy: 92.7%

95% CI: (0.9206, 0.9345)



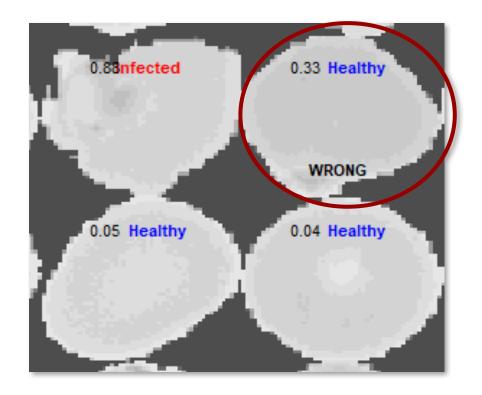
Impressive results!



PROBLEM

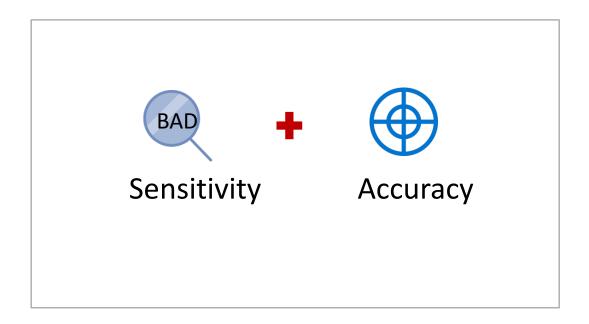
Setting the threshold of the classifier

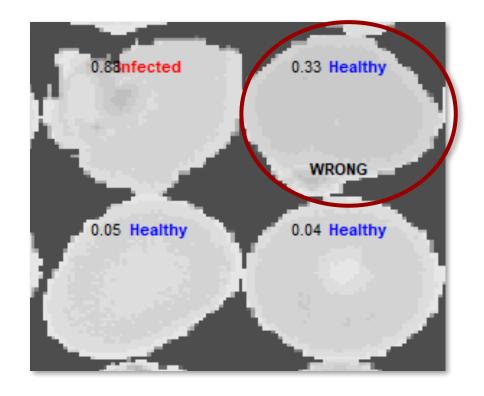
- CNN assigns probability to each image
- Default threshold of 0.50
- >0.50 = Infected, <0.50 = Healthy
- It is extremely dangerous to misclassify an infected person as healthy (different costs)
- The percentage of infected correctly classified is known as "Sensitivity" BAD



Setting the threshold of the classifier

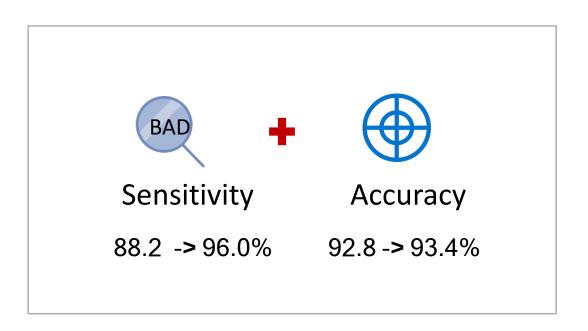
What is the threshold to maximize

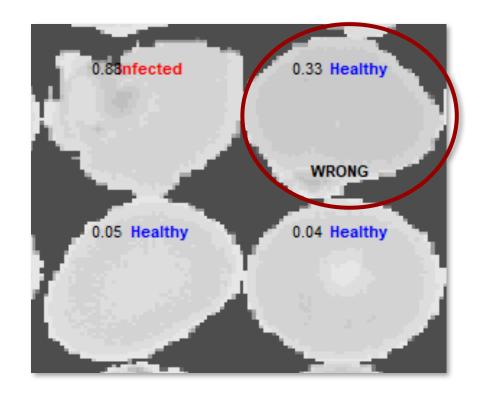




Setting the threshold of the classifier

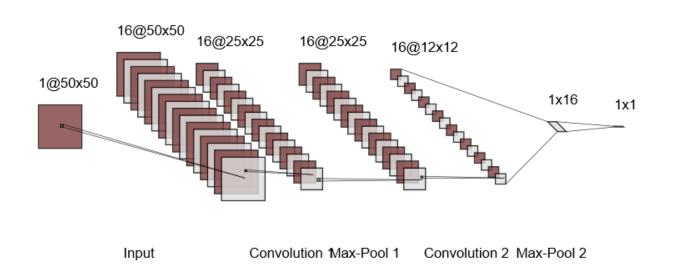
Threshold = 0.18

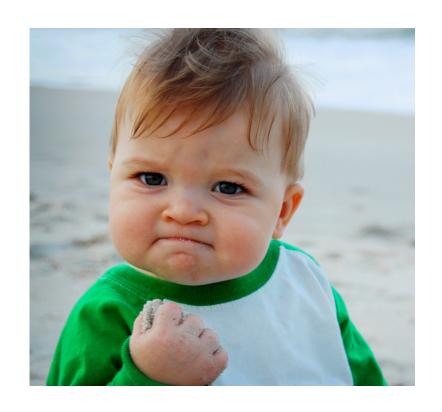




Model summary

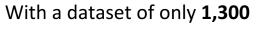
Our CNN correctly identifies 96% of infected cells in an instant!





Comparison to Previous Work

Smaller Dataset

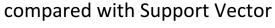




images, overfitting was highly likely.

Comparison:SVM

The results from the CNN were



Machine(SVM) (92% accuracy).

98% Accuracy

Higher accuracy could be due to higher image resolutions and more computationally intensive CNNs

PROBLEM

(GoogleNet)





Larger Dataset

Our dataset was 20 times larger, which is more representative and makes overfitting less likely.

Comparison: Logistic Regression

We first used logistic regression and then feature engineering on our dataset, and compared the results to CNN.

93% Accuracy

With an accuracy of 93% and sensitivity of 96%, we believe that this model is suitable for practical use.

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Limitations of our work



Trade-off between accuracy and computational power



Model cannot differentiate between malignant and benign infections



Limited computational power



Time constraints



Binary results

Conclusion

Automated Diagnosis

With automated diagnosis through CNN, we no longer have to rely on the experience of laboratorians.

Fewer Deaths

All this will lead to a reduction in the number of worldwide malaria-related deaths annually.



Higher Accuracy

Diagnoses will be more accurate, even in areas which are unfamiliar with the disease

Fewer false +/-

With fewer false positives and negatives, we avoid overprescription and delayed medication, which are major causes of malaria-related deaths.

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Thanks for your attention.