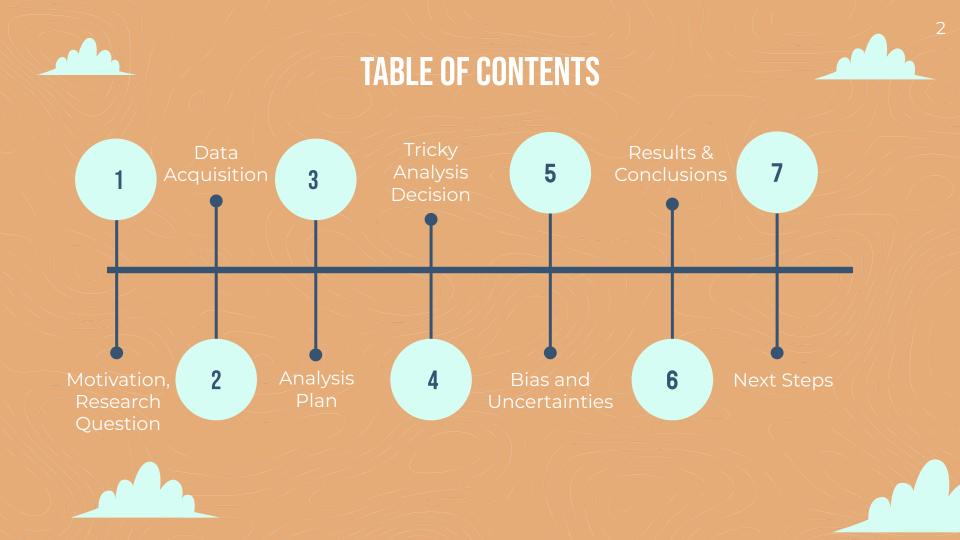


Group 7: Alex Smithgall (Leader), Andre Chuabio, Sam Rea

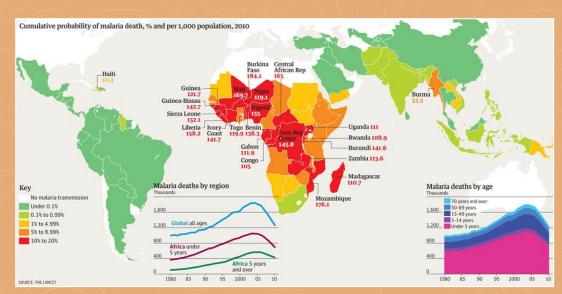
DS 4002 4/23/24





BACKGROUND

- 94% of Malaria cases, 95% of deaths in Sub-Saharan Africa
 - "Getting treatment early for mild malaria can stop the infection from becoming severe"
- Identifiable through
 Microscopy reading a
 blood smear, hard to do in
 rural areas
- Africa: many healthcare workers with limited training, RDTs potentially unreliable



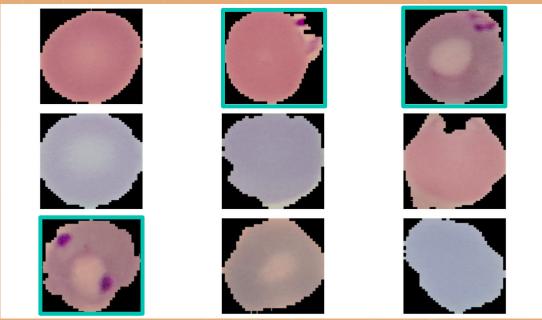


OUTLINE

Research Question	What level of specificity can we achieve in classifying malaria cells using deep learning algorithms?
Hypothesis	We will be able to identify cells infected with malaria with 95% accuracy
Approach	We will use TensorFlow and the Keras package in R to train a neural network image classification model, which will determine if cells are infected or not



DATA ACQUISITION



27,558 images, 2988x5312 JPEGs: 50/50 Parasitized/Uninfected
Official source is NIH but found tidier version on Kaggle (organized by subfolder)





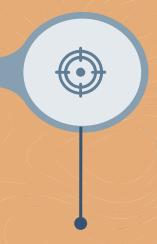
Establish Dataset: data, split into train/tes.



resolution, standardize



Modeling: Classification with 25



Evaluation: >0.95



TRICKY ANALYSIS DECISION

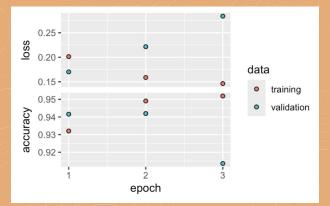


ISSUE

- Balancing between image resolution and time to run model
- How many Epochs to run the model

SOLUTION

- Compromised at 256x256 pixels (blurrier)
- Ran 25 epochs to reduce variability







BIAS AND UNCERTAINTY EVALUATION

CELL SELECTION

- Quality of cell images dependant on the preparer
- Possible false negatives due to low Malaria incidence

MODEL OVERFITTING

- Volatility in validation accuracy could increase validation split
- Used dropout layer to reduce overfitting

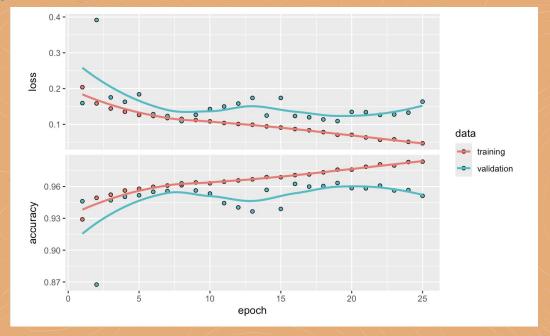




RESULTS

ACCURACY: 0.9834 (TRAINING), ~0.95 (TESTING)

```
Epoch 1/25
689/689 F===
          ========= ] - 9893s 14s/step - loss: 0.2038 - accuracy: 0.9290
l_accuracy: 0.9461
Epoch 2/25
689/689 F===
        l_accuracy: 0.8675
Epoch 3/25
l_accuracy: 0.9470
Epoch 4/25
l_accuracy: 0.9503
Epoch 5/25
l_accuracy: 0.9517
Epoch 21/25
689/689 [======== ] - 9528s 14s/step - loss: 0.0634 - accuracy: 0.9786
val_loss: 0.1341 - val_accuracy: 0.9583
Epoch 22/25
689/689 [=======] - 9406s 14s/step - loss: 0.0568 - accuracy: 0.9809
val_loss: 0.1265 - val_accuracy: 0.9608
Epoch 23/25
689/689 [========= ] - 9637s 14s/step - loss: 0.0581 - accuracy: 0.9798
val_loss: 0.1276 - val_accuracy: 0.9563
Epoch 24/25
val_loss: 0.1327 - val_accuracy: 0.9566
Epoch 25/25
val_loss: 0.1635 - val_accuracy: 0.9512
```



NEXT STEPS



CONDUCT REAL-LIFE SAMPLES



REDUCE OVERFITTING

(Gather more data, run more epochs, experiment with resolution scaling)



LOOK INTO MORE IN-DEPTH CLASSIFICATION

REFERENCES

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[2] "TensorFlow for R - Image classification from scratch." Accessed: Apr. 12, 2024. [Online]. Available: https://tensorflow.rstudio.com/examples/image_classification_from_scrat

[3] "Fact sheet about malaria." Accessed: Apr. 21, 2024. [Online]. Available: https://www.who.int/news-room/fact-sheets/detail/malaria

[4] P. J. Rosenthal, "How Do We Best Diagnose Malaria in Africa?," Am J Trop Med Hyg, vol. 86, no. 2, pp 192–193, Feb. 2012, doi: 10.4269/ajtmh.2012.11-0619.

[5] J. B. Parr *et al.*, "Analysis of false-negative rapid diagnostic tests for symptomatic malaria in the Democratic Republic of the Congo," *Sci Rep*, vol. 11, no. 1, p. 6495, Mar. 2021, doi: 10.1038/s41598-021-85913-z

Project GitHub: https://github.com/samrea5/Project-3-Identifying-Malaria-Infections-with-Image-Classification/tree/main

