# NDEV84212

Bsc Hons Data Science: Project Presentation

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# Problem Statement

- About 90% of all malaria deaths in the world today occur in Africa south of the Sahara.
- The majority of infections in Africa are caused by Plasmodium falciparum.
- Identifying parasite species and their stage is very important in scutinizing the properties of malaria
- The process is labor intensive and time consuming

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## Why is it a data science problem

- The problem requires a machine to diagnose a disease based on microscope images of bacilli.
- A data science problem is a problem that involves data miing, cleaning and predictive modelling while also providing insights, recommendations and classifications in the process.

## Why the solution requires the skills of a data scientist

- The end result is to have a working model that has been trained to accurately recognise different bacilli.
- The process involves data gymnastics, and flexibility through complex matrix computations and manipulations.

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# Role of Maths

The convolution of two functions, $f(t)$ and $g(t)$, is given by:

$$(f * g)(t) = \int_{-\infty}^{\infty} f(\tau)g(t-\tau)d\tau$$

In discrete time, this is given by:

$$(f * g)(n) = \sum_{m=-\infty}^{\infty} f(m)g(n-m)$$

Note, however, that in general CNNs don't use *convolution*, but instead use *cross-correlation*. Colloquially, instead of "flip-and-drag," CNNs just "drag." For real-valued functions, cross-correlation is defined by:

$$(f \star g)(n) = \sum_{m=-\infty}^{\infty} f(m)g(n+m)$$

We'll follow the field's convention and call this operation convolution.

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The 2D convolution (formally: cross-correlation) is given by:

$$(f * g)(i,j) = \sum_{m=-\infty}^{\infty} \sum_{n=-\infty}^{\infty} f(m,n)g(i+m, j+n)$$

This generalizes to higher dimensions as well. Note also: these “convolutions” are not commutative.

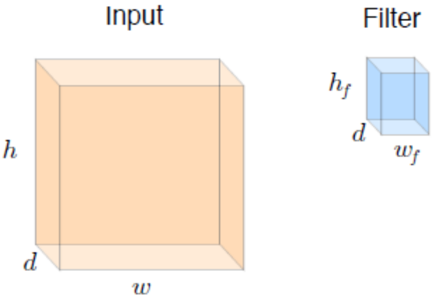
Example: Note, we assume that outside of each grid are zero values (that are not drawn). Now, dragging across the top row, we get:

$$\begin{array}{|c|c|c|}\hline 1 & 1 & 1 \\ \hline 1 & 1 & 1 \\ \hline 1 & 1 & 1 \\ \hline \end{array} * \begin{array}{|c|c|}\hline w & x \\ \hline y & z \\ \hline \end{array} = \begin{array}{|c|c|c|c|}\hline z & y+z & y+z & y \\ \hline & & & \\ \hline & & & \\ \hline & & & \\ \hline \end{array}$$

# Convolutional Layer

This convolution operation (typically in 3D, since images often come with a width and height as well as *depth* for the R, G, B channels) defines the "convolutional layer" of a CNN. The convolutional layer defines a collection of filters (or activation maps), each with the same dimension as the input.

- Say the input was of dimensionality $(w, h, d)$.
- Say the filter dimensionality is $(w_f, h_f, d)$. So that the filter operates on a small region of the input, typically $w_f < w$.
- The depths being equal means that the output of this convolution operation is 2D.



# Data Acquisition

## Data Sources

- The data was acquired from **AI research**: "air.ug/microscopy/"
- It is structured since the data consists of images and annotations.
- The data classifies as big data since each category of disease consists of over 2000 images, each image consisting of multiple bounding boxes in order to indicate parasites and bacilli.

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# Data Architecture

A one-off customized adapter for any camera and microscope combination is created in order to capture the images from the microscope.

*Image capture in progress at Mulago National Referral Hospital*

The captured images then preprocessed, before being fed to a model, annotations need to be made.

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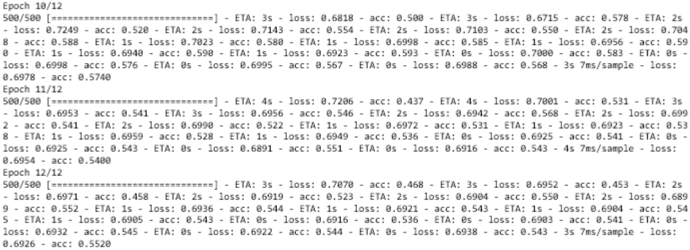
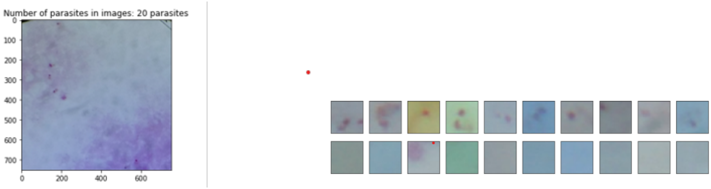
# Data Analysis

## Model Performance

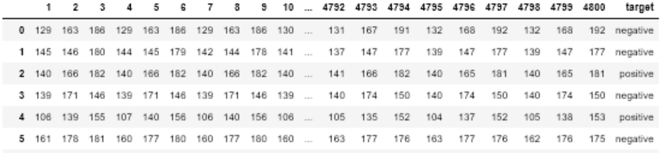


```
Epoch 10/12
500/500 [==============================] - ETA: 3s - loss: 0.6818 - acc: 0.500 - ETA: 3s - loss: 0.6715 - acc: 0.578 - ETA: 2s
- loss: 0.7249 - acc: 0.520 - ETA: 2s - loss: 0.7143 - acc: 0.554 - ETA: 2s - loss: 0.7103 - acc: 0.550 - ETA: 2s - loss: 0.704
8 - acc: 0.588 - ETA: 1s - loss: 0.7023 - acc: 0.580 - ETA: 1s - loss: 0.6998 - acc: 0.585 - ETA: 1s - loss: 0.6956 - acc: 0.59
0 - ETA: 1s - loss: 0.6940 - acc: 0.590 - ETA: 1s - loss: 0.6923 - acc: 0.593 - ETA: 0s - loss: 0.7000 - acc: 0.583 - ETA: 0s -
loss: 0.6998 - acc: 0.576 - ETA: 0s - loss: 0.6995 - acc: 0.567 - ETA: 0s - loss: 0.6988 - acc: 0.568 - 3s 7ms/sample - loss:
0.6978 - acc: 0.5740
Epoch 11/12
500/500 [==============================] - ETA: 4s - loss: 0.7206 - acc: 0.437 - ETA: 4s - loss: 0.7001 - acc: 0.531 - ETA: 3s
- loss: 0.6953 - acc: 0.541 - ETA: 3s - loss: 0.6956 - acc: 0.546 - ETA: 2s - loss: 0.6942 - acc: 0.568 - ETA: 2s - loss: 0.699
2 - acc: 0.541 - ETA: 2s - loss: 0.6990 - acc: 0.522 - ETA: 1s - loss: 0.6972 - acc: 0.531 - ETA: 1s - loss: 0.6923 - acc: 0.53
8 - ETA: 1s - loss: 0.6959 - acc: 0.528 - ETA: 1s - loss: 0.6949 - acc: 0.536 - ETA: 0s - loss: 0.6925 - acc: 0.541 - ETA: 0s -
loss: 0.6925 - acc: 0.543 - ETA: 0s - loss: 0.6891 - acc: 0.551 - ETA: 0s - loss: 0.6916 - acc: 0.543 - 4s 7ms/sample - loss:
0.6954 - acc: 0.5400
Epoch 12/12
500/500 [==============================] - ETA: 3s - loss: 0.7070 - acc: 0.468 - ETA: 3s - loss: 0.6952 - acc: 0.453 - ETA: 2s
- loss: 0.6971 - acc: 0.458 - ETA: 2s - loss: 0.6919 - acc: 0.523 - ETA: 2s - loss: 0.6904 - acc: 0.550 - ETA: 2s - loss: 0.689
9 - acc: 0.552 - ETA: 1s - loss: 0.6936 - acc: 0.544 - ETA: 1s - loss: 0.6921 - acc: 0.543 - ETA: 1s - loss: 0.6904 - acc: 0.54
5 - ETA: 1s - loss: 0.6905 - acc: 0.543 - ETA: 0s - loss: 0.6916 - acc: 0.536 - ETA: 0s - loss: 0.6903 - acc: 0.541 - ETA: 0s -
loss: 0.6932 - acc: 0.545 - ETA: 0s - loss: 0.6922 - acc: 0.544 - ETA: 0s - loss: 0.6938 - acc: 0.543 - 3s 7ms/sample - loss:
0.6926 - acc: 0.5520
```



**(a)** Parasites

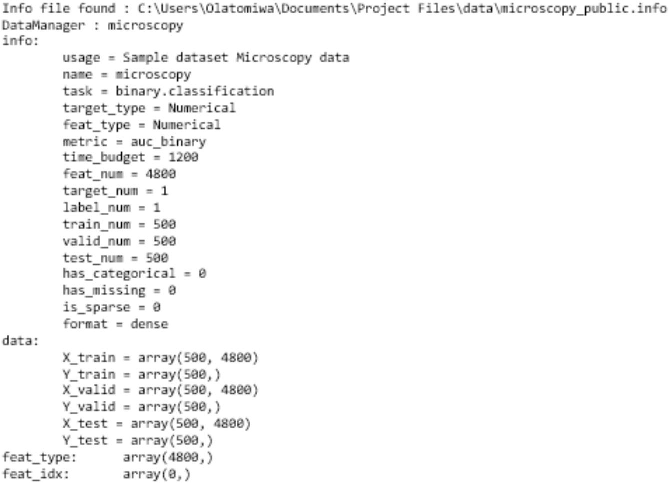
## The Data



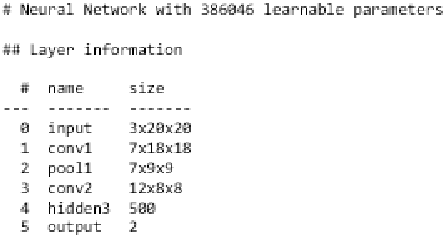
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | ... | 4792 | 4793 | 4794 | 4795 | 4796 | 4797 | 4798 | 4799 | 4800 | target |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | 129 | 163 | 186 | 129 | 163 | 186 | 129 | 163 | 186 | 130 | ... | 131 | 167 | 191 | 132 | 168 | 192 | 132 | 168 | 192 | negative |
| 1 | 145 | 146 | 180 | 144 | 145 | 179 | 142 | 144 | 178 | 141 | ... | 137 | 147 | 177 | 139 | 147 | 177 | 139 | 147 | 177 | negative |
| 2 | 140 | 166 | 182 | 140 | 166 | 182 | 140 | 166 | 182 | 140 | ... | 141 | 166 | 182 | 140 | 165 | 181 | 140 | 165 | 181 | positive |
| 3 | 139 | 171 | 146 | 139 | 171 | 146 | 139 | 171 | 146 | 139 | ... | 140 | 174 | 150 | 140 | 174 | 150 | 140 | 174 | 150 | negative |
| 4 | 106 | 139 | 155 | 107 | 140 | 156 | 106 | 140 | 156 | 106 | ... | 105 | 135 | 152 | 104 | 137 | 152 | 105 | 138 | 153 | positive |
| 5 | 161 | 178 | 181 | 160 | 177 | 180 | 160 | 177 | 180 | 160 | ... | 163 | 177 | 176 | 163 | 177 | 176 | 162 | 176 | 175 | negative |

+ The Dataset stores an array with each row corresponding to a vectorized feature for each image.
+ Converting the 2d feature vector into one or more 1D feature vectors
+ The number of rows equal the number of images.

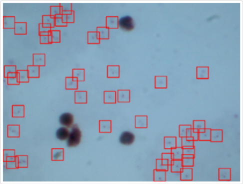
# Pre-processing



```
Info file found : C:\Users\Olatomiwa\Documents\Project Files\data\microscopy_public.info
DataManager : microscopy
info:
        usage = Sample dataset Microscopy data
        name = microscopy
        task = binary.classification
        target_type = Numerical
        feat_type = Numerical
        metric = auc_binary
        time_budget = 1200
        feat_num = 4800
        target_num = 1
        label_num = 1
        train_num = 500
        valid_num = 500
        test_num = 500
        has_categorical = 0
        has_missing = 0
        is_sparse = 0
        format = dense
data:
        X_train = array(500, 4800)
        Y_train = array(500,)
        X_valid = array(500, 4800)
        Y_valid = array(500,)
        X_test = array(500, 4800)
        Y_test = array(500,)
feat_type:      array(4800,)
feat_idx:       array(0,)
```



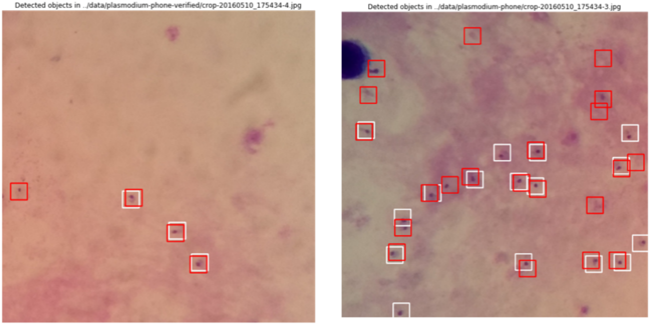
```
# Neural Network with 386046 learnable parameters

## Layer information

  #  name     size
---  -------  -------
  0  input    3x20x20
  1  conv1    7x18x18
  2  pool1    7x9x9
  3  conv2    12x8x8
  4  hidden3  500
  5  output   2
```



*Detection of plasmodium falciparum in thick blood smear image.*

**(a)** Model Parameters and the Image

# Predictions


Detected objects in ../data/plasmodium-phone-verified/crop-20160510_175434-4.jpg
Detected objects in ../data/plasmodium-phone/crop-20160510_175434-3.jpg

**(a)** Parasites Predictions

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