## Capstone Project **Malaria Detection**



Final Report

## Executive Summary

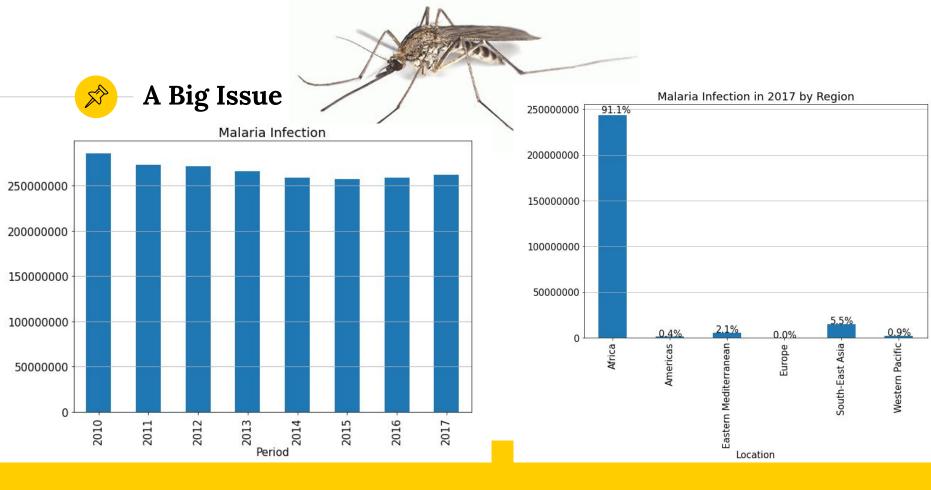
MALARIA DETECTION



## **Defining the Problem**

### **MALARIA**

• Is caused by **Plasmodium parasites** transmitted to humans through the bites of infected female Anopheles mosquitoes.



## 229,000,000

Malaria cases

400,000

Malaria related deaths

in

2019



Working at 60 cases/hour a doctor will clear only

## 120,000 cases/yr

he will need to work

## 1,900 years

to clear all the cases in

In

## 2019

alone



A single computer working at a rate of

# 60,000 cases/hr

## 201 days

Saving approximately

## \$380 Million

and potentially

400,000 lives



# Problem and Solution Summary



## **Proposed Approach**

### **POTENTIAL TECHNIQUES**

An **automated system** can help with the early and accurate detection of malaria. Applications of automated classification techniques using Machine Learning (ML) and Artificial Intelligence (AI) have consistently shown higher accuracy than manual classification. It would therefore be highly beneficial to propose a method that performs malaria detection using **Deep Learning Algorithms**.

#### **OVERALL SOLUTION DESIGN**

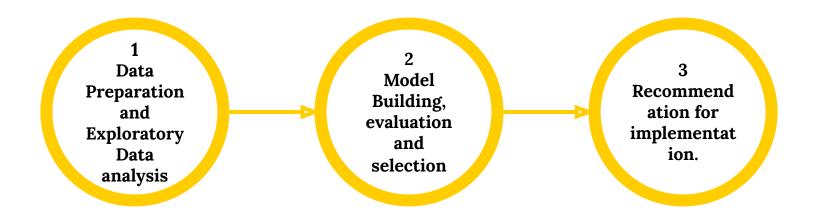
We will be using building a **convolution neural network (CNN) model** to classify between infected and non-infected blood cell samples from the images. This is a binary classification problem so we will be using a sigmoid activation function. Our process will be **Data Preparation > Exploratory Data analysis > Model Building > Model evaluation > Model selection > Summary of potential benefits > Recommendation for implementation.** 

#### **MEASURES OF SUCCESS**

We will attempt various models and **test accuracy with a loss score**. We will also use a 20% validation split for each model to see if training and validation accuracy improve together to determine if the model is overfitting.



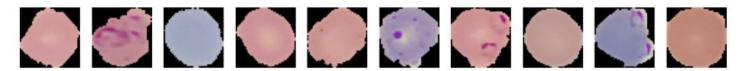
## **Proposed Approach**



See appendix detailed slides of steps 1 & 2. We will look at the second half of steps 2 and 3 today.



#### PRINTING OUT SOME OF THE IMAGES AND LOOKING AT THE ASSOCIATED LABELS - AND IT'S CORRECTLY LABELLED



label for each of the above image: [0 1 0 0 0 1 1 0 1 0]

- . We print out a random set of images and compared with the labels and they correspond.
- Next we will take a look at the dataset and check the shape it should be 4D arrays and should not need to be further reshaped.

Training set: (24958, 224, 224, 3) (24958,) Test set: (2600, 224, 224, 3) (2600,)

## NEXT WE CHECK TO SEE IF OUR DATA IS BALANCED BETWEEN POSITIVE AND NEGATIVE CASES AND WE SEE THAT WE HAVE AN EQUAL NUMBER OF POSITIVE AND NEGATIVE CASES

Positive cases in the training set : 12479 Negative cases in the training set : 12479 Positive cases in the test set : 1300 Negative cases in the test set : 1300



#### **MODEL COMPARISONS**

We did 4 Convolutional Neural Network models and saw the results progressive improved. Let's compare the models to evaluate various techniques and each model's performance. We used the Leaky Relu activation function for the hidden layers and a Sigmoid activation function for the output layer. Below we see the adjustments we made for each model.

CNN Model 1
Sequential Model
Layer 1 16 nodes
Layer 2 32 nodes
Max Pooling Layer
Flatten
Dense Layer 32 node

### es Sigmoid Activation

## **CNN Model2** Sequential Model Layer 1 16 nodes + 20% Dropout Layer Layer 2 32 nodes + 20% Dropout Layer Max Pooling Laver Flatten Dense Layer 32 nodes +50% Dropout Layer.

Sigmoid Activation

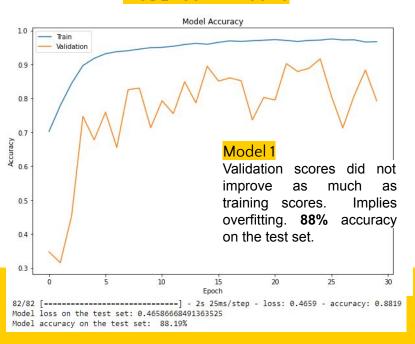
#### **CNN Model3 CNN Model4** Sequential Model Sequential Model Laver 1 16 nodes Laver 1 16 nodes + 32 Node Laver + 20% Dropout Layer + Max Pooling Laver 32 Node Layer + 25% Dropout Layer Layer 2 32 nodes + 64 Node Laver + 25% Dropout Layer Max Pooling Layer Flatten Dense Layer 32 nodes

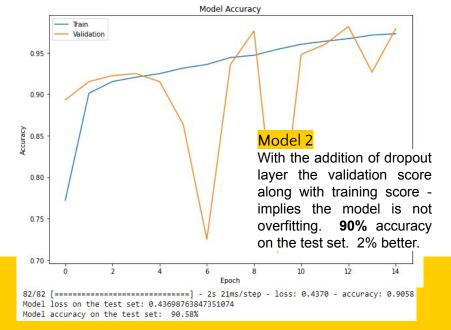
50% Dropout Laver

Sigmoid Activation

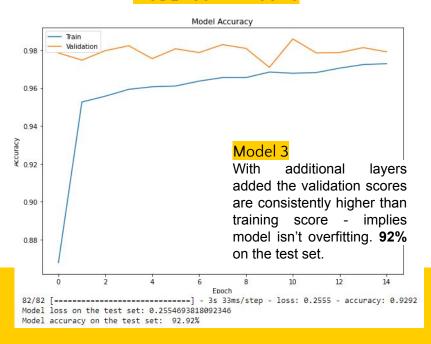
## + 64 nodes + 20% Dropout Layer Max Pooling Layer Flatten Dense Laver 32 nodes +50% Dropout Laver Sigmoid Activation

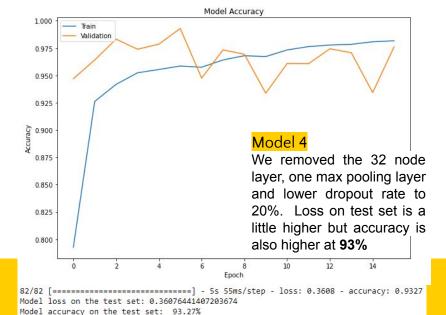














#### **MODEL COMPARISONS**

We did 2 Hyperparameter tuned **Convolutional Neural Network** models and 2 transfer learning models. The model architectures are informed by hyperparameter tuning methods and the improved iteratively based on the results. Let's compare the models to evaluate various techniques and each model's performance.

Random Search	<b>Bayesian Optimazation</b>	Transfer Learning	<b>Bayesian / Transfer Learning</b>
Sequential Model	Sequential Model	Sequential Model	Sequential Model
Layer 1 112 nodes	Layer 1 128 nodes		
+ 30% Dropout Layer	+ 40% Dropout Layer	VGG16 Model	VGG16 Model
Layer 2 160 nodes	Layer 2 160 nodes		
+ Max Pooling Layer	+ Max Pooling Layer	Flatten	Flatten
+ 30% Dropout Layer	+ 40% Dropout Layer		
Layers 3 & 4 32 nodes	Layers 3 & 4 32 nodes	Dense Layer 32 nodes	Dense Layer 112 nodes
+ Max Pooling Layer	+ Max Pooling Layer	30% Dropout Layer	20% Dropout Layer
+ 30% Dropout Layer	+ 40% Dropout Layer	Sigmoid Activation	Sigmoid Activation

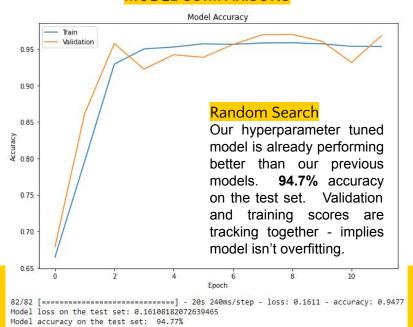
Dense Layer 112 nodes 30% Dropout Layer Sigmoid Activation

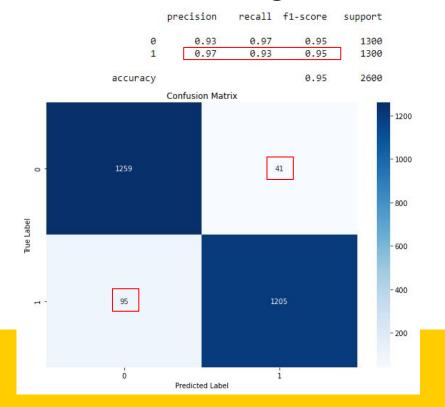
Flatten

Dense Layer 128 nodes 40% Dropout Layer Sigmoid Activation

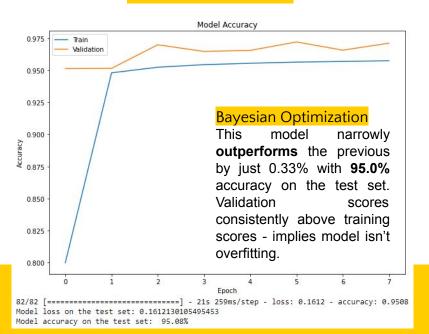
Flatten

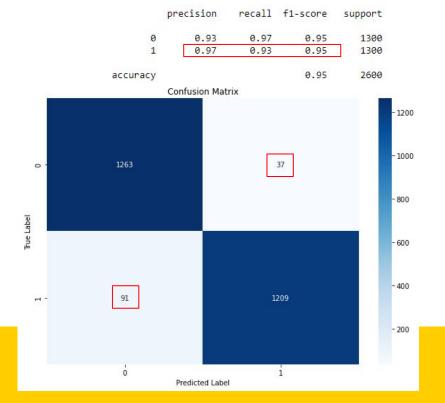






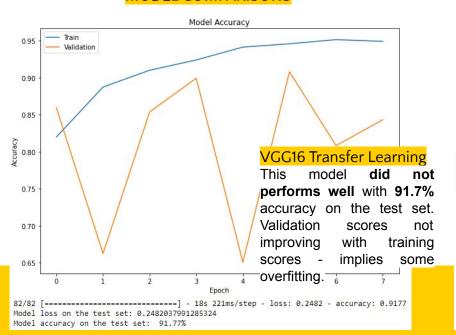


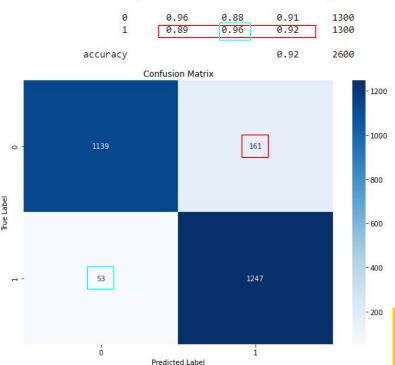






#### **MODEL COMPARISONS**

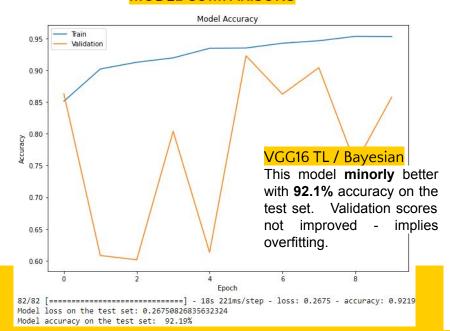


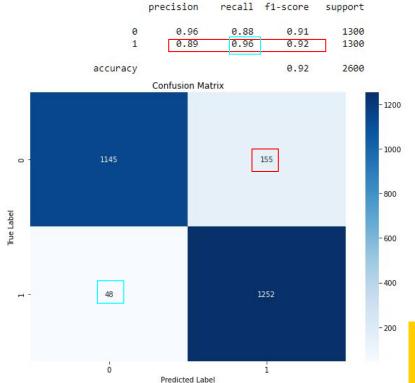


precision

recall f1-score support





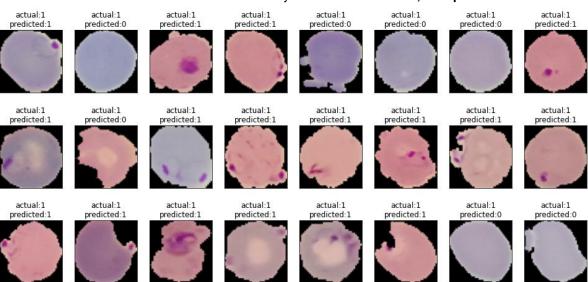




## **Model Choice**

### **BAYESIAN OPTIMIZED MODEL (THE 2nd MODEL)**

Overall it is the most effective model with a accuracy rate with a 93% recall, 97% precision and 95% f1-score on the test set.



## Recommendations for Implementation



## Conclusion

#### **BENEFITS AND RECOMMENDATIONS**

- We've built an automated system can help with the early and accurate detection of malaria using a Neural Network automated classification techniques and evaluated our models through validation and test scores against actual labels.
- We noted that it can **significantly reduce the time** for addressing the problem significantly from **1,900 years** to just **201 days** taking on 2019's caseload.
- It presents a cost savings of approximately \$380 million dollars a year in man hours.
- Most importantly, it can save lives. Potentially 400,000 lives in 2019 alone.

#### **IMPLEMENTATION**

- The model requires images to be taken in a color format that can be converted to 64x64 image.
- It is recommended that a physician or trained health professional examine the scan following detection of malaria infection by the model to confirm accuracy of diagnosis.
- The model should be periodically retrained with new data to maintain accuracy.

## 4 — Appendix



## **Data Exploration**

#### DATA DESCRIPTION

There are a total of **24,958** train and **2,600** test images (colored) with **an equal number** of parasitized and uninfected instances, where:

- The parasitized cells contain the Plasmodium parasite
- The uninfected cells are free of the Plasmodium parasites but could contain other impurities

#### PREPPING THE DATASET

- The original dataset is available as .png files organized in folders.
- Since the data is already split into train and the test dataset in respective folders and further split into parasitized and uninfected folders. We will need to import from our folders and prep.
- We will convert all images to the same size and to 4D arrays so that they can be used as an input for the
  convolutional neural network. Then we will need to create the labels for both types of images to be able to
  train and test the model.

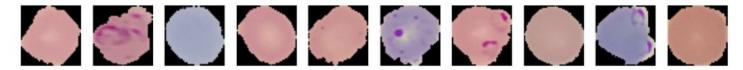


## **Data Exploration**

```
#We will run the same code for "parasitized" as well as "uninfected" folders within the "train" folder
                    for folder_name in ['/parasitized/', '/uninfected/']:
                        #Path of the folder
                        images_path = os.listdir(train_dir + folder name)
                        for i, image name in enumerate(images path):
                            try:
                                #Opening each image using the path of that image
LOADING THE IMAGES
                                image = Image.open(train dir + folder name + image name)
                                #Resizing each image to (224,224)
SIZING THE IMAGES
                                image = image.resize((SIZE, SIZE))
                                #Converting images to arrays and appending that array to the empty list defined above
CONVERTING TO AN ARRAY
                                train images.append(np.array(image))
                                #Creating labels for parasitized and uninfected images
ADDING CORRECT LABELS
                                if folder name=='/parasitized/':
                                    train_labels.append(1)
                                else:
                                    train labels.append(0)
                            except Exception:
                                pass
                    #Converting lists to arrays
                    train images = np.array(train images)
                    train labels = np.array(train labels)
```



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label for each of the above image: [0 1 0 0 0 1 1 0 1 0]

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#### **OVERALL SOLUTION DESIGN**

We will be using building a convolution neural network (CNN) model to classify between infected and non-infected blood cell samples from the images. This is a binary classification problem so we will be using a sigmoid activation function.

#### **MEASURES OF SUCCESS**

We will attempt various models and test accuracy with a loss score. We will also use a 20% validation split for each model to see if training and validation accuracy improve together to determine if the model is overfitting.



## **Data Preparation**

#### **OPTIMIZING THE IMAGE SIZE**

As we build our CNN models we learn that we expend much less computational resources by resizing our image from 224x224 to 64x64. Below we compare the 9th and 10th epoch and we can see that the larger image had comparable and even slightly lower accuracy score but took 10 times longer to process. This lead me to build the rest of the models using 64x64 image size.

```
Epoch 9/10
624/624 - 501s - loss: 0.0507 - accuracy: 0.9834 - val_loss: 0.6188 - val_accuracy: 0.8233
Epoch 10/10
624/624 - 502s - loss: 0.0560 - accuracy: 0.9827 - val_loss: 0.7765 - val_accuracy: 0.7841
624/624 - 48s - loss: 0.1621 - accuracy: 0.9404 - val_loss: 0.4836 - val_accuracy: 0.8257
Epoch 9/30
624/624 - 47s - loss: 0.1539 - accuracy: 0.9452 - val_loss: 0.4271 - val_accuracy: 0.8301
Epoch 10/30
```

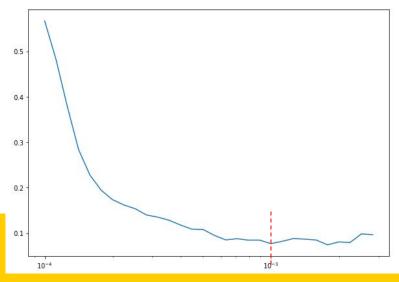


## **Refined Insight**

### **OPTIMIZING THE LEARNING RATE**

Early on in the model building process, we defined a function to test out different learning rates to find the best learning rate for the model. We plotted our learning rate verse the loss and we found that the loss plateaus at 10^-3,

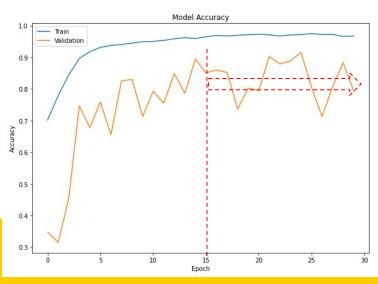
so we used 0.001 as our learning rate.





### **OPTIMIZING THE NUMBER OF EPOCHS**

We also started with a higher number of epochs and plotted accuracy per epoch and we found that our accuracy starts to taper off starting at 15 epochs so we set our model to train up to 15 epochs.





#### **MODEL COMPARISONS**

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+50% Dropout Layer.

Sigmoid Activation

## **CNN Model3** Sequential Model Laver 1 16 nodes + 32 Node Laver + Max Pooling Laver + 25% Dropout Layer Layer 2 32 nodes + 64 Node Laver + 25% Dropout Layer Max Pooling Layer Flatten

Dense Layer 32 nodes 50% Dropout Laver Sigmoid Activation

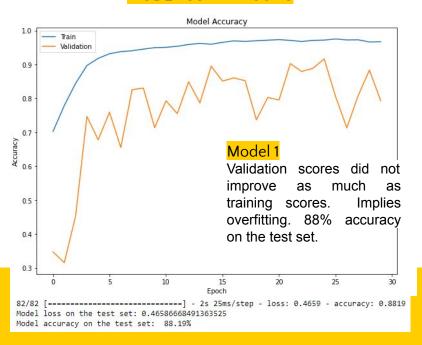
### **CNN Model4**

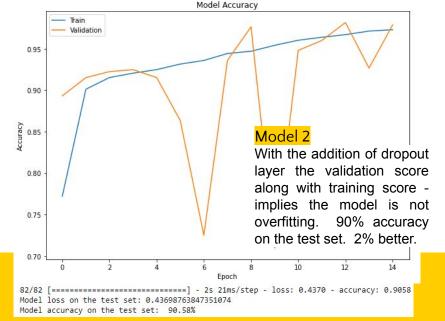
Sequential Model Laver 1 16 nodes + 20% Dropout Layer 32 Node Layer + 64 nodes

+ 20% Dropout Layer Max Pooling Layer Flatten

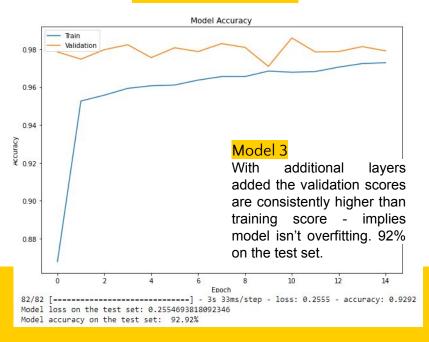
Dense Laver 32 nodes +50% Dropout Laver Sigmoid Activation

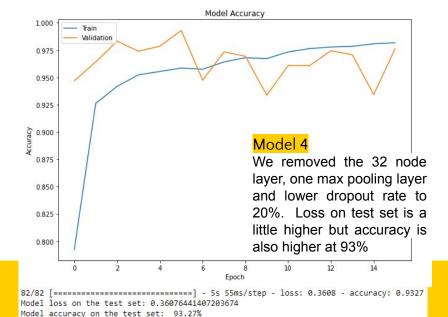








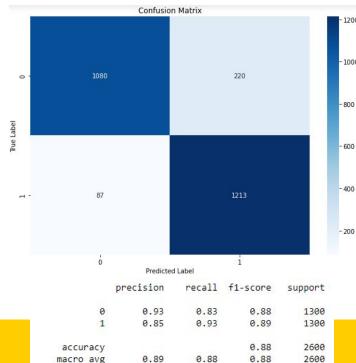






weighted avg

## **Comparison of Various Techniques**



0.89

0.88

0.88

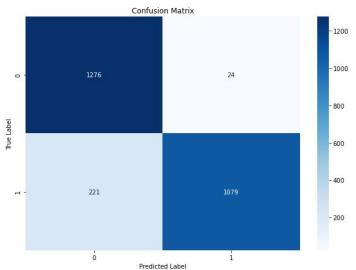
2600

#### Model 1

Since having false negatives would be worse than false positives in malaria detection, we want to emphasize Recall score. This model has 93% recall, 85% precision and 89% f1-score on the test set.

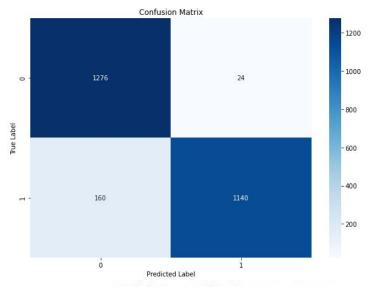
### Model 2

In comparison, model 2 has 83% recall, 98% precision and 90% f1-score. It has much more false negatives than model which is not optimal.



	precision	recall	f1-score	support	
0	0.85	0.98	0.91	1300	
1	0.98	0.83	0.90	1300	
accuracy			0.91	2600	
macro avg	0.92	0.91	0.91	2600	
weighted avg	0.92	0.91	0.91	2600	





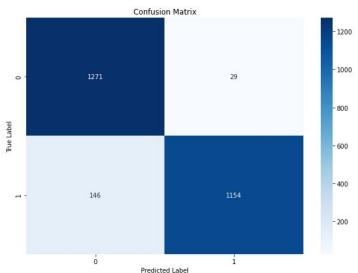
recall f1-score precision 0 0.89 0.98 0.93 1300 0.98 0.88 0.93 1300 0.93 2600 accuracy macro avg 0.93 0.93 0.93 2600 weighted avg 0.93 0.93 0.93 2600

#### Model 3

model 3 has 88% recall, 98% precision and 93% f1-score. It's an improvement on model 2.

### Model 4

model 4 has 89% recall, 98% precision and 93% f1-score. It has a little more false positives but it also has less false negative than model 3, which is a good thing.



	precision	recall	f1-score	support	
0	0.90	0.98	0.94	1300	
1	0.98	0.89	0.93	1300	
accuracy			0.93	2600	
macro avg	0.94	0.93	0.93	2600	
weighted avg	0.94	0.93	0.93	2600	3