

MALARIA DETECTION USING DEEP LEARNING

SMARTBRIDGE AL PROJECT

Team Brogrammers

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Project Introduction

Malaria is a life-threatening disease that is spread by the Plasmodium parasites. It is detected by trained microscopists who analyse microscopic blood smear images. Modern deep learning techniques may be used to do this analysis automatically. The need for the trained personnel can be greatly reduced with the development of an automatic accurate and efficient model. In our project, we have developed an automated convolutional neural network (CNN) based model which shall predict if a person has malaria using the microscopic blood smear images.

Our deep learning-based model can detect malarial parasites from microscopic images with an accuracy of 96.38%. For a practical and real-world application, we have made a website with which our model has been integrated with using flask.

Problem Statement

Implement Deep Learning Techniques to detect malaria using IBM Cloud

Solution

Malaria can be detected by analyzing microscopic blood smear images. This process can be automated by using convolutional neural networks (CNN) model which shall use a training dataset of images to get a high accuracy in prediction as it becomes really important in the field of medicine to get diagnosed properly. We have made a website which allows the user to upload the blood smear image and our model will predict if malaria is detected or not

Literature Survey

1. **Dong, Y., Jiang, Z., Shen, H., Pan, W. D., Williams, L. A., Reddy, V. V., ... & Bryan, A. W. (2017, February). Evaluations of deep convolutional neural networks for automatic identification of malaria infected cells. In *2017 IEEE EMBS international conference on biomedical & health informatics (BHI)* (pp. 101-104). IEEE.**

This paper studied automatic identification of malaria infected cells using deep learning methods. We used whole slide images of thin blood stains to compile an dataset of malaria-infected red blood cells and non-infected cells, as labeled by a group of four pathologists. We evaluated three types of well-known convolutional neural networks, including the LeNet, AlexNet and GoogLeNet. Simulation results showed that all these deep convolution neural networks achieved classification accuracies of over 95%, higher than the accuracy of about 92% attainable by using the support vector machine method. Moreover, the deep learning methods have the advantage of being able to automatically learn the features from the input data, thereby requiring minimal inputs from human experts for automated malaria diagnosis.

2. **Vijayalakshmi, A. (2020). Deep learning approach to detect malaria from microscopic images. *Multimedia Tools and Applications*, 79(21), 15297-15317.**

Malaria is an infectious disease which is caused by plasmodium parasite. Several image processing and machine learning based techniques have been employed to diagnose malaria, using its spatial features extracted from microscopic images. In this work, a novel deep neural network model is introduced for identifying infected falciparum malaria parasite using transfer learning approach. This proposed transfer learning approach can be achieved by unifying existing Visual Geometry Group (VGG) network and Support Vector Machine (SVM). Implementation of this unification is carried out by using “Train top layers and freeze out rest of the layers” strategy. Here, the pre-trained VGG facilitates the role of expert learning model and SVM as domain specific learning model. Initial ‘k’ layers of pre-trained VGG are retained and (n-k) layers are replaced with SVM. To evaluate the proposed VGG-SVM model, a malaria digital corpus has been generated by acquiring blood smear images of infected and non-infected malaria patients and compared with state-of-the-art Convolutional Neural Network (CNN) models. Malaria digital corpus images were used to analyse the performance of VGG19-SVM, resulting in classification accuracy of 93.1% in identification of infected falciparum malaria. Unification of VGG19-SVM shows superiority over the existing CNN models in all performance indicators such as accuracy, sensitivity, specificity, precision and F-Score. The obtained result shows the potential of transfer learning in the field of medical image analysis, especially malaria diagnosis.

3. **Masud, M., Alhumyani, H., Alshamrani, S. S., Cheikhrouhou, O., Ibrahim, S., Muhammad, G., ... & Shorfuzzaman, M. (2020). Leveraging deep learning techniques for malaria parasite detection using mobile application. *Wireless Communications and Mobile Computing*, 2020.**

Malaria is a contagious disease that affects millions of lives every year. Traditional diagnosis of malaria in laboratory requires an experienced person and careful inspection to discriminate healthy and infected red blood cells (RBCs). It is also very time-consuming and may produce inaccurate reports due to human errors. Cognitive computing and deep learning algorithms simulate human intelligence to make better human decisions in applications like sentiment analysis, speech recognition, face detection, disease detection, and prediction. Due to the advancement of cognitive computing and machine learning techniques, they are now widely used to detect and predict early disease symptoms in healthcare field. With the early prediction results, healthcare professionals can provide better decisions for patient diagnosis and treatment. Machine learning algorithms also aid the humans to process huge and complex medical datasets and then analyze them into clinical insights. This paper looks for leveraging deep learning algorithms for detecting a deadly disease, malaria, for mobile healthcare solution of patients building an effective mobile system. The objective of this paper is to show how deep learning architecture such as convolutional neural network (CNN) which can be useful in real-time malaria detection effectively and accurately from input images and to reduce manual labor with a mobile application. To this end, we evaluate the performance of a custom CNN model using a cyclical stochastic gradient descent (SGD) optimizer with an automatic learning rate finder and obtain an accuracy of 97.30% in classifying healthy and infected cell images with a high degree of precision and sensitivity. This outcome of the paper will facilitate microscopy diagnosis of malaria to a mobile application so that reliability of the treatment and lack of medical expertise can be solved.

4. **Poostchi, M., Silamut, K., Maude, R. J., Jaeger, S., & Thoma, G. (2018). Image analysis and machine learning for detecting malaria. *Translational Research*, 194, 36-55.**

Malaria remains a major burden on global health, with roughly 200 million cases worldwide and more than 400,000 deaths per year. Besides biomedical research and political efforts, modern information technology is playing a key role in many attempts at fighting the disease. One of the barriers toward a successful mortality reduction has been inadequate malaria diagnosis in particular. To improve diagnosis, image analysis software and machine learning methods have been used to quantify parasitemia in microscopic blood slides. This article gives an overview of these techniques and discusses the current developments in image analysis and machine learning for microscopic malaria diagnosis. We organize the different approaches published in the

literature according to the techniques used for imaging, image preprocessing, parasite detection and cell segmentation, feature computation, and automatic cell classification. Readers will find the different techniques listed in tables, with the relevant articles cited next to them, for both thin and thick blood smear images. We also discussed the latest developments in sections devoted to deep learning and smartphone technology for future malaria diagnosis.

5. **Shekar, G., Revathy, S., & Goud, E. K. (2020, June). Malaria Detection using Deep Learning. In 2020 4th International Conference on Trends in Electronics and Informatics (ICOEI)(48184) (pp. 746-750). IEEE.**

Malaria is the deadliest disease in the earth and big hectic work for the health department. The traditional way of diagnosing malaria is by schematic examining blood smears of human beings for parasite-infected red blood cells under the microscope by lab or qualified technicians. This process is inefficient and the diagnosis depends on the experience and well knowledgeable person needed for the examination. Deep Learning algorithms have been applied to malaria blood smears for diagnosis before. However, practical performance has not been sufficient so far. This paper proposes a new and highly robust machine learning model based on a convolutional neural network (CNN) which automatically classifies and predicts infected cells in thin blood smears on standard microscope slides. A ten-fold cross-validation layer of the convolutional neural network on 27,558 single-cell images is used to understand the parameter of the cell. Three types of CNN models are compared based on their accuracy and select the precise accurate - Basic CNN, VGG-19 Frozen CNN, and VGG-19 Fine Tuned CNN. Then by comparing the accuracy of the three models, the model with a higher rate of accuracy is acquired.

Experimental Investigation

While working on the solution we investigated on the what is AL and what is ML and how to build models using them and how to do image processing. And mainly we had studied about the CNN because our solution mainly need this so we worked on these aspects.

Artificial Intelligence: Artificial intelligence (AI) is the simulation of human intelligence processes by machines, especially computer systems enabling it to even mimic human behaviour. Its applications lie in fields of Computer Vision, Natural Language Processing, Robotics, Speech Recognition, etc.

Basic Operation of Neural Networks: Neural Networks (NN) form the base of deep learning, a subfield of machine learning where the algorithms are inspired by the structure of the human brain. NN take in data, train themselves to recognize the patterns in this data and then predict the outputs for a new set of similar data. NN are made up of layers of neurons. These neurons are the

core processing units of the network.

Transfer Learning: A major assumption in many machine learning and data mining algorithms is that the training and future data must be in the same feature space and have the same distribution. However, in many real-world applications, this assumption may not hold. For example, we sometimes have a classification task in one domain of interest, but we only have sufficient training data in another domain of interest, where the latter data may be in a different feature space or follow a different data distribution. In such cases, knowledge transfer, if done successfully, would greatly improve the performance of learning by avoiding much expensive data labelling efforts. In recent years, transfer learning has emerged as a new learning framework to address this problem.

Convolutional Neural Network: Classifier models can be basically divided into two categories respectively which are generative models based on hand-crafted features and discriminative models based on traditional learning such as support vector machine (SVM), Random Forest (RF) and Convolutional Neural Network (CNN). One difficulty with methods based on hand-crafted features is that they often require the computation of a large number of features in order to be accurate when used with many traditional machine learning techniques. This can make them slow to compute and expensive memory-wise. More efficient techniques employ lower numbers of features, using dimensionality reduction like PCA (Principle Component Analysis) or feature selection methods, but the reduction in the number of features is often at the cost of reduced accuracy. Brain tumor segmentation employ discriminative models because unlike generative modelling approaches, these approaches exploit little prior knowledge on the brain's anatomy and instead rely mostly on the extraction of [a large number of] low level image features, directly modelling the relationship between these features and the label of a given voxel.

Activation Function: Sigmoid function ranges from 0 to 1 and is used to predict probability as an output in case of binary classification while Softmax function is used for multi-class classification. tanh function ranges from -1 to 1 and is considered better than sigmoid in binary classification using feed forward algorithm. ReLU (Rectified Linear Unit) ranges from 0 to infinity and Leaky ReLU (better version of ReLU) ranges- from -infinity to +infinity. ReLU

stands for Rectified Linear Unit for a non-linear operation.

The output is $f(x) = \max(0, x)$. ReLU's purpose is to introduce non-linearity in our ConvNet. Since, the real world data would want our ConvNet to learn would be non-negative linear values. There are other nonlinear functions such as tanh or sigmoid that can also be used instead of ReLU. Most of the data scientists use ReLU since performance wise ReLU is better than the other two. Stride is the number of pixels that would move over the input matrix one at a time. Sometimes filter does not fit perfectly fit the input image. We have two options: either pad the picture with zeros (zero-padding) so that it fits or drop the part of the image where the filter did not fit. This is called valid padding which keeps only valid part of the image.

Hardware and Software Requirements

Hardware

Processor: Intel® Core™ i3-2350M CPU @ 2.30GHz

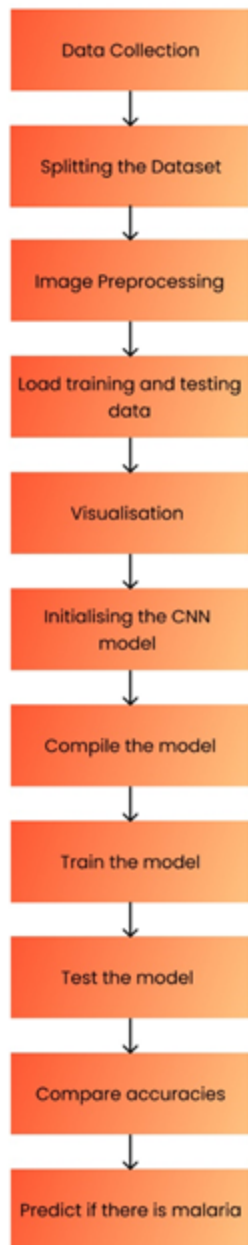
Installed memory (RAM) 4.00GB

System Type: 64-bit Operating System

Software

- Python-3 (with libraries like keras, numpy, pandas, opencv, matplotlib, tensorflow)
- HTML
- CSS
- Bootstrap
- Flask
- IBM Cloud
- IBM Watson Studio
- Spyder
- Jupyter Notebook

Flowchart



Conclusion

We were successfully able to predict if a person has malaria using the model we created.

We integrated the CNN model with the website we created for ease of use.

The testing and validation accuracy were quite commendable (96.38%) and the predictions were always correct for as many times we tried. We trained our model for epochs to get the best and most accurate results.

Results

Model

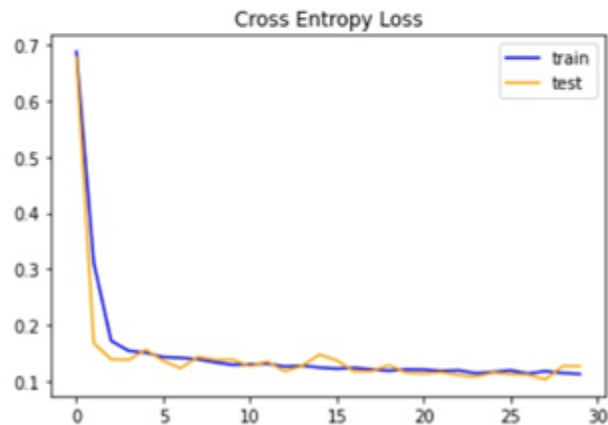
```
Epoch 14/30
344/344 [=====] - 387s 1s/step - loss: 0.1271 - acc: 0.9595 - val_loss: 0.1269 - val_acc: 0.9602
Epoch 15/30
344/344 [=====] - 391s 1s/step - loss: 0.1237 - acc: 0.9615 - val_loss: 0.1469 - val_acc: 0.9602
Epoch 16/30
344/344 [=====] - 391s 1s/step - loss: 0.1218 - acc: 0.9617 - val_loss: 0.1365 - val_acc: 0.9615
Epoch 17/30
344/344 [=====] - 389s 1s/step - loss: 0.1231 - acc: 0.9609 - val_loss: 0.1167 - val_acc: 0.9618
Epoch 18/30
344/344 [=====] - 391s 1s/step - loss: 0.1202 - acc: 0.9606 - val_loss: 0.1173 - val_acc: 0.9635
Epoch 19/30
344/344 [=====] - 390s 1s/step - loss: 0.1180 - acc: 0.9622 - val_loss: 0.1280 - val_acc: 0.9622
Epoch 20/30
344/344 [=====] - 385s 1s/step - loss: 0.1203 - acc: 0.9611 - val_loss: 0.1144 - val_acc: 0.9613
Epoch 21/30
344/344 [=====] - 386s 1s/step - loss: 0.1202 - acc: 0.9617 - val_loss: 0.1128 - val_acc: 0.9617
Epoch 22/30
344/344 [=====] - 384s 1s/step - loss: 0.1176 - acc: 0.9626 - val_loss: 0.1155 - val_acc: 0.9606
Epoch 23/30
344/344 [=====] - 386s 1s/step - loss: 0.1186 - acc: 0.9607 - val_loss: 0.1102 - val_acc: 0.9624
Epoch 24/30
344/344 [=====] - 385s 1s/step - loss: 0.1137 - acc: 0.9631 - val_loss: 0.1072 - val_acc: 0.9618
Epoch 25/30
344/344 [=====] - 385s 1s/step - loss: 0.1159 - acc: 0.9619 - val_loss: 0.1148 - val_acc: 0.9622
Epoch 26/30
344/344 [=====] - 386s 1s/step - loss: 0.1190 - acc: 0.9622 - val_loss: 0.1117 - val_acc: 0.9628
Epoch 27/30
344/344 [=====] - 384s 1s/step - loss: 0.1130 - acc: 0.9627 - val_loss: 0.1111 - val_acc: 0.9620
Epoch 28/30
344/344 [=====] - 386s 1s/step - loss: 0.1171 - acc: 0.9613 - val_loss: 0.1025 - val_acc: 0.9620
Epoch 29/30
344/344 [=====] - 385s 1s/step - loss: 0.1142 - acc: 0.9629 - val_loss: 0.1263 - val_acc: 0.9626
Epoch 30/30
344/344 [=====] - 386s 1s/step - loss: 0.1121 - acc: 0.9638 - val_loss: 0.1262 - val_acc: 0.9618
```


Graphs

```
In [23]: # Plotting the accuracies
import matplotlib.pyplot as plt

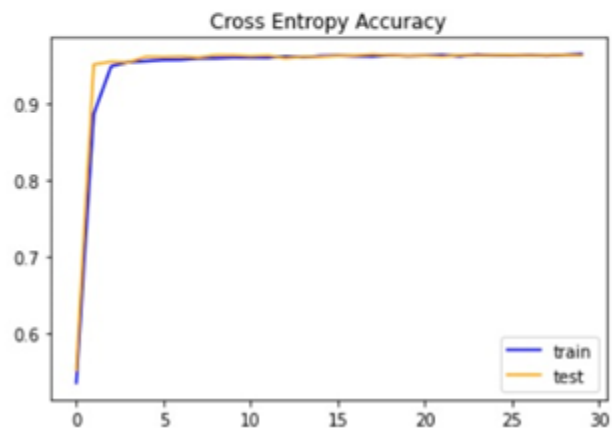
# plot training and testing loss
plt.title('Cross Entropy Loss')
plt.plot(hist.history['loss'], color='blue', label='train')
plt.plot(hist.history['val_loss'], color='orange', label='test')
plt.legend()
```

Out[23]: <matplotlib.legend.Legend at 0x7f627508fe90>



```
In [25]: # plot training and testing accuracy
plt.title('Cross Entropy Accuracy')
plt.plot(hist.history['acc'], color='blue', label='train')
plt.plot(hist.history['val_acc'], color='orange', label='test')
plt.legend()
```

Out[25]: <matplotlib.legend.Legend at 0x7f6257e8d8d0>



Website

Malaria Detection using DL

[About](#)[Prevention](#)[Predict](#)

Know more about Malaria, how to prevent it and its prediction

Bites can kill



- ✓

Asymptomatic malaria
Caused by all Plasmodium species, the patient has circulating parasites but no symptoms.
- 🎯

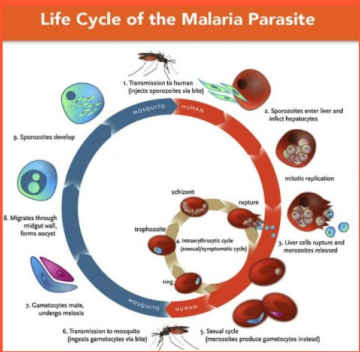
Complications
Severe anaemia and end-organ damage, coma, pulmonary complications and hypoglycaemia
- 💖

Take help
Consult your doctor and follow prescribed medicines

Use a mosquito net over the bed if your bedroom is not air-conditioned or screened. Treat the mosquito net with the insecticide permethrin. Spray an insecticide or repellent on clothing, as mosquitoes may bite through thin clothing.



Can Malaria Be Prevented?



Can Malaria Be Prevented?

Easy way to predict malaria using deep learning techniques



© Copyright 2021 Malaria Detection

Apply insect repellent to exposed skin. The recommended repellent contains 20-35% percent N,N-Diethyl-meta-toluamide (DEET). Wear long-sleeved clothing and long pants if you are outdoors at night.



Stay safe

Can Malaria Be Prevented?

Check whether the person is infected with malaria or not

Interactive, simple and quick way to predict malaria

PREDICTION

Upload image and check whether it is infected or not with malaria



The prediction is : uninfected

Check whether the person is infected with malaria or not

Interactive, simple and quick way to predict malaria

PREDICTION

Upload image and check whether it is infected or not with malaria



The prediction is : infected

Future Scope

This project presents convolutional model for malaria parasite detection which takes into consideration not only classification accuracy but also aim to be computationally efficient.

This model can be used in hospitals along with other disease diagnosing algorithms or models in a combined interface for easy, automated and early detection of diseases. This will not only help the doctors efficiently diagnose and treat the patients, but is also efficient in terms of time. One can increase the number of epochs or the dataset size and use appropriate layers to get a more accurate model with next to none error.

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