Group 4: Malaria Cell Image Recognition

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Motivation

- Malaria is a blood disease caused by the *Plasmodium* parasites transmitted through the bite of female Anopheles mosquito. However, the accuracy of using microscope depends on smear quality and expertise in classifying and counting parasitized and uninfected cells. Such an examination could be arduous for large-scale diagnoses resulting in poor quality. By adopting machine learning techniques, the efficiency and accuracy of diagnosing malaria could be improved, which is of great significance for poor areas.
- Using dataset from NIH, we implemented machine learning models, including CNN, VGG16, Xception, and ResNet, to train and recognize infected cells, achieving high accuracy over 97%.

Data

- Our dataset is from U.S. National Library of Medicine, collected from 150 infected and 50 healthy patients, containing 27,558 images of various sizes, pre-classified into two folders: parasitized and uninfected.
- We implement data augmentation to increase the dataset from 27,558 to 11,0232 by rotating original image to create new data. We also enhanced the contrast of the RGB image to boost the feature extraction, and manually labeled infected as 1, uninfected as 0. We use 20% data as test set and 20% as evaluation set.
- Source: https://ceb.nlm.nih.gov/repositories/malaria-datasets/

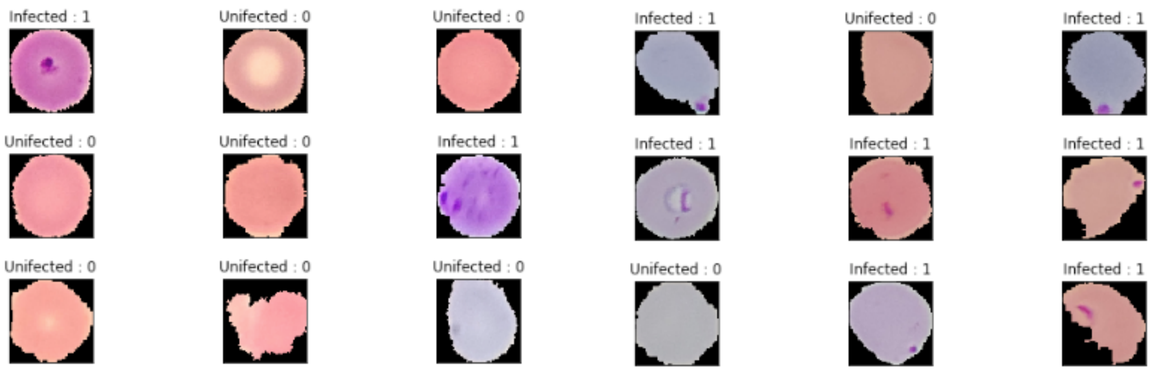

Figure 1 Enhanced RGB images

Figure 2 Original RGB images

Feature

Input features are RGB three-channel pixels. Features would be extracted by each convolutional layers using convolutional kernels. Each feature size is varied, depending on the size of kernel.

Model

- **Convolutional Neural Network (CNN)**

Boosted by TensorFlow Estimator, our Convolutional Neural Network takes inputs of 64 * 64 * 3 dimensional image, and trains using 4 convolutional layers, 4 pooling layers, and 2 dense layers. Specifications are as followed.

	Conv layers	Pooling layers	Dense layers
1	Filters: 64 Kernel size: 5*5	Pool size: 2*2 Strides: 2	Units: 256 Activation: relu
2	Filters: 32 Kernel size: 5*5	Pool size: 2*2 Strides: 2	Units: 128 Activation: relu
3	Filters: 32 Kernel size: 5*5	Pool size: 2*2 Strides: 2	
4	Filters: 32 Kernel size: 5*5	Pool size: 2*2 Strides: 2	

Table 1 CNN specifications

- **Xception**

Invented by Google, Xception is an Extreme version of Inception. With a modified depthwise separable convolution, it is even better than Inception-v3 for ImageNet. We implemented a Xception in Keras.

- **VGG16**

VGG16 is a convolutional neural network modeled by K. Simonyan and A.Zisserman from the University of Oxford. It made improvement by using multiple 3 * 3 kernel-sized filter. We implemented a VGG16 with modified fully-connected layers in Keras.

- **ResNet**

ResNet solves the degradation problem that with the network depth increasing, accuracy gets saturated and then degrades rapidly. Because of its depth, it performs better than traditional CNN. We implemented a ResNet with modified fully-connected layers to further explore the accuracy in Keras.

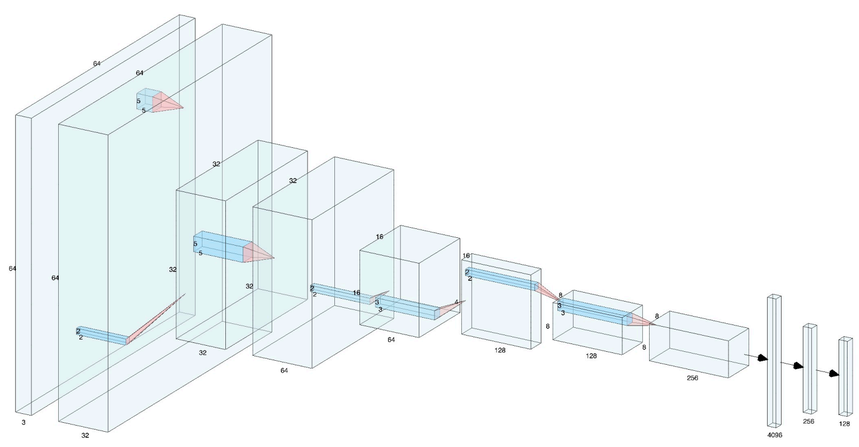

Figure 3 CNN model example

Result

- For each model, we trained 30 epoch, with batch size as 100. Because of the limitation of hardware, we had to restrict the data size of ResNet to the half of others.
- Spontaneously, our traditional CNN achieved 92% accuracy, which is the lowest. Xception is the best model, but a little overfitting occurred.
- Ranking: Xception > ResNet > VGG16 > CNN

	Train Size	Test Size	Train Error	Test Error	Train Acc	Test Acc
CNN	70548	22047	0.0657	0.28258	97.73%	92.15%
VGG16	70548	22047	0.1133	0.1325	95.93%	95.13%
ResNet	35274	19843	0.0110	0.2858	99.60%	96.60%
Xception	70548	22047	0.0031	0.1565	99.91%	97.57%

Table 2 Model Result

Discussion

- In general, we trained four models to do malaria cell image recognition: CNN, VGG16, ResNet and Xception. The highest accuracy is over 97% by Xception. Our model performed well on the dataset, however, overfitting problem still occurs when dealing with extremely deep neural networks like Xception and ResNet, which are needed to be improved by further fine-tuning steps.

Future

- More work needs to be done in the future to improve and fix the overfitting problem when training on the very deep networks like Xception and ResNet. There are many approaches to be explored, including data augmentation, regularization, dropout, etc.
- Other aspects, including the effect from optimizer, kernel size, learning rate, as well as the loss function, need also to be experimented.

Reference

- Rajaraman, Sivaramakrishnan, et al. "Pre-trained convolutional neural networks as feature extractors toward improved malaria parasite detection in thin blood smear images." *PeerJ* 6 (2018): e4568.
- Rajaraman S, Jaeger S, Antani SK. 2019. Performance evaluation of deep neural ensembles toward malaria parasite detection in thin-blood smear images. *PeerJ* 7:e6977

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NIH U.S. National Library of Medicine