Evaluations of Deep Convolutional Neural Networks for Automatic Identification of Malaria Infected Cells

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- Problem Statement
- Machine Learning for Automated Classification of Malaria Infected Cells
- Wholeslide Images
- Dataset of Cell Images for Malaria Infection
- Deep Convolutional Neural Networks
- Evaluation Results and Case Study
- Conclusion





Problem Statement

- 214 million malaria cases, causing 438,000 death in 2015 (source: WHO)
- Reliable malaria diagnoses require necessary training / specialized human resources
- Unfortunately, in many malaria-predominant areas, such resources are inadequate and frequently unavailable
- Whole slide imaging (WSI):
 - Scans conventional glass slides
 - Produces <u>high-resolution</u> digital slides
 - The most recent pathology imaging modality, available worldwide
- WSI images allow for highly-accurate automated identification of malaria infected cells.





Machine Learning for Malaria Detection

- Machine learning algorithms have been shown to be very capable for building <u>automated diagnostic systems for malaria</u>.
- Classification accuracy of feature-based supervised learning methods:
 - 84% (SVM)
 - 83.5% (Naïve Bayes Classifier)
 - 85% (Three-layer Neural Network)
- Deep learning methods:
 - can extract hierarchical representation of the data
 - higher layers represent increasingly abstract concepts
 - higher layers become invariant to transformations and scales
- <u>NO publicly available high-resolution datasets to train and test deep</u> <u>neural networks for malaria detection</u> – need to build one!
- Plan: to evaluate several well-known deep convolution neural networks using a high-resolution dataset.



Red blood cell samples





Wholeslide Images of Malaria Infection

Entire slide with cropped region delineated in green



Whole Slide Image for malaria infected red blood cells from UAB

Image of 258×258 with 100X magnification







Compilation of a Pathologist Curated Dataset



Link to the dataset



- Single-cell image extraction:
 - Apply image morphological operations

Dataset curation:

- Four UAB experienced pathologists
- Each single-cell image scored by at least two pathologists
- To include an image in "infected" set, all reviewers must mark positively (excluded otherwise).
- Similarly, to be "non-infected", all reviewers must mark negatively.
- Final dataset:
 - 1,034 infected cells
 - 1,531 non-infected cells



Three Convolutional NN's to be Evaluated

CNN	LeNet-5	AlexNet	GoogLeNet
Year Proposed	1998	2012	2014
# of Layers	4	8	22
Top 5 Errors on ILSVRC	?	16.4%	6.7%
# of Convolutional Layers	3	5	21
Convolutional Kernel Size	5	11, 5, 3	7, 1, 3, 5
# of Fully Connected Layers	1	3	1
# of Parameters	3,628,072	20,176,258	5,975,602
Dropout	No	Yes	Yes
Data Augmentation	No	Yes	Yes
Inception	No	No	Yes
Local Response Normalization	No	Yes	Yes





Training and Verification of CNN's



Label	Training	Testing
Infected	517	517
Normal	765	766

Note: 25% of the training set used for verification.

- The dataset is still too small.
- Overfitting issue.
- LeNet-5 has no drop-out.





Evaluation Results

		Ground Truth			
		Positive	Negative	Accuracy	
LeNet-5	Positive	493	25	96.18%	
	Negative	24	741		
AlexNet	Positive	502	39	95.79%	
	Negative	15	727		
GoogLeNet	Positive	503	10	09 120/	
	Negative	14	756	98.13%	
SVM	Positive	500	90	01 66%	
	Negative	17	676	91.00%	

SVM Features:

ranked from high to low

- Hu's moment 7,5,3,6
- MinIntensity
- Shannon's Entropy
- Hu's moment 2

See reference below.

V. Muralidharan, Y. Dong, and W. D. Pan, "A comparison of feature selection methods for machine learning based automatic malarial cell recognition in wholeslide images," *IEEE BHI-16*.





Computational Aspect

- SVM involves feature selection and feature extraction.
- Three CNN running times (in seconds):

CNN	LeNet-5	AlexNet	GoogLeNet
Training- Validation	7	28	141
Testing	5	5	19

More parameters means longer training and testing time.









Features Learned (LeNet-5)













Convolutional Layer 1 and Histogram





Features Learned (LeNet-5)













Convolutional Layer 2 and Histogram





Conclusion

Advantage of using CNN:

- About 98% accuracy achieved with GoogleNet, significantly higher than SVM.
- Tradeoff between computational complexity and accuracy.
- Deep learning methods allow features to be automatically extracted, which is not possible with traditional methods.

Further Work:

• Build a larger dataset for the study, with the goal of achieving reliable and accurate automated malaria diagnosis.





Thanks!



