Lossless Compression of Curated Erythrocyte Images Using Deep Autoencoders for Malaria Infection Diagnosis

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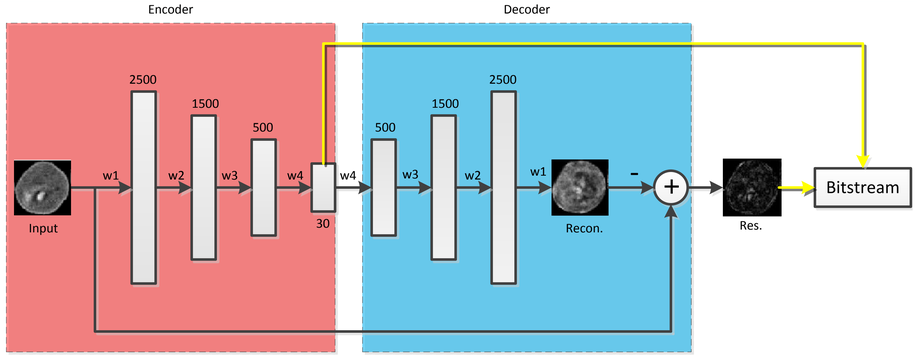
Introduction

- While autoencoders have been used as a generative machine learning technique for dimensionality reduction, they are *lossy* in nature.
- we proposed a novel image coding scheme by using stacked autoencoders (SAE), where the reconstruction residuals were Golomb-Rice coded to achieve lossless compression.
- As a case study for telemedicine applications, we compressed labeled erythrocyte (red-blood cell) images from a database curated by pathologists for malaria infection diagnosis.
- We compared the compression bitrates against several state-of-the-art lossless image compression methods.

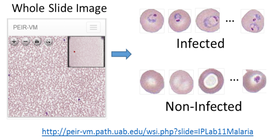
Lossless Image Compressor based on Stacked Autoencoders

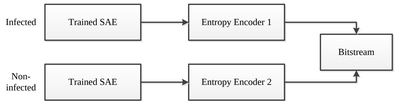


The lossless image compressor based on Stacked Autoencoders using Restricted Boltzmann Machines. The compressor takes an input image and generates the compressed bitstream. The so-called "encoder" is the 1st component of the compressor. The encoder reduces the input image to very low dimensional (e.g., a 30-point) vector. The 2nd component of the compressor is the "decoder", which reconstructs an approximate version of the original image. To achieve lossless compression, we employed a Golomb-Rice Code to code the residual images. The 30-point vectors were binary coded.

Malaria Infected and Non-Infected Red Blood Cells

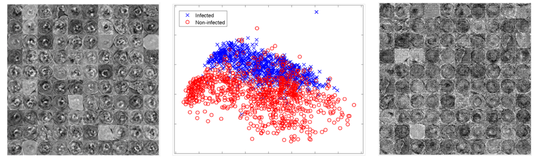
Malaria is a life-threatening disease caused by parasites transmitted to people through mosquitoes. In 2015, there were 214 million cases of malaria and 438,000 deaths. There has been a growing interest in building automated malaria diagnostic systems. Whole slide imaging, which scans conventional glass slides to produce high-resolution digital slides, has recently been used to diagnose malaria.



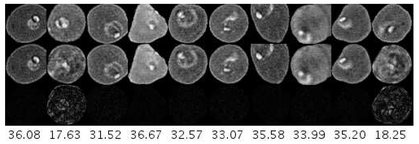


Separate training of neural networks offered higher compression than the mixed scheme, since common features could be more easily learned from the images of the same class.

Features Learned and Approximation Results

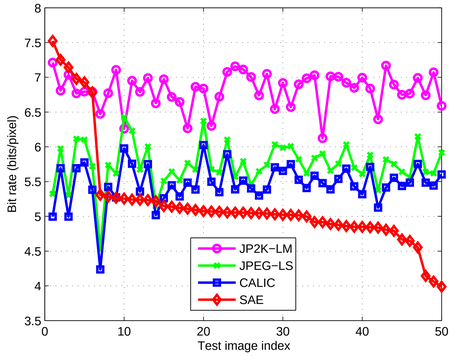


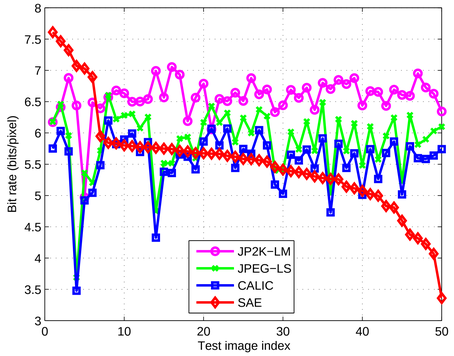
(Left) and (Right): Weighs learned at the first layer of the SAE for infected and non-infected cell images, respectively. (Middle) Distribution of the 2D representations after training the SAE (2500-1500-500-2) on 1,000 infected and 1,000 non-infected cell images.



Randomly selected infected cell images. (Top) Original images; (Middle) Reconstructed images; (Bottom) Absolute residual images and PSNR values.

Compression Results of Infected and Non-Infected Cells





We chose a 2500-1500-500-30 network architecture. For each type of images, 1,000 labeled images were divided into two sets: 900 for training and 100 for testing. The number of epochs was set to 1,000 for pre-training and fine-tuning. (Left) Infected cells; (Right) Non-infected cells.

Cell Type	Proposed	CALIC	JPEG-LS	JP2K-LM
Infected	5.1729	5.4391	5.6921	6.2320
Non-Infected	5.5135	5.6068	5.9632	6.4195

Conclusions

- **This might be the first attempt to achieve lossless data compression by using a deep learning technique**.
- For infected cell images, the proposed method achieved 4.9%, 9.1% and 17.0% lower bit rates than CALIC, JPEG-LS and JPEG 2000-LM, respectively.
- Nonetheless, the compression performance on non-infected cell images was not as remarkable.
- For a small number of images, the proposed method underperformed. The reason might be that in these images, intra-image correlations might be stronger than inter-image correlations, thus local prediction methods tend to compress better.
- In terms of computational complexity, the proposed method took about about 30 ms on average for testing.
- A hybrid approach would be beneficial.