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HUMAN BLOOD CELLS RECOGNITION BY USING DEEP LEARNING

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Abstract - . A CNN-based framework is built to automatically classify the blood cell images into subtypes of the cells. Experiments are conducted on a dataset of 13k images of blood cells with their subtypes, and the results show that our proposed model provide better results in terms of evaluation parameters.

RED BLOOD CELLS(RBC'S)

WHITE BLOOD CELLS(WBC'S)

PLATELETS

Key Words: Convolutional Neural Networks, Maxpooling,Flattening. Residual Learning.

1.INTRODUCTION

CNNs are one of the best learning algorithms for understanding image content and have shown exemplary performance in image segmentation, classification, detection, and retrieval related tasks. The success of CNNs has captured attention beyond academia. In industry, companies such as Google, Microsoft, AT&T, NEC, and Facebook have developed active research groups for exploring new architectures of CNN At present, most of the frontrunners of image processing and computer vision (CV) competitions are employing deep CNN based models. The attractive feature of CNN is its ability to exploit spatial or temporal correlation in data. The topology of CNN is divided into multiple learning stages composed of a combination of the convolutional layers, non- linear processing units, and subsampling layers. CNN is a feedforward multilayered hierarchical network, where each layer, using a bank of convolutional kernels, performs multiple transformations. Convolution operation helps in the extraction of useful features from locally correlated data points. The output of the convolutional kernels is then assigned to the non-linear processing unit (activation function), which not only helps in learning abstractions but also embeds non-linearity in the feature space.

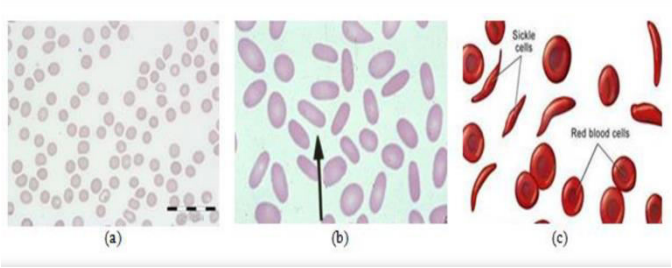
2. Body of Paper

In general, databases that are used in developing blood cell classification systems rely on microscopic cell images. The variety of information in these images makes cell identification difficult for machines due to the different sizes, shapes and colors. However, as our novel approach to cell identification is based on simulating a human expert's visual recognition, who is normally able to identify the three types of cells despite the above problems, the different morphological features, sizes and rotations of cells are not considered as an obstacle in this work and are left to the neural network to learn via global pattern averaging.

The work in this paper is divided in four stages. 1) Image processing 2) convolution 3)Maxpooling 4)Flattening. An image can be considered as a matrix of light intensity levels that can be manipulated using computer algorithms in MATLAB. The human blood consists of three major components of blood cells which are red blood cell (RBC), white blood cell (WBC) and platelets. Red blood cell has the major percentage in the human blood and conducts various functions in human body such as transporting oxygen throughout the body, carrying carbon dioxide and waste products away from cells and tissue. Normal shape of the RBC is biconcave disks with about 7 to 8μm in diameter and 2.2 μm thick . Considering the abnormal RBC morphology give a sign of anaemia, reduction of haemoglobin (a protein that bind with oxygen molecule in RBC), and secondary effect of several other disorders. From medical perspective, the RBC diagnosis contributes information about various blood related disease. For instance, the shape of RBCs and its deformability has connection to the relevant disease more especially anaemia and secondary effect of several other disorder . Anaemia and blood related disorders are common in almost 24.5% of world population. This make all pathological laboratories the current method of blood smear analysis relies on visually inspecting the blood smear slide under the microscope. The method is time consuming, laborious, expensive and it requires skilled technicians.

The convolutional layer is composed of a set of convolutional kernels where each neuron acts as a kernel. Max pooling is a pooling operation that selects the maximum element from the region of the feature map covered by the filter.

Flattening is converting the data into a 1-dimensional array for inputting it to the next layer. We flatten the output of the convolutional layers to create a single long feature vector. And it is connected to the final classification model, which is called a fully-connected layer.



Figures shows the human blood cells.a)normalblood cells, b) and c) abnormal blood cells.

3. CONCLUSIONS

We were able to use a simple CNN model to classify the blood cells in our dataset with an accuracy of 98% just based on image level data. We hope the results and methodology provide a glimpse into how promising Deep Learning techniques are in the field of cell imaging and classification.While the model and problem statement discussed is simple, we believe they can be extended to more challenging problems with multiple classes, more varied lighting conditions, and new cell types. In particular, we are extremely excited about using such techniques in not just datasets of BCs but a wide variety of other cells such as platelets, sickle cells, and even tumor cells.Apply Deep Learning to healthcare in a meaningful, valuable way. Most importantly we hope that we can enable:

- Faster iteration cycles and improvements.
- Increased accessibility to high quality, quantitative assessments.
- Lower costs and better patient outcomes.

Our proposed model can automatically classify the blood cell images into subtypes of the cells with high accuracy,precision and other evaluation parameters. This proposed model can be very beneficial for blood diagnosis in the medical field that can save a lot of time. We believe that there is always room for improvement in every field so as well in this field also. Researchers may implement this work on large dataset that may out perform the current results.

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