Deep Learning Based Cell Classification for Future Vision Implemented Lab-on-a-Chip Devices

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Cell sensing and classification are significant in pathology detection in the biomedical industry. This paper presents the use of deep learning techniques in the classification of healthy red blood cells (hRBCs) and sickle cells (SCs). Fully connected and convolutional models are proposed and designed for this application. Two datasets containing 40 images and 297 images are prepared using photomicrographs of a human blood smear to train and test the models. In comparison to the fully connected model, the convolutional model produced successful results. The possibility of implementing artificial intelligence (AI) in pathology detection with a larger dataset using a similar software configuration is identified. RStudio software, KERAS library, and Tensor Flow are used as the R language programming tool, artificial neural network interface and the backend respectively. Use of validation split in convolutional models is also studied, and significant variations of accuracy are observed. Yet the maximum testing accuracy remains unchanged in the study due to the lower number of images in the datasets utilized.

Keywords: *red blood cell classification, sickle cell disease, deep learning, convolutional neural network, tensor flow*