Optimizing Cell Quantification in Biological Assays Using a Convolutional Neural Network

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Modern research laboratories place a strong emphasis on image-processing, which commands a great deal of human resources and time on a daily basis. Fluorescence Confocal Microscopes, a tool with a variety of scientific research applications, image tissues in slices, thereby allowing for the quantification and localization of cells or regions of interest (ROIs) in three dimensions within any assay. Microscope outputs are difficult to decipher as a result of superposition of datasets and the retention of signal throughout multiple image slices. Human processing of these images requires extensive concentration and consumes finite resources. Machine learning provides the tools required to ameliorate and accelerate the efficient completion of this task. Convolutional Neural Networks, which are designed to mimic human vision, can be used to identify these features autonomously. Using data from studies of retinal development in mice from Dr. Kay's Lab at Duke University, a neural network model was trained to perform the aforementioned task. Iterative training of the model using multiple datasets improves the accuracy and efficiency of cell counts and classifications. The CUDA native interface, a library allowing access to computational hardware, and the Google Cloud Compute platform, which hosts the hardware itself, provide the tools necessary to create, implement and facilitate the model training. Overlay of neural network outputs is expected to provide additional insight into gene expression during critical periods in development. However, this same framework is also designed to handle a multitude of image-processing tasks, with potential applications in pathology, environmental management, and geology.

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