Semantic Segmentation of Cell Painted Organelles using DeepLabv3plus Model

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Cell painting based high content fluorescence imaging technique offers deep insight into the functional and biological changes in subcellular structures. However, advanced instrumentation and the limited availability of suitable fluorescent dyes restricts the tool to comprehensively characterize the cell morphology. Therefore, generating fluorescent specific organelle images using transmitted light microscopy provides an alternative solution for clinical applications. In this work, the utility of semantic segmentation deep network for predicting the Endoplasmic Reticulum (ER), cytoplasm and nuclei from a composite image is investigated. To perform this study, a public dataset consisting of 3456 composite images are considered from Broad Bioimage Benchmark collection. The pixel wise labeling is carried out with the generated binary masks for ER, cytoplasm and nuclei. DeepLabv3plus architecture with Atrous Spatial Pyramid Pooling (ASPP) and depth wise separable convolution is used as a learning model to perform semantic segmentation. The accuracy and loss function at different learning rates are analyzed and the segmentation results are validated using Jaccard index, mean Boundary F (BF) score and dice index. The trained model achieved 97.86% accuracy with a loss of 0.07 at the learning rate of 0.01. Mean BF score, dice index and Jaccard index for nuclei, ER and cytoplasm are (0.98, 0.94, 0.88), (0.97, 0.82, 0.7) and (0.95, 0.88, 0.66) respectively. The obtained results indicate that the adopted methodology could delineate the subcellular structures by accurately detecting sharp object boundaries. Therefore, this study could be useful for predicting the cell painted images from transmitted light microscopy without the requirement of fluorescent labeling.