

Abstract

Advances in medical imaging have increased its role in improving diagnosis and care decisions. Biomedical researchers continue to refine and improve imaging methods to better understand disease mechanisms and identify biomarkers and therapeutic targets. Biopsies are essential for the diagnosis of many diseases, and are precious resources to investigate how the architecture and cellular content of tissues reflect disease progression and therapeutic response. Fully harnessing the information contained within biomedical images relies upon sophisticated image processing and statistical analyses to quantify hallmark features and patterns that may otherwise escape physicians and researchers.

A central challenge is the development of high-performance image segmentation approaches, which enable computational tools to discern individual cells within complex tissue microenvironments. Conventional image segmentation relies on machine learning (ML) for cellular edge detection, which often requires customization for each image and tissue type while deep-learning (DL) methods use neural networks to predict the flow of pixels from the center of each cell to its boundary. As the quality of image segmentation directly impacts the reliability of downstream quantification in spatial analysis, evaluating the performance and adaptability of different segmentation methods is critical to advancing single-cell resolution studies in complex tissues.

This paper explores the effectiveness of Cellpose, a DL segmentation tool, benchmarked with the machine-learning software Ilastik, utilizing high-parameter images of prostate tumor biopsies. A range of models available through Cellpose, including default models, tuned, and custom trained, were developed and evaluated by comparing cell counts across selected Imaging Mass Cytometry (IMC) images from the VIC dataset. The results indicate that Cellpose can achieve similar cell counts to Ilastik, with substantially less training data, pointing to superior efficiency of DL segmentation methods. This study serves as a first step towards evaluating whether cell segmentation based on DL methods can eventually streamline or replace the machine-learning methods in existing segmentation workflows.