Contribution ID: **41** Type: **Poster**

Analysis and Segmentation of Nucleus with U-Net

Tuesday 9 April 2024 17:50 (20 minutes)

The nucleus, responsible for a cell's genetic instructions and vital functions such as gene expression and replication, plays a crucial role in understanding cellular mechanisms and discovering problems related to diseases. Even with advanced 3D imaging techniques such as soft X-ray tomography (SXT) providing detailed insights into the structure of cellular components, specifically the nucleus, remains a significant challenge [1-2]. Due to differences in DNA packing, the nucleus exhibits significant variations in its intensity and texture, making it difficult to perform segmentation without manual input. Manual segmentation, requiring specialized expertise, consumes extensive time and resources [1, 3-5]. Automatic and accurate automatic segmentation not only aims to simplify analysis but also holds the potential to unlock a deeper exploration of cellular complexities at statistically significant sample sizes. Addressing these challenges could potentially revolutionize our understanding of cellular functions and pathologies.

Previously, we have shown that by a combination of semi-automatically segmented training datasets and machine learning automatic cytoplasm segmentation of diverse cells is possible [6]. In this study, we further explore deep-learning techniques automatic segmentation of cell nucleus. Utilizing the U-Net [7], and an open-source tool 3D Slicer [8], we use morphological contour interpolation based on a few annotated slices, to create training data and with high efficiency to accurately segment nucleus labeled.
Our work on the automatic segmentation of cell nuclei enables monitoring and analysis of DNA packing associated with aging, disease, environment, or genetics. Using dice coefficient and morphological parameters we show that our pipeline can accurately segment the nucleus of human immune T-cells and murine microglia BV-2 segmentation with potential for automatic segmentation across more divergent cell types.

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Primary authors: EROZAN, Ayse; Dr WEINHARDT, Venera; Prof. HEUVELINE, Vincent

Presenter: EROZAN, Ayse

Session Classification: Posters

Track Classification: MLC