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Volumetric Semantic Instance Segmentation of the Plasma Membrane of **HeLa** Cells

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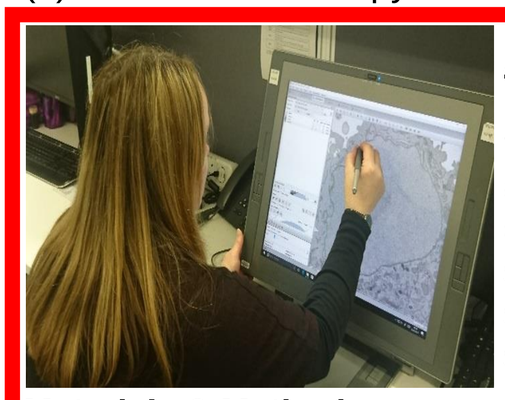
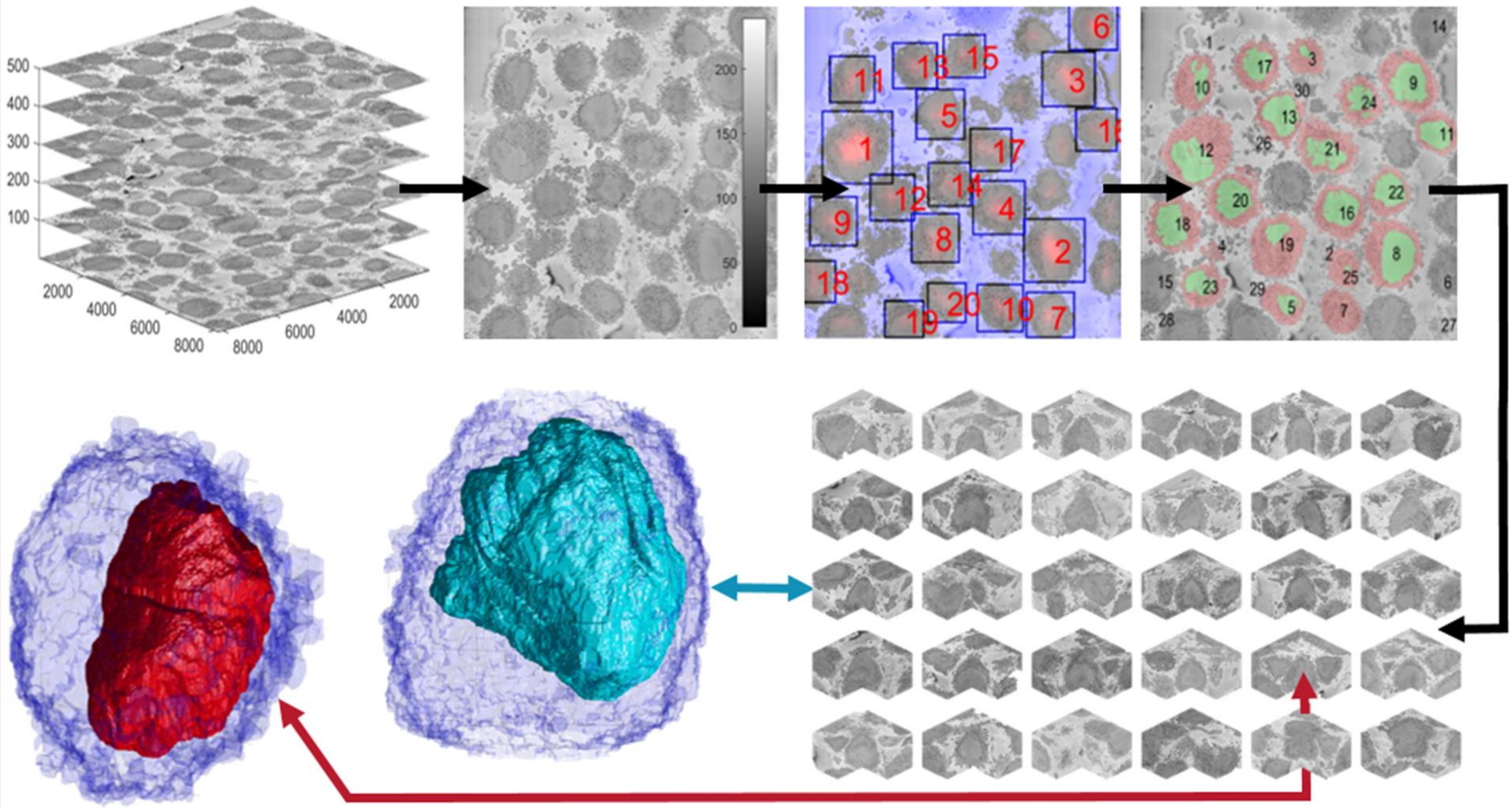


Abstract

Modern Electron Microscopes (EM) can acquire very high-resolution images and a core facility can produce tens of thousands of data sets that can easily exceed gigabytes of data every month. The identification of individual cells, and the shape of the cell are of great interest to scientists, as the structure of the cell may reveal some conditions of health or disease. Despite the significant disadvantages in time and inter- and intra-user variability, manual or semi-automatic delineation of the plasma membrane is widely used. In this work, an unsupervised volumetric semantic instance segmentation of the plasma membrane of HeLa cells as observed with Serial block face scanning electron microscopy (SBF SEM) is described.

Materials & Methods

The data sets consisted of **EM images of cervical cancer cells called "HeLa" cells**. Wild type HeLa cells were prepared and embedded in Durcupan resin following the method of the National Centre for Microscopy and Imaging Research (NCMIR). SBF SEM data was collected using a 3View2XP (Gatan, Pleasanton, CA) attached to a Sigma VP SEM (Zeiss, Cambridge). Images were acquired at 8192 x 8192 pixels over a total of 518 slices, with 10 x 10 x 50 nm voxel size and the intensity of each voxel was between 0 and 255. The resin background of the images was segmented at different slices of a 3D stack of 518 slices with 8192 x 8192 pixels each. The background was used to create a distance map, which helped identify and rank the cells by their size at each slice. The centroids of the cells detected at different slices were linked to identify them as a single cell that spanned a number of slices. A subset of these cells, i.e., the largest ones and those not close to the edges were selected for further processing. The selected cells were then automatically cropped to smaller regions of interest of 2000 x 2000 x 300 voxels that were treated as cell instances. Then, for each of these volumes, the nucleus was segmented, and the cell was separated from any neighbouring cells through a series of traditional image processing steps that followed the plasma membrane. The segmentation process was repeated for all the regions of interest previously selected.



Results & Future Work

- **For one cell for which the ground truth was available, the algorithm provided excellent results in Accuracy (AC) and the Jaccard similarity Index (JI): nucleus: JI =0.9665, AC =0.9975, cell including nucleus JI =0.8711, AC =0.9655, cell excluding nucleus JI =0.8094, AC =0.9629.**
- **A limitation of the algorithm for the plasma membrane segmentation was the presence of background. In samples with tightly packed cells, this may not be available.**
- **All the code and data were released openly through https://github.com/reyesaldasoro/Hela-Cell-Segmentation, https://doi.org/10.5281/zenodo.4590903, and http://dx.doi.org/10.6019/EMPIAR-10094.**
- **The framework is not restricted to HeLa cells as other cells from any electron imaging modality could be also analysed.**
- **Future work will consider the analysis of the other cellular structures such as Golgi apparatus, mitochondria and the chromatin in the nucleus.**

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