From volume electron microscopy datasets to segmentation models, feature quantification, and data reuse

Dr. Ilya Belevich[1], Kirk Czymmek[2], Johanna Bischof[3], Aastha Mathur[3], Lucy Collinson[4], Eija Jokitalo[1]
[1]University of Helsinki, Helsinki, Finland, [2]Donald Danforth Plant Science Center, Saint Louis, USA, [3]Euro-BioImaging ERIC Bio-Hub, EMBL, Heidelberg, Germany, [4]Francis Crick Institute, London, UK

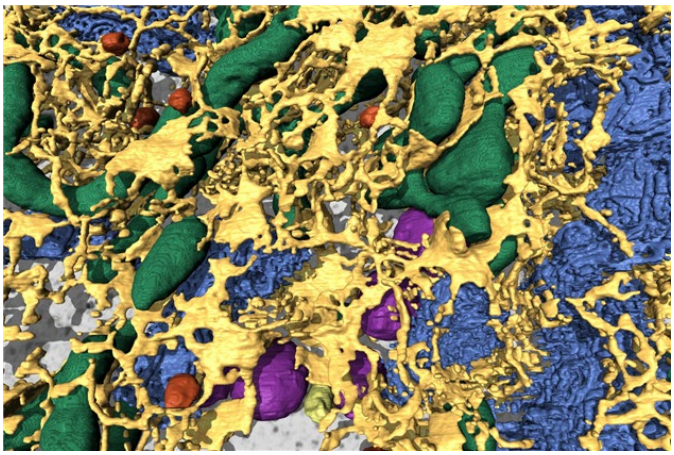
Advancements in microscopy techniques have led to the generation of ever-increasing amount of data, demanding efficient analysis methods. Image segmentation tools, particularly those powered by Artificial Intelligence (AI), have become critical components for processing this data. However, segmentation is just the first step in unlocking the wealth of information hidden within these complex datasets. Quantitative analysis methodologies are essential for extracting meaningful biological insights.

Here delves into the power of AI-driven segmentation for quantitative analysis in electron microscopy. We demonstrate the segmentation of a U2OS cell FIB-SEM dataset [1] using a newly developed tools within Microscopy Image Browser (MIB) [2]. Our approach leverages the "segment-anything" model [3] for ground truth generation of training labels alongside a newly developed 2.5D deep learning workflow for image segmentation in DeepMIB tool [4] of MIB. This powerful combination allows for efficient generation of accurate models for various cellular organelles, including mitochondria, endoplasmic reticulum (ER), Golgi apparatus, nuclear envelope, lysosomes, and peroxisomes [5]. These models serve as the foundation for in-depth quantitative analysis.

Moving beyond segmentation, we explore potential analysis pathways. A typical pipeline might begin with volumetric analysis of organelles, providing valuable information about their size and distribution. This analysis can be further extended by developing custom methods to quantify specific features relevant to cell biology research. Examples include measuring the density of nuclear pores, quantifying the sheet-to-tubule ratio of the ER, or analyzing the contact points between ER and mitochondria.

In addition, we showcase the immense potential of large-volume electron microscopy data, extending its utility beyond the scope of the original research project. Sharing these datasets responsibly is crucial for unlocking their full potential and enabling broader scientific exploration. By fostering responsible data sharing practices [5], we can collectively extract even deeper insights from these rich datasets, leading to significant advancements in our understanding of cellular biology.

Graphic:



Keywords:

volume microscopy deep learning FIB-SEM

Reference:

1. Belevich I, Schertel A, Zaversek T, Szyrynska N, Saarnio S, Jokitalo E, Human bone osteosarcoma epithelial cell (U2-OS), EMPIAR, doi: 10.6019/EMPIAR-11746
2. Belevich I, Joensuu M, Kumar D, Vihinen H, Jokitalo E. Microscopy Image Browser: A Platform for Segmentation and Analysis of Multidimensional Datasets. PLoS Biol. 2016 Jan 4;14(1):e1002340. doi: 10.1371/journal.pbio.1002340
3. Kirillov A, Mintun E, Ravi N, Mao H, Rolland C, Gustafson L, Xiao T, Whitehead S, Berg AC, Lo W-Y, Dollár P, Girshick R, Segment Anything, arXiv:2304.02643, doi: 10.48550/arXiv.2304.02643
4. Belevich I, Jokitalo E. DeepMIB: User-friendly and open-source software for training of deep learning network for biological image segmentation. PLoS Comput Biol. 2021 Mar 2;17(3):e1008374. doi: 10.1371/journal.pcbi.1008374
5. Czymmek KJ, Belevich I, Bischof J, Mathur A, Collinson L, Jokitalo E., Accelerating data sharing and reuse in volume electron microscopy. Nat Cell Biol. 2024 Apr 12. doi: 10.1038/s41556-024-01381-3