3D ConvNets improve macromolecule localization in 3D cellular cryo-electron tomograms

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KEYWORDS: cryo-electron tomography, deep learning, 3D analysis

Cryo-electron tomography (cryo-ET) allows one to capture 3D images of cells in a close to native state, at sub-nanometer resolution. However, noise and artifact levels are such that heavy computational processing is needed to access the image content [1]. We propose a deep learning framework to accurately and jointly localize multiple types and states of macromolecules in cellular cryo-electron tomograms. We compare this framework to the commonly-used template matching method on both synthetic and experimental data. On synthetic image data, we show that our framework is very fast and produces superior detection results. On experimental data, the detection results obtained by our method correspond to an overlap rate of 86% with the expert annotations. In addition, we show that our method can be combined to template matching procedures to reliably increase the number of expected detections. In our experiments, this strategy was able to find additional 24.3% membrane-bound ribosomes that were missed or discarded during manual annotation.

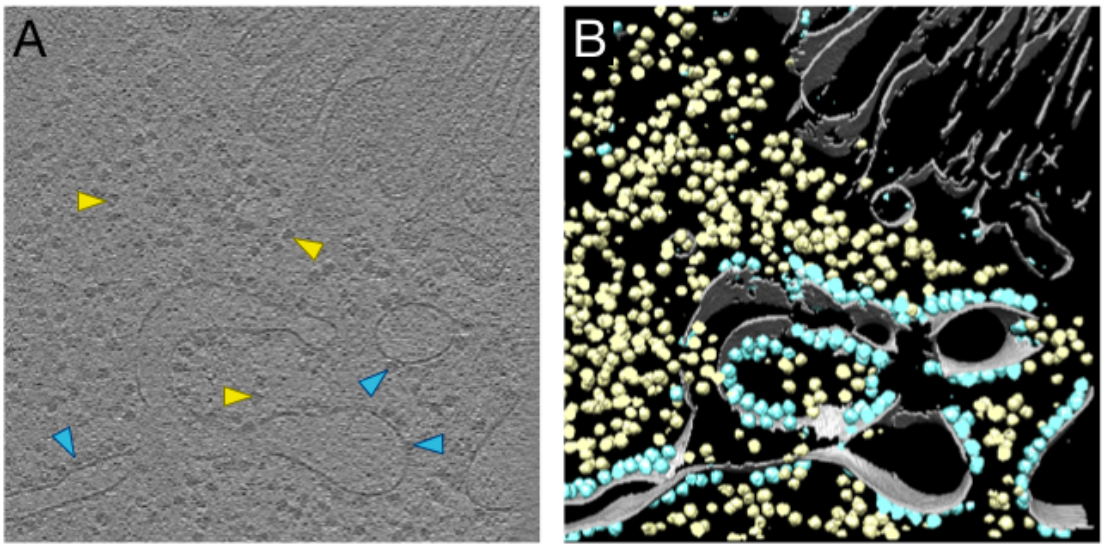

Figure 1. Chlamydomonas cell. (A) Tomogram slice; blue arrows indicate membrane-bound ribosomes; yellow arrows indicate cytoplasmic ribosomes. (B) Corresponding voxelwise classification obtained by our 3D CNN, performed for 3 classes: mb-ribos (blue), ct-ribos (yellow) and membrane (gray).

[1] D. Vanhecke and al., *Cryo-electron tomography: methodology, developments and biological applications*, Journal of Microscopy, vol. 242, Pt. 3, pp. 221-227, 2011.