McGill UNIVERSITY

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Computational challenges in high-resolution cryogenic electron microscopy

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X-ray crystallography has represented the dominant technique for obtaining high-resolution information of macromolecular complexes. Cryo-electron microscopy (cryo-EM) was traditionally used to shed light into the morphology of large protein complexes that resisted crystallization, albeit at substantially lower resolutions than crystallography. However, recent technological advances, mainly in computation and instrumentation levels, are now allowing cryo-EM to start being a competitive technique in terms of the level of details that can provide. Nevertheless, we should not rest on laurels as important challenges remains unsolved in cryo-EM and we need to encourage further progress to promote this technique to the next "omics" technology in structural biology. These challenges include among others: 1) development of high-thorughtput high-resolution computational methods, allowing in a close future the "one-push-one-map" phylosophy; 2) implementation of new image processing methods to obtain high-resolution reconstructions using Volta phase plates with defocused samples; 3) new computational approaches to deal with both discrete and continous heterogenerous samples; 4) development of robust 3D map validation methods. This seminar will introduce the computational improvements that have excited this field of cryo-EM, the computational challenges that are currently limiting its potential, and possible solutions to face them.

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Strathcona Anatomy Building
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