



Seminar/Talk

MissAlignment learns to straighten out cryo-ET tilt series

Marten Chaillet

Hubrecht Institute

Host: Alicia Michael

Cryo-electron tomography (cryo-ET) is used to visualize complex cellular environments at macromolecular resolution. However, due to limitations of the microscope, computational image alignment is crucial for data interpretation. Existing reference-free alignment algorithms aim to maximize similarity between adjacent tilt images for improved registration. This often proves ineffective due to limited information overlap between images and inaccurate assumptions about the sample. Meanwhile, human experts can easily recognize misalignment. We introduce a new machine learning-based approach for training similar intuition and using it to improve alignment. MissAlignment trains a convolutional neural network to score the alignment accuracy using a contrastive loss metric that doesn't require well-aligned ground truth. Back-propagation from this score is then used to optimize individual image alignment parameters. Our method demonstrates significantly improved alignment compared to existing techniques, leading to superior performance in all downstream analysis tasks. This advancement substantially enhances the robustness of cryo-ET data processing, making the technique applicable to a broader range of samples.

Friday, January 23, 2026 10:00am - 11:00am

Office Bldg West / Ground floor / Heinzl Seminar Room



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