Cryo-EM Course
at the Laboratory for BioMolecular Structure (LBMS)
June 14-17th, 2022
Brookhaven National Laboratory

Cryo-ET data collection and reconstruction demonstration

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Department of Microbial Pathogenesis
Microbial Sciences Institute
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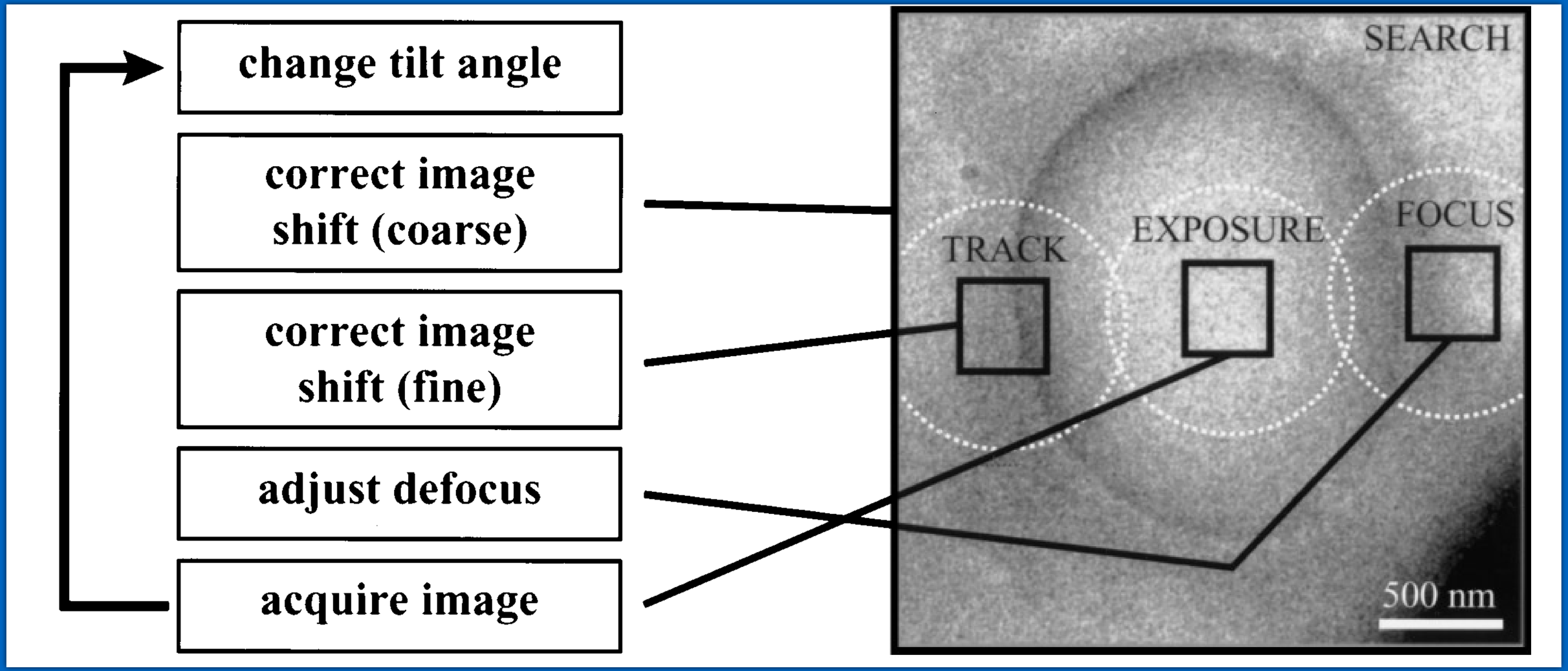
Cryo-ET data collection



Koster et al., JSB 1997

Many cryo-ET data acquisition packages

SerialEM

UCSF Tomo
Leginon
FEI tomography
EM-Manu

SerialEM

Automated electron microscope tomography using robust prediction of specimen movements

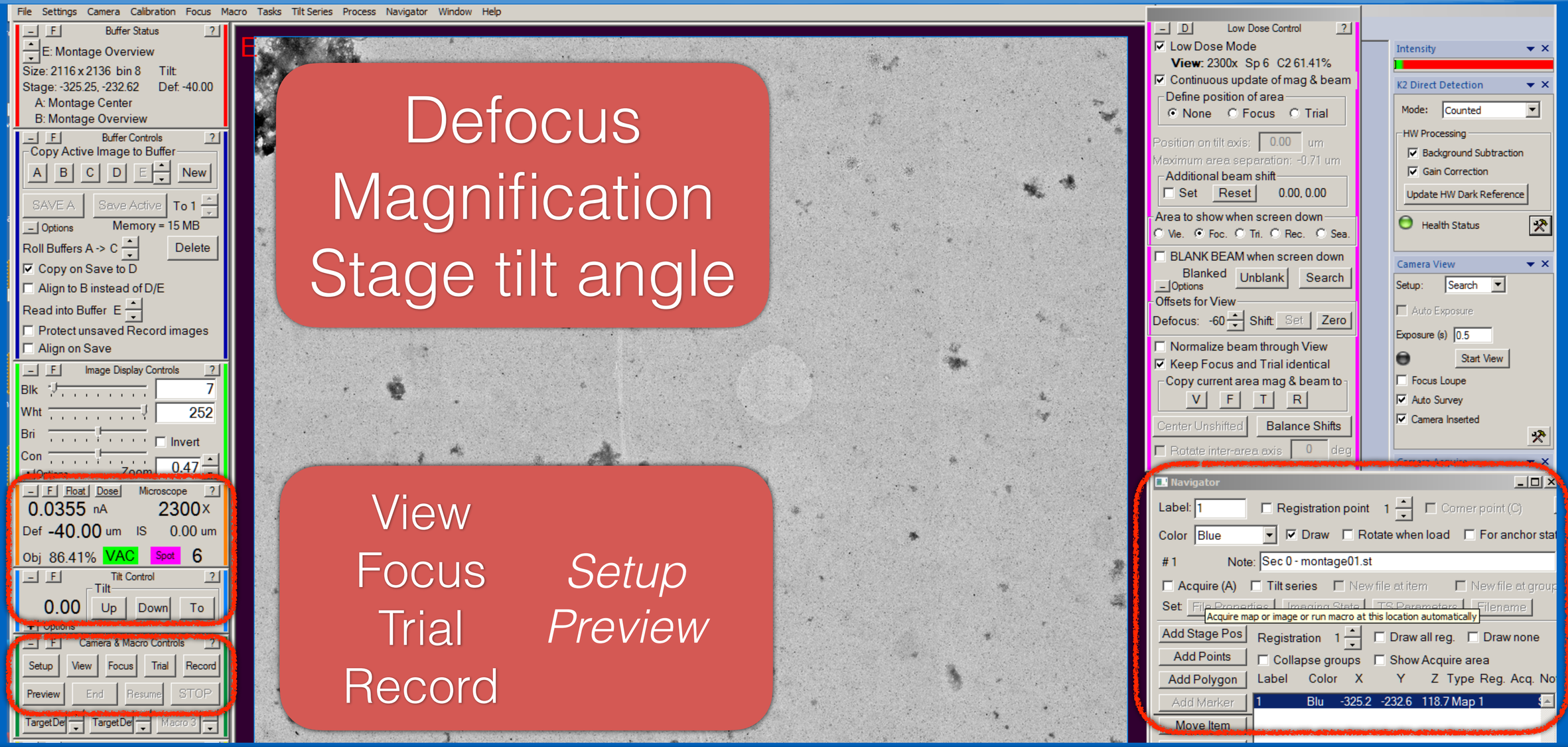
2005

David N. Mastronarde *

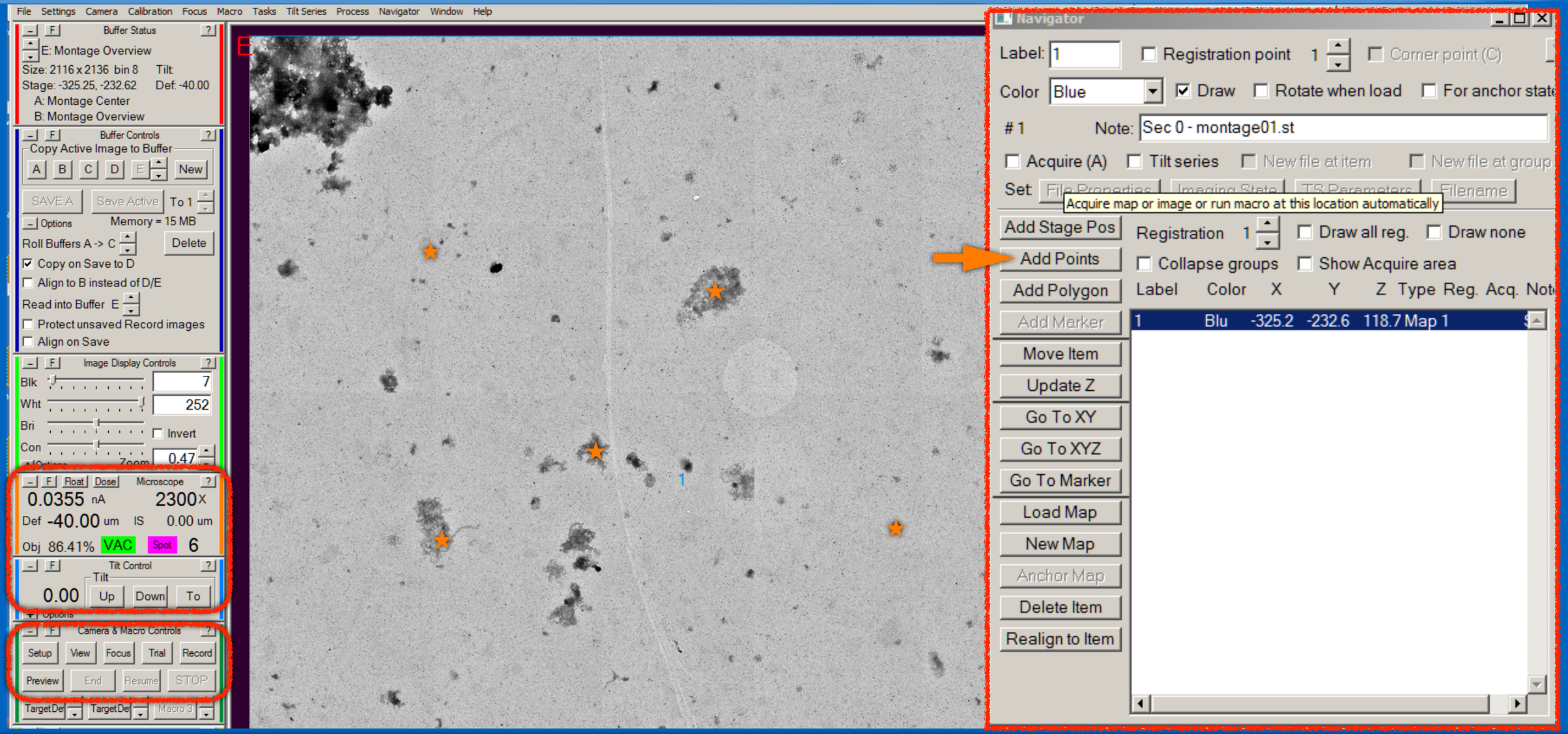
Boulder Laboratory for Three-Dimensional Electron Microscopy of Cells, Department of Molecular, Cellular, and Developmental Biology, University of Colorado, Boulder, CO 80309, USA

SerialEM provides a flexible interface. The script capability provides a relatively easy way to add commands requested by users.

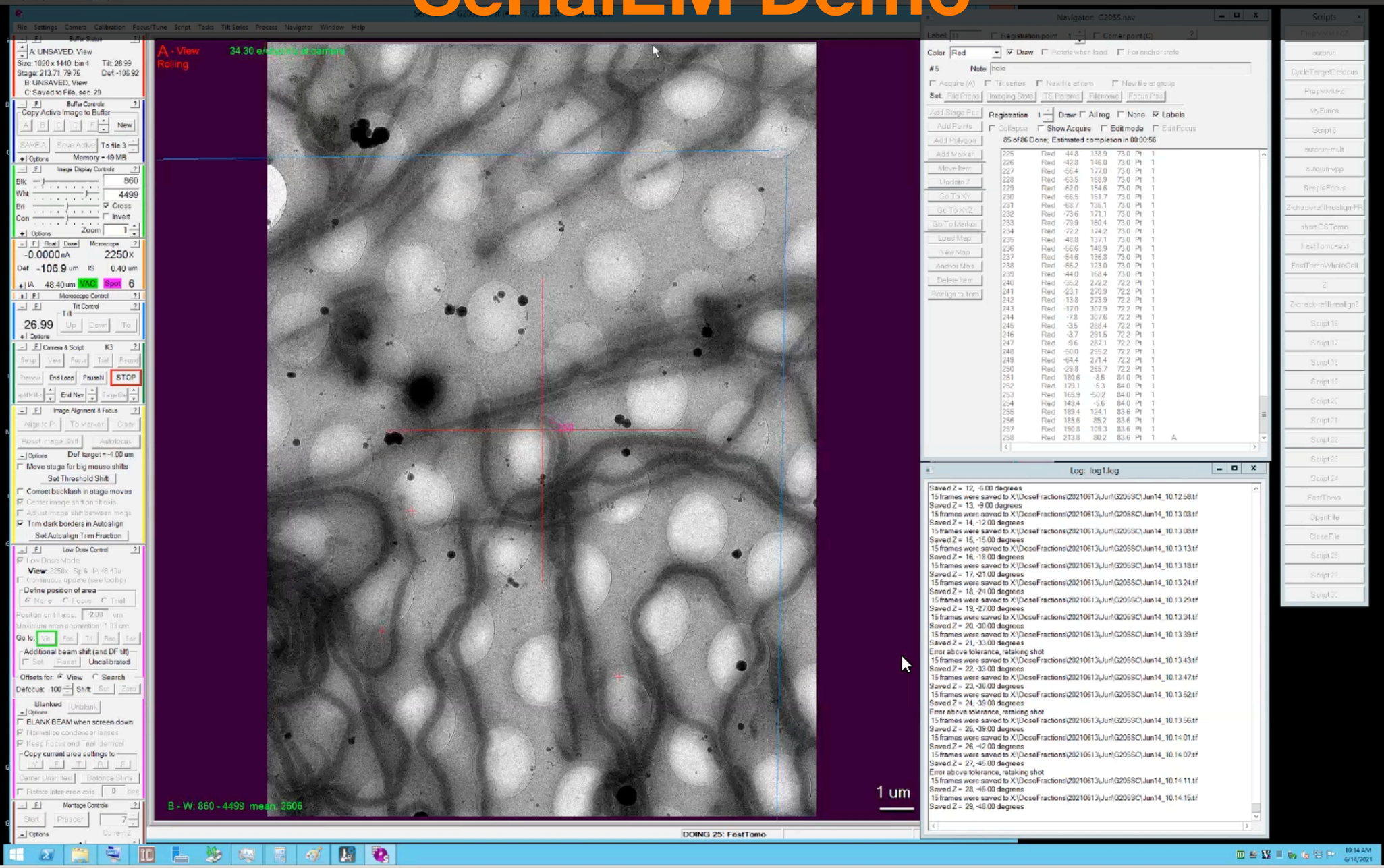
SerialEM (David Mastronarde)



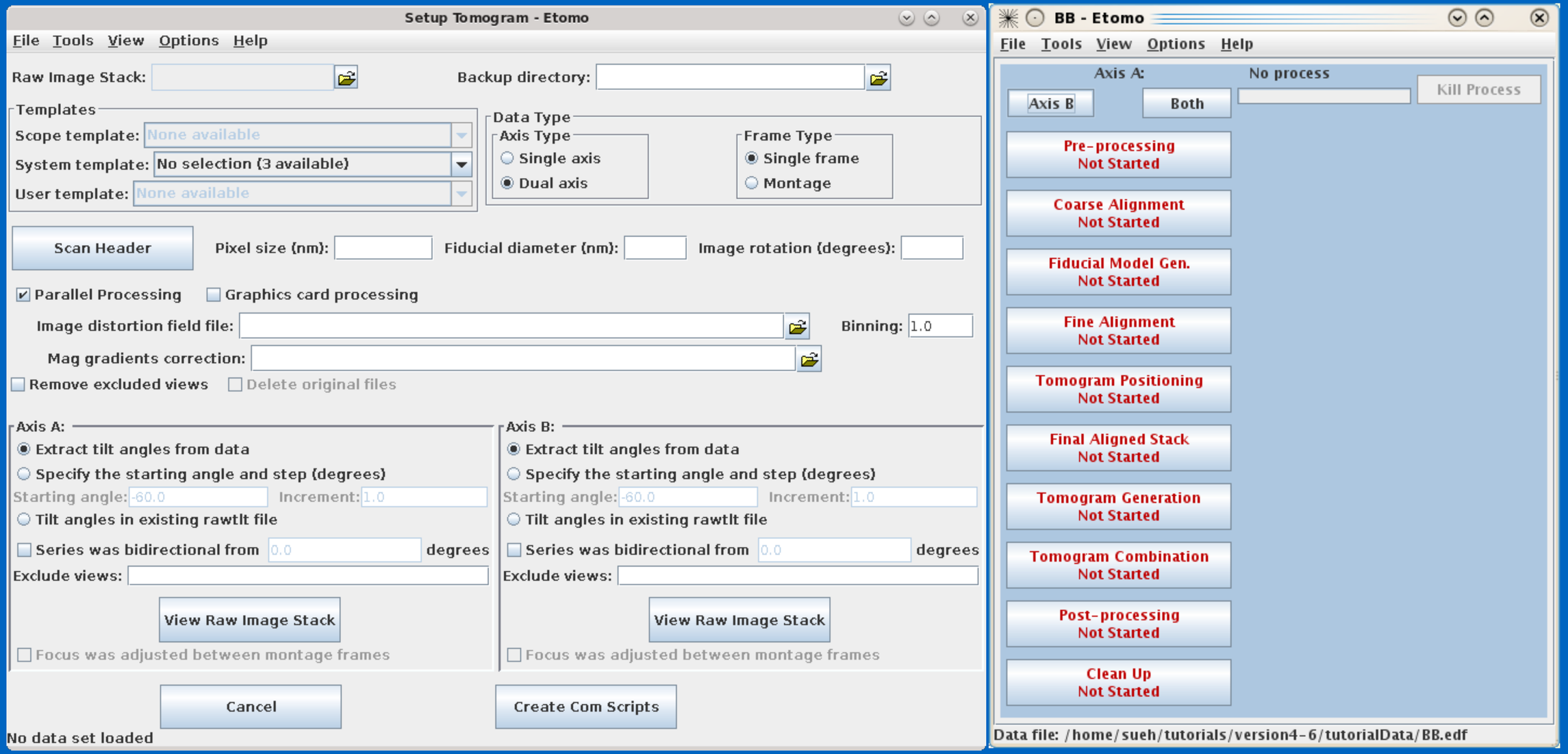
SerialEM — Navigator



SerialEM Demo



Aligning tilt seires (IMOD)



Aligning tilt seires (AreTomo)

AreTomo -InMrc original_tilt.mrc -OutMrc aligned_tilt.mrc

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AreTomo: An integrated software package for automated marker-free, motion-corrected cryo-electron tomographic alignment and reconstruction

Shawn Zheng[1,2] Georg Wolff [3] Garrett Greenan[1] Zhen Chen[1] Frank G. A. Faas[3] Montserrat Bárcena[3] Abraham J. Koster[3] Yifan Cheng[1,2,*] David Agard[1,*]

Thanks

- **Any questions?**