



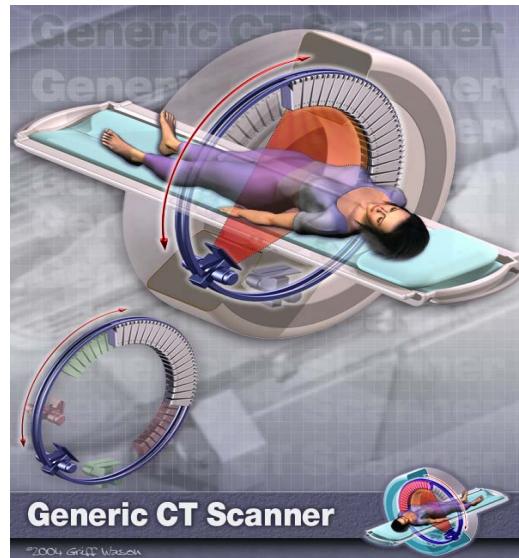
Lecture 8: Tomography (part 1)

- 1. Principles of Electron Tomography**
- 2. Sample Preparation**
- 3. Data Acquisition**
- 4. Tomogram Reconstruction**
- 5. Tomogram Denoising**

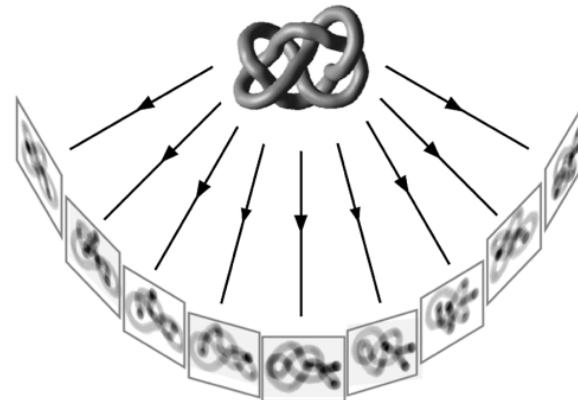
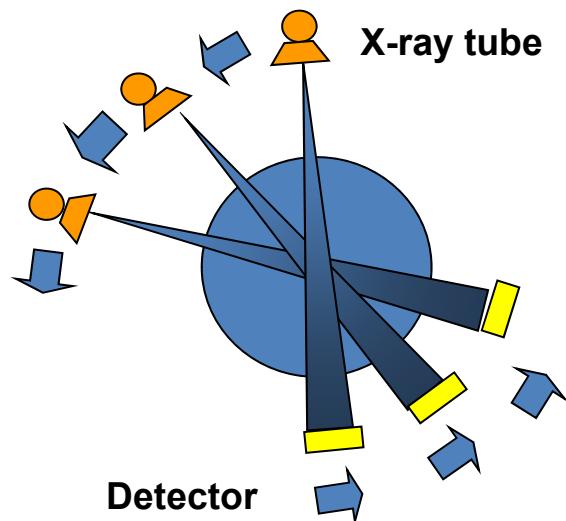


Principles of EM Tomography

Computer Tomography

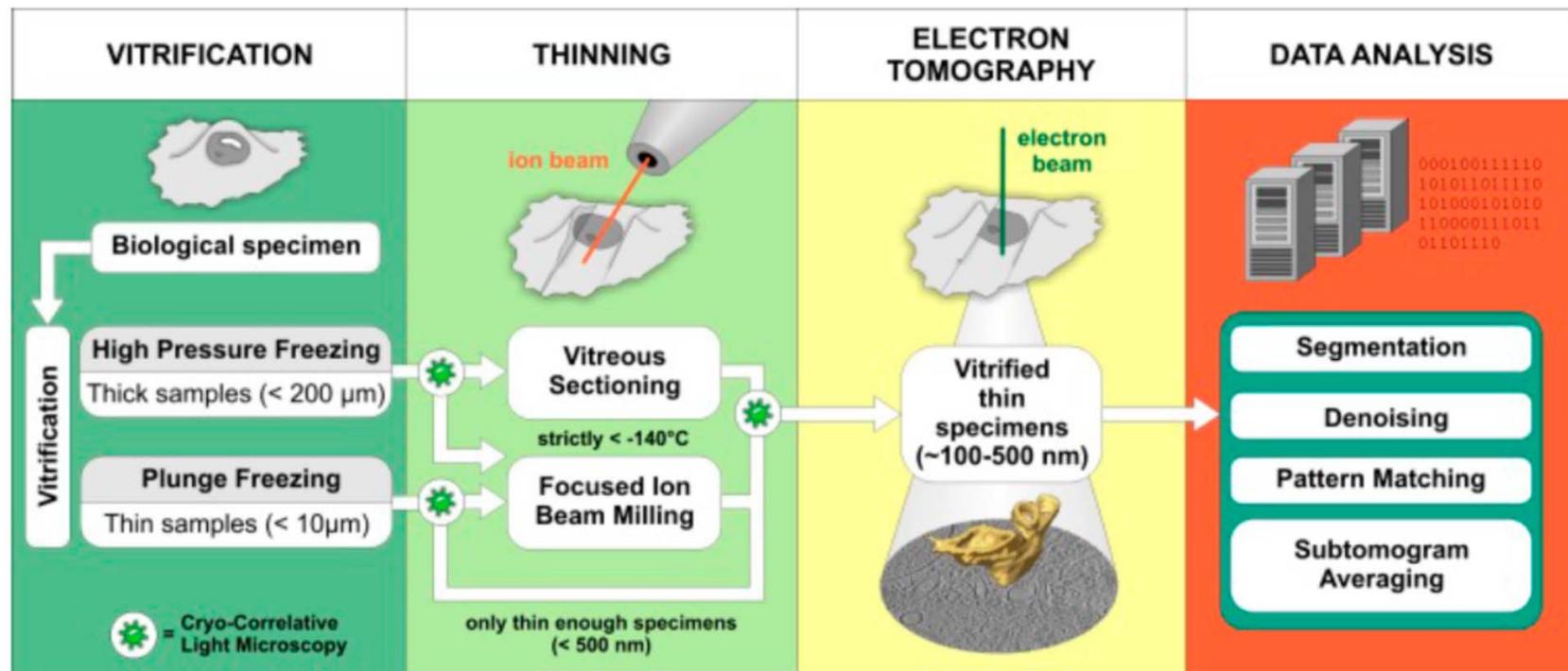


Electron Tomography





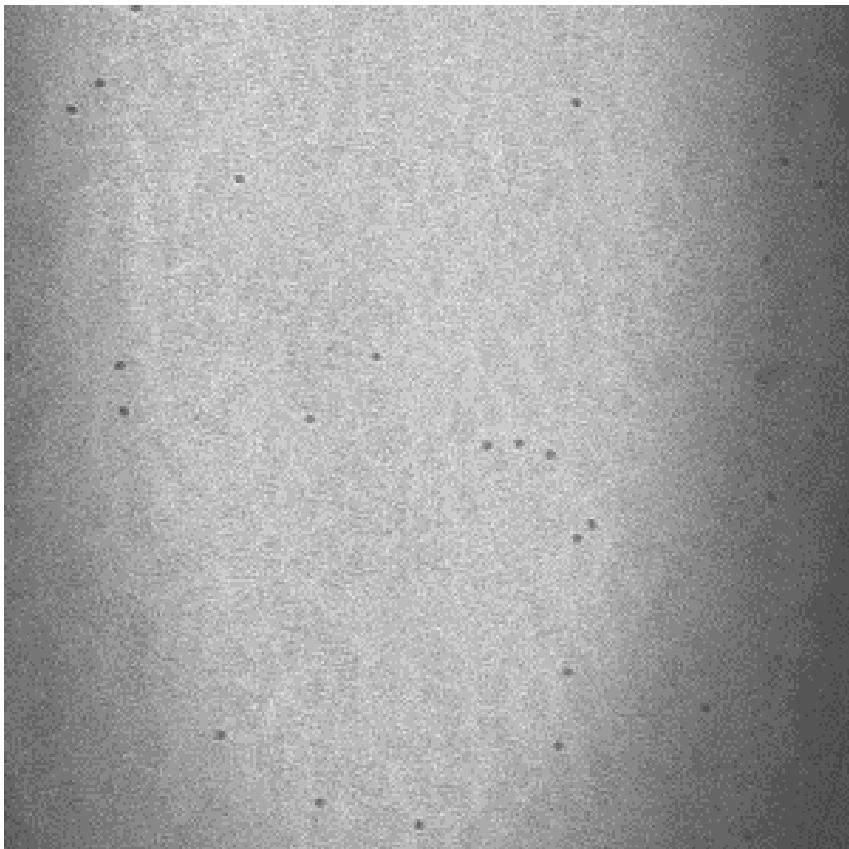
Workflow in Electron Tomography



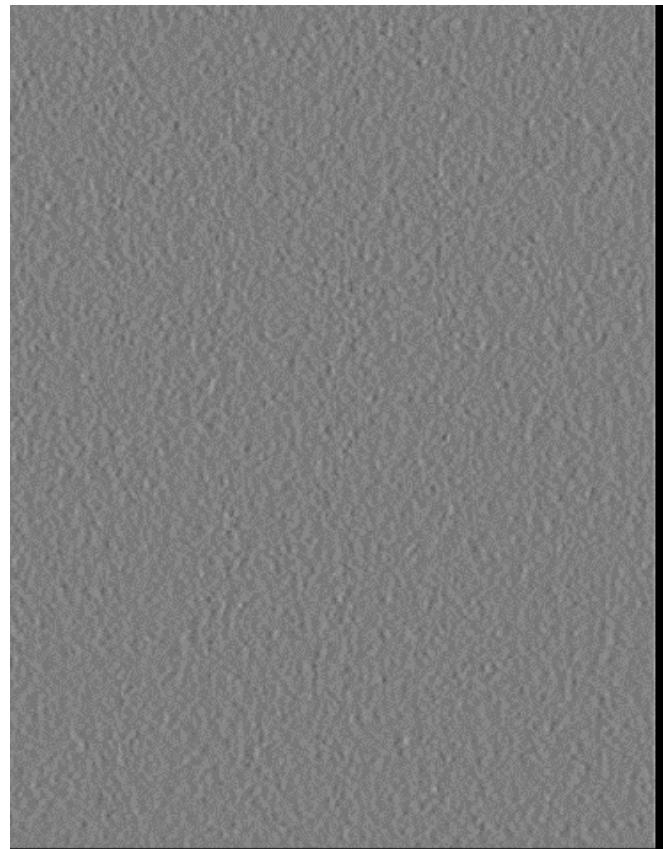


Principles of Electron Tomography

Aligned Tilt Series

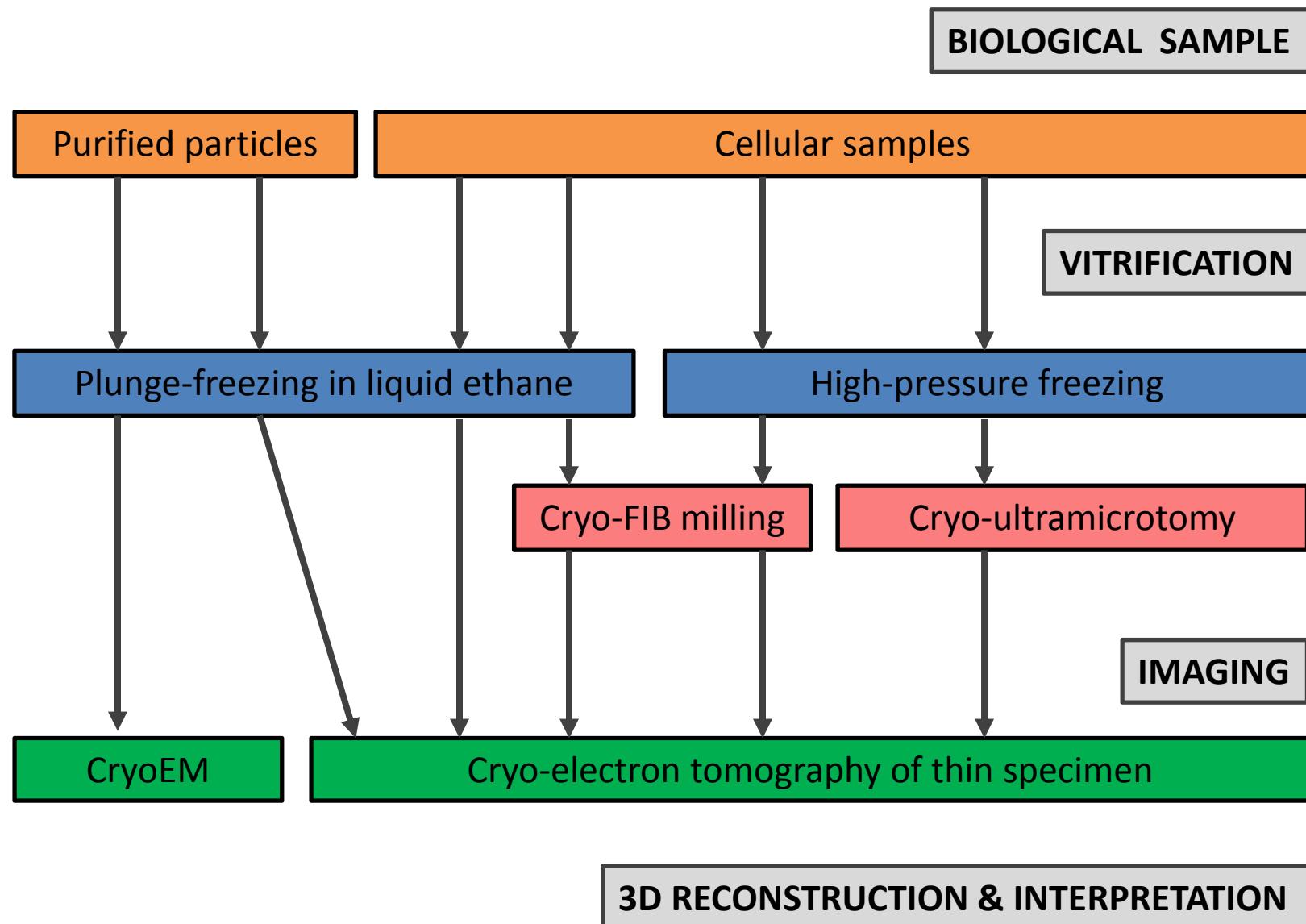


Reconstructed Tomogram



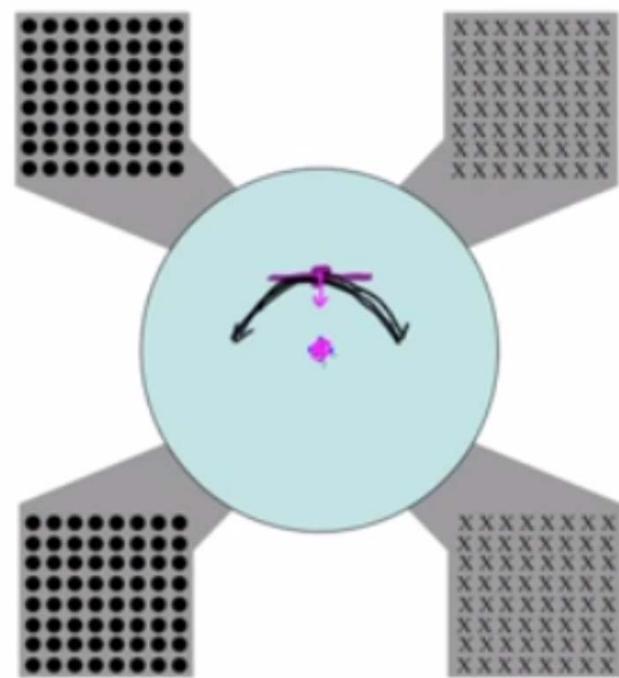
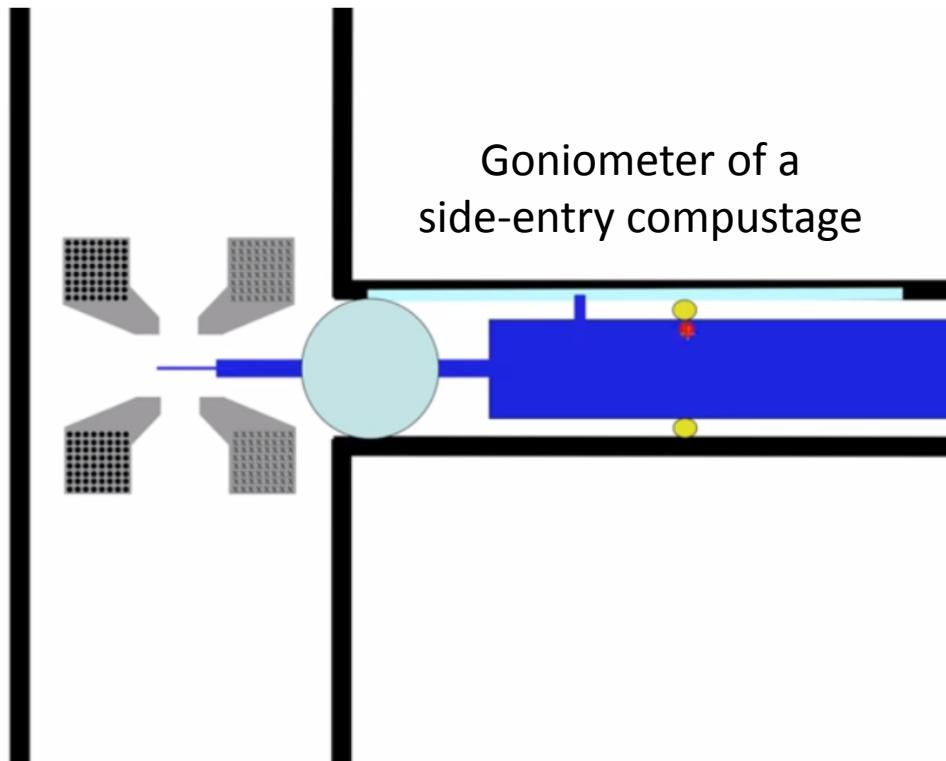


Sample Preparation for CryoET





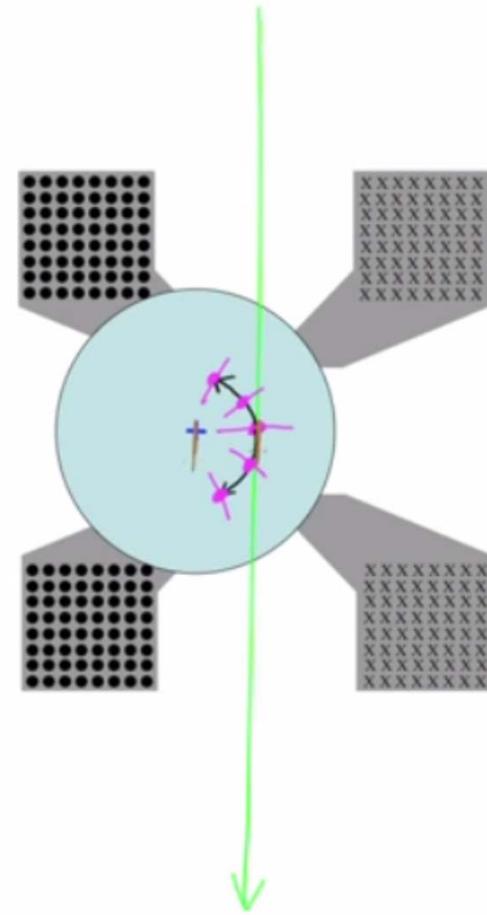
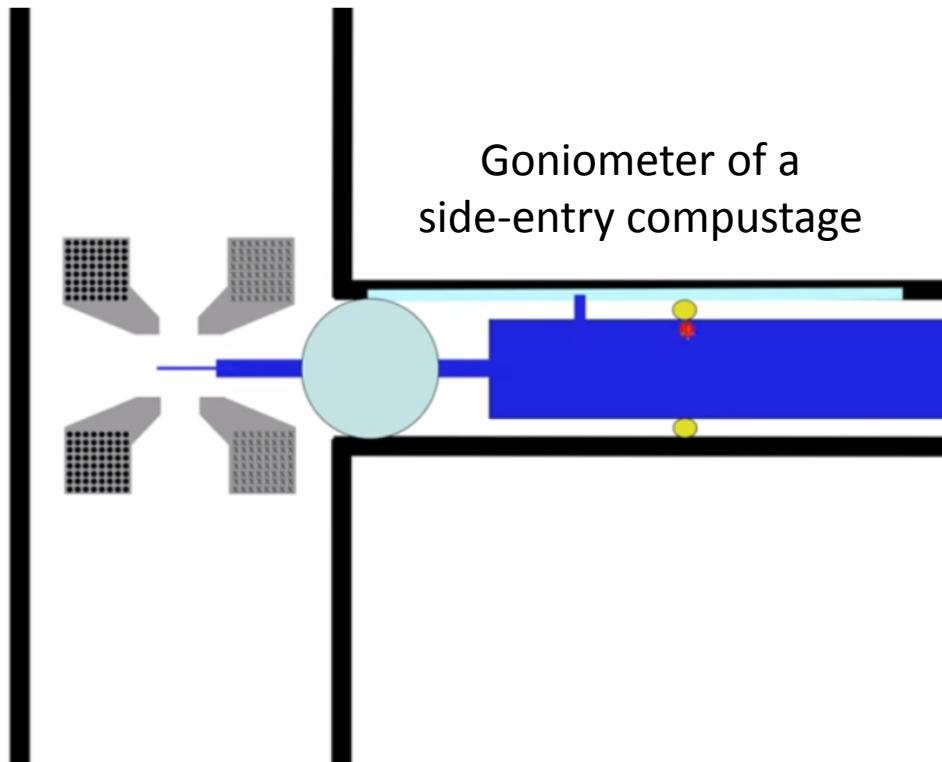
Acquisition of Tilt Series



Eucentric height



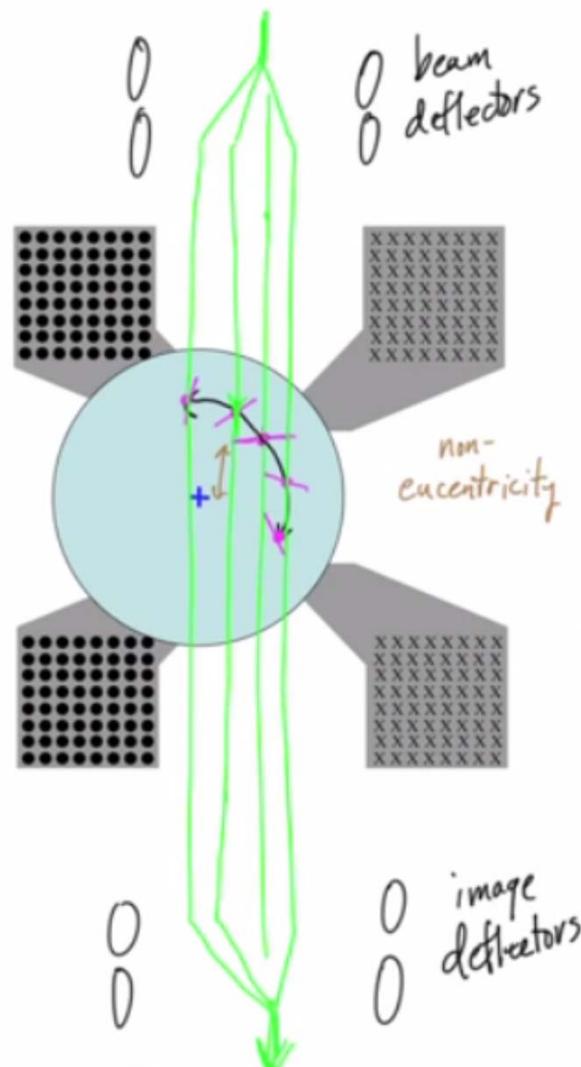
Acquisition of Tilt Series



Tilt axis offset

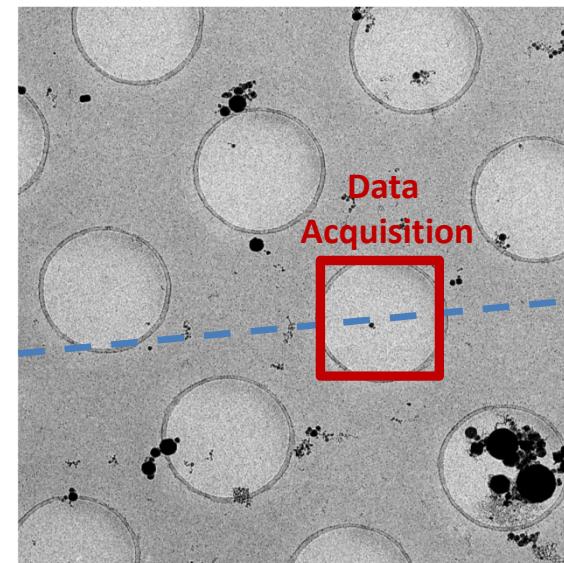


Acquisition of Tilt Series



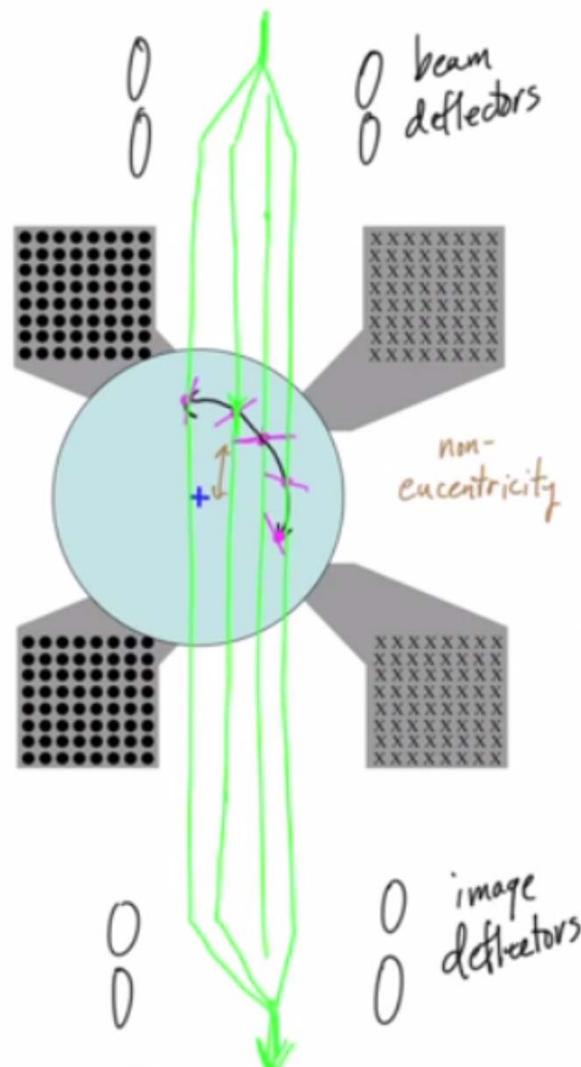
Predictive Method

- Collect few initial tilt images
- Determine image shifts
- Fit shift to a model of tilt geometry
- Predict and apply beam/image shifts
- Collect further images, refine model



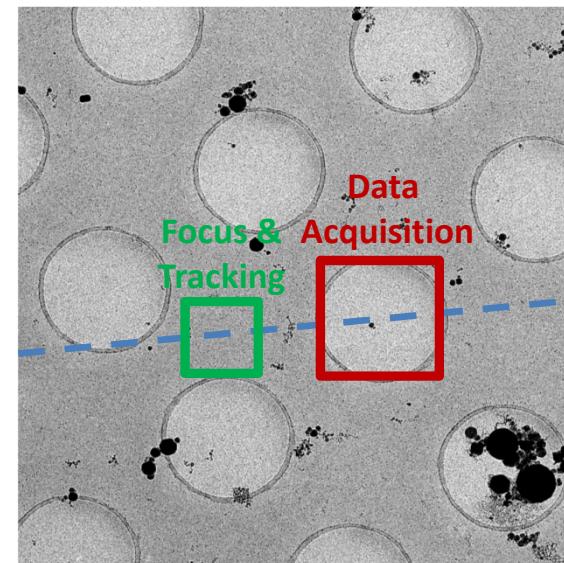


Acquisition of Tilt Series



Focus Position Method

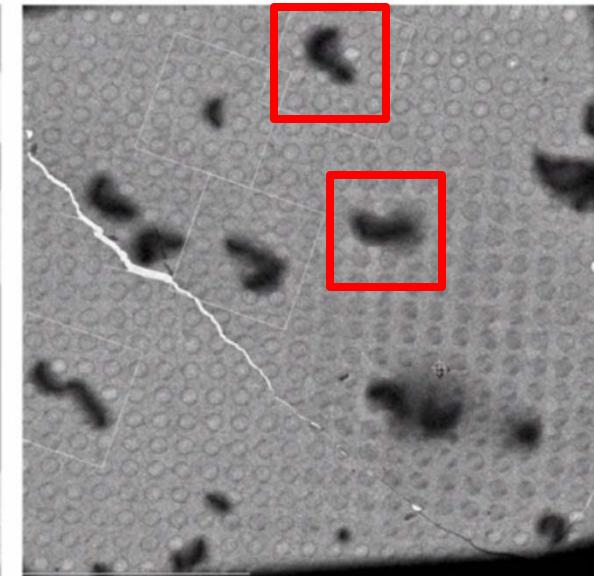
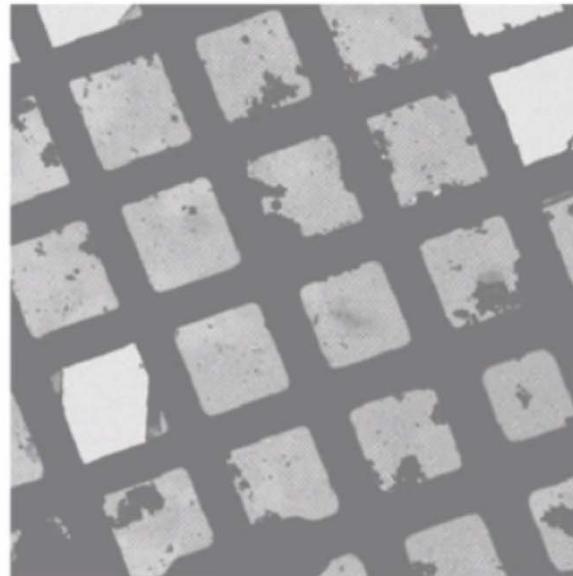
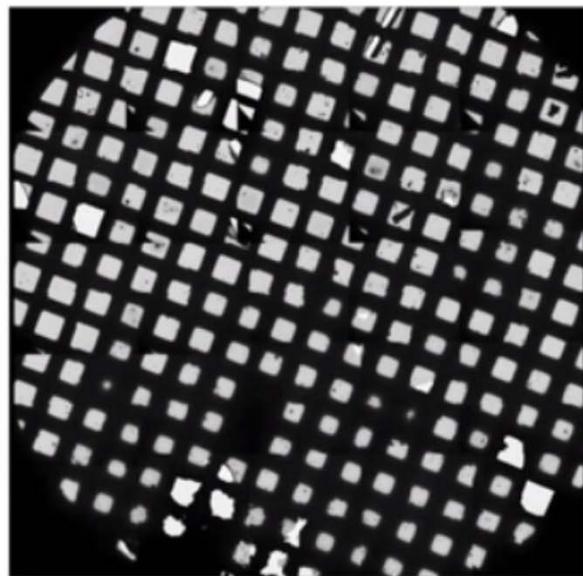
- Move to Focus, focus and center
- Move to Record, collect image
- Tilt, move to Focus, focus, center
- Move to Record, collect image
- Refine model of beam/image shifts





Automated Data Collection

Identify the target area of interest



Set parameters for data collection:

Range of tilt angles: -60° to $+60^\circ$

Angular step: 1° or 2°

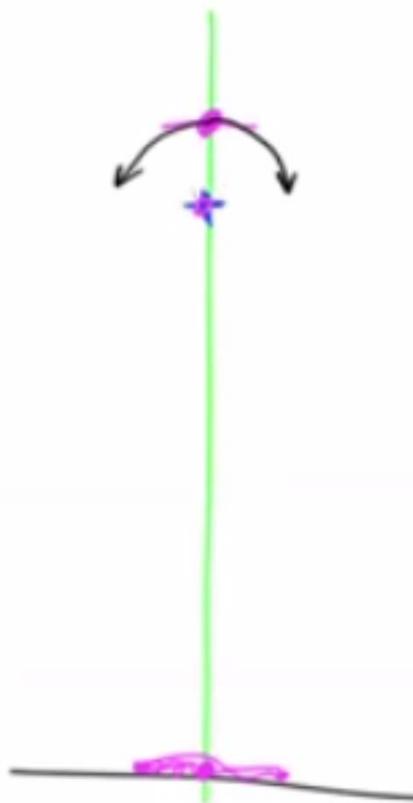
Dose per image: $0.5\text{-}2.0 \text{ e}^-/\text{Å}^2$

Dose distribution: uniform vs. tilt-dependent

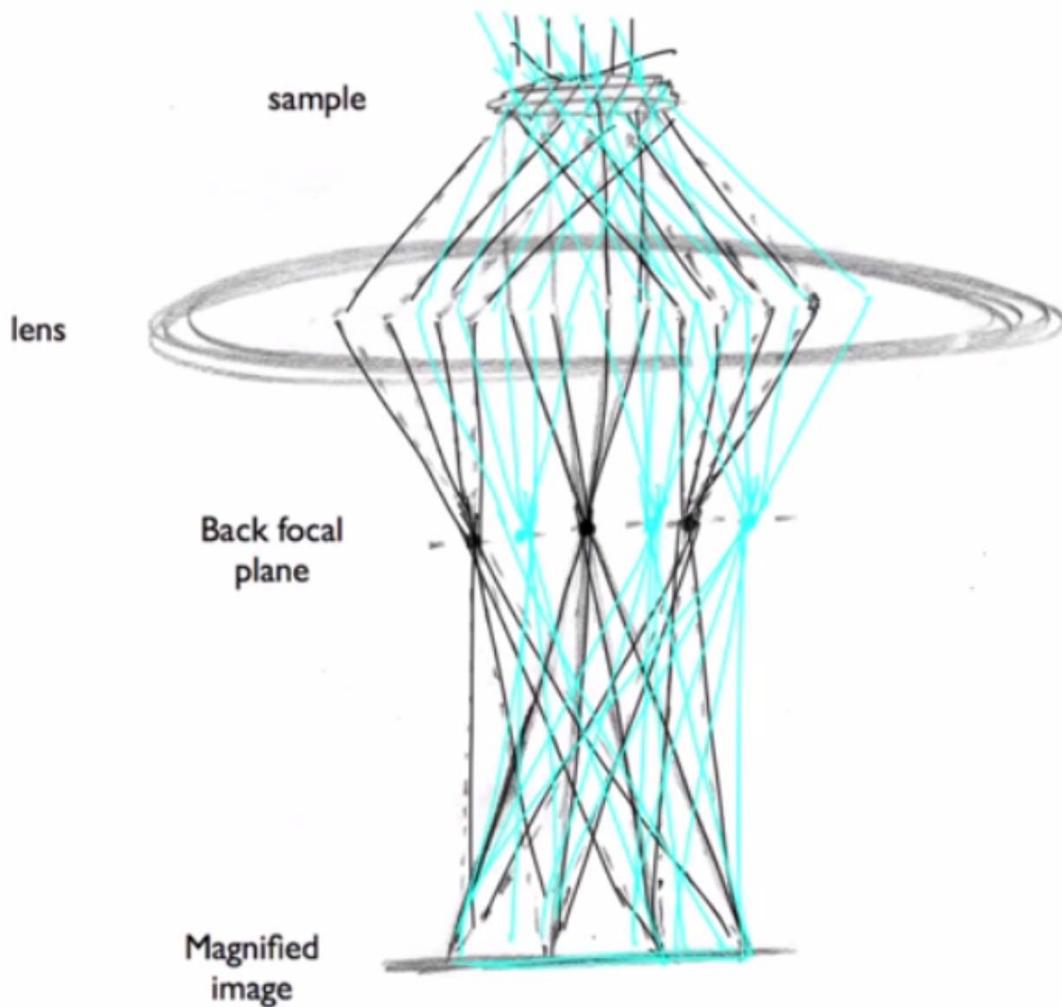


Automated Data Collection

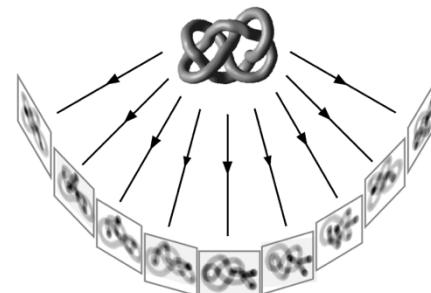
Automated determination of the Eucentric height



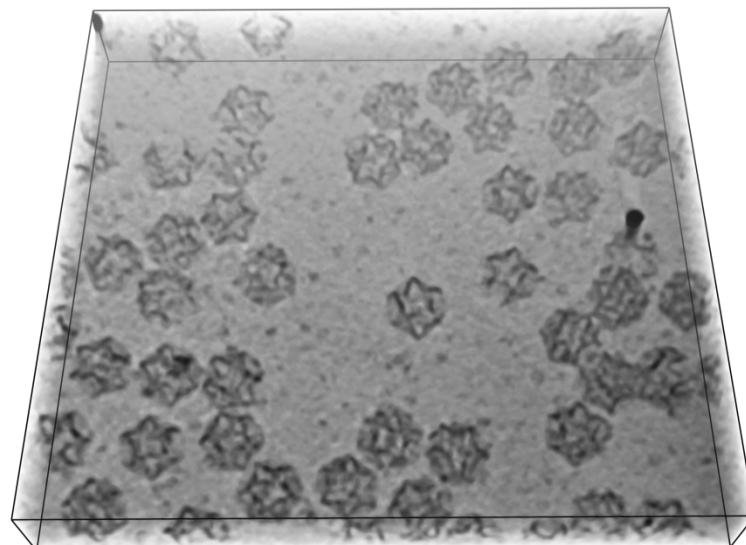
Automated focusing



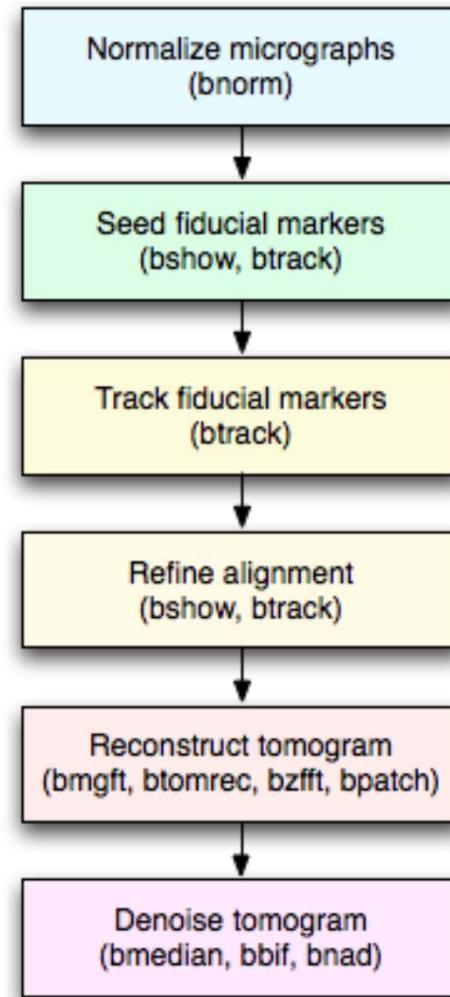
Electron Tomography



Data acquisition (tilt series)

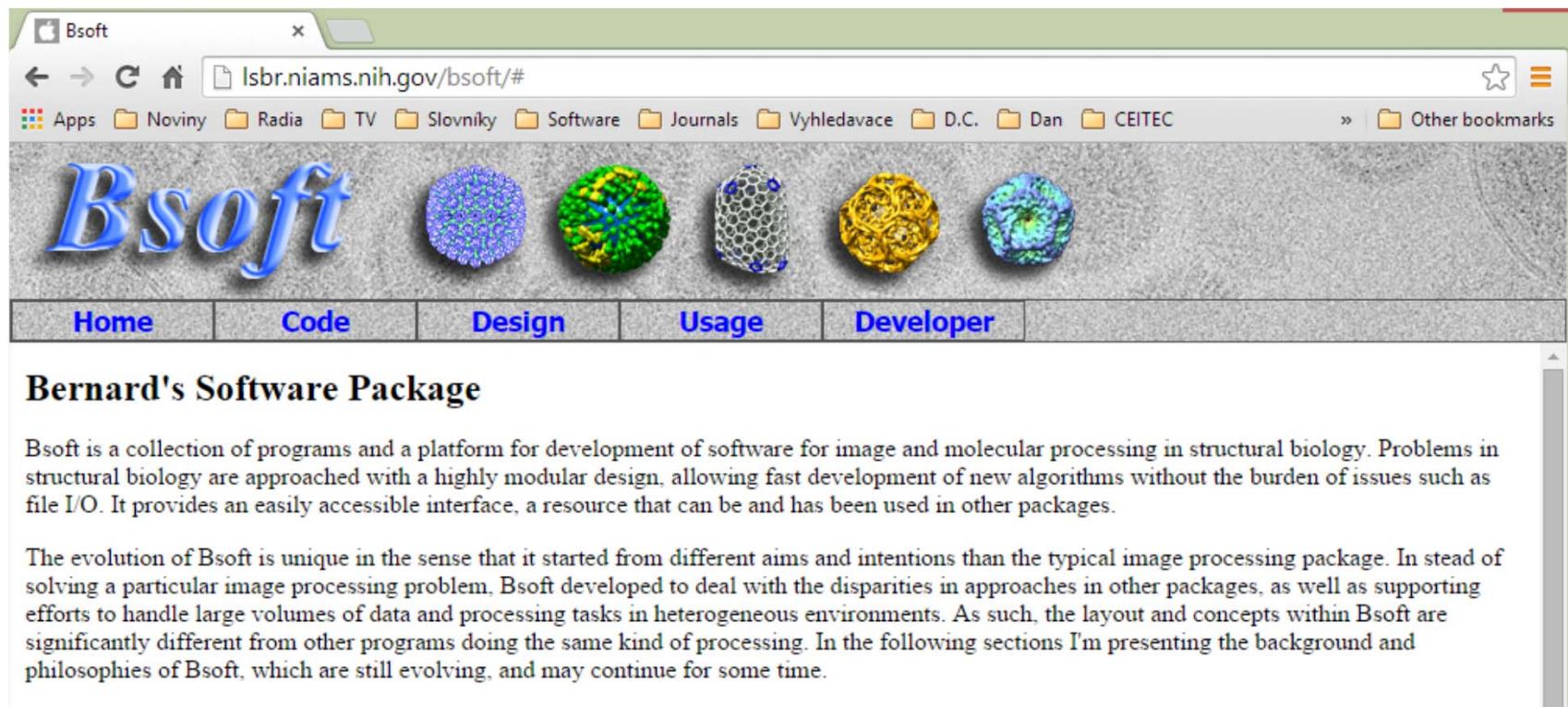


Reconstructed tomogram



Tomogram reconstruction workflow
(IMOD, Bsoft, EMAN2, Xmipp)

Image processing in Bsoft

A screenshot of a web browser window showing the Bsoft homepage. The title bar says "Bsoft". The address bar shows "lsbr.nih.gov/bsoft/#". The menu bar includes "Apps", "Noviny", "Radia", "TV", "Slovníky", "Software", "Journals", "Vyhledavace", "D.C.", "Dan", "CEITEC", and "Other bookmarks". Below the menu is a banner with the word "Bsoft" in large blue letters and five small molecular models. A navigation bar at the bottom has tabs for "Home", "Code", "Design", "Usage", and "Developer".

Bernard's Software Package

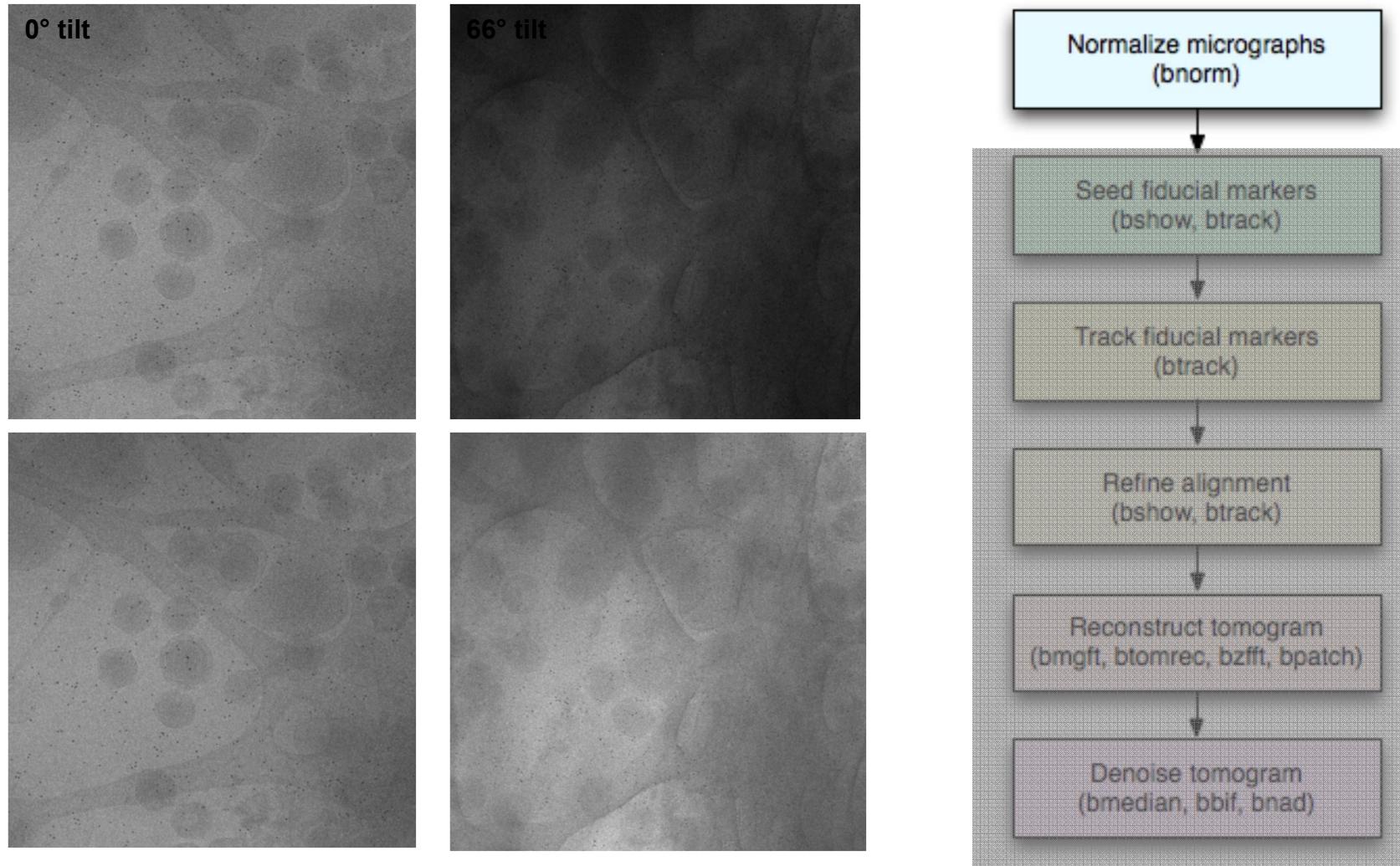
Bsoft is a collection of programs and a platform for development of software for image and molecular processing in structural biology. Problems in structural biology are approached with a highly modular design, allowing fast development of new algorithms without the burden of issues such as file I/O. It provides an easily accessible interface, a resource that can be and has been used in other packages.

The evolution of Bsoft is unique in the sense that it started from different aims and intentions than the typical image processing package. In stead of solving a particular image processing problem, Bsoft developed to deal with the disparities in approaches in other packages, as well as supporting efforts to handle large volumes of data and processing tasks in heterogeneous environments. As such, the layout and concepts within Bsoft are significantly different from other programs doing the same kind of processing. In the following sections I'm presenting the background and philosophies of Bsoft, which are still evolving, and may continue for some time.

Images are stored in pif/mrc/tif files as a set of 2D images or as slices of a 3D image.

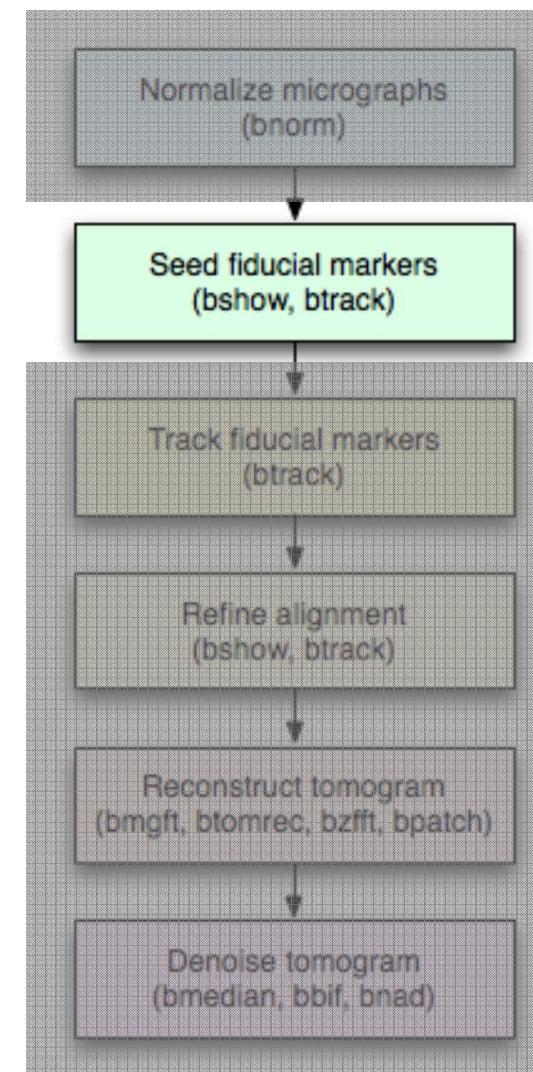
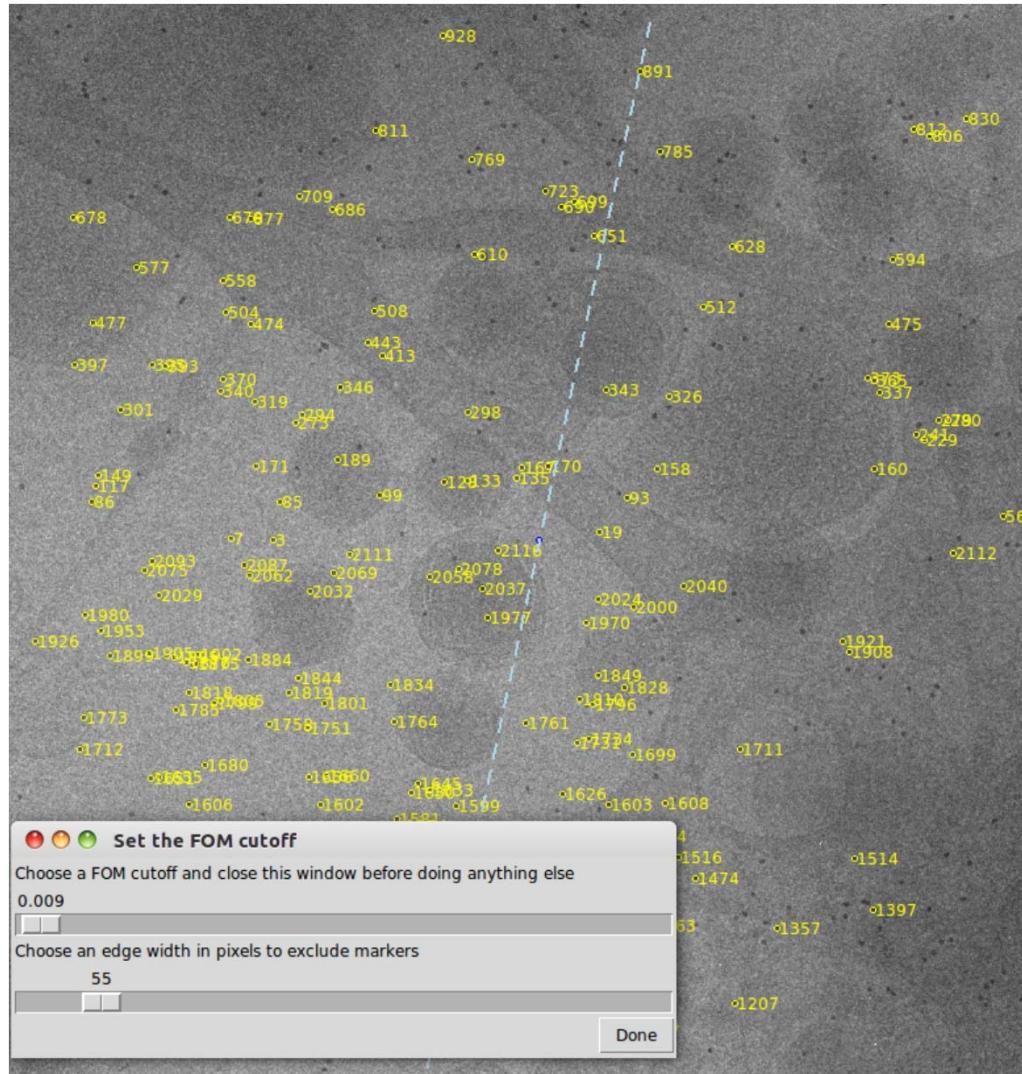
Parameters are stored in **ASCII star files** with predetermined organization for **micrographs, reconstructions and models**.

Preprocessing of collected data

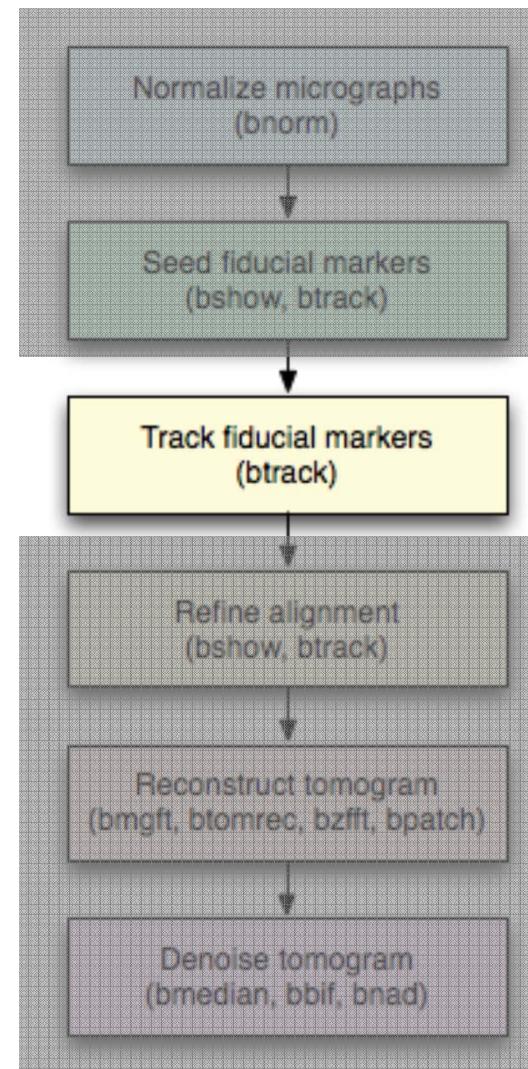
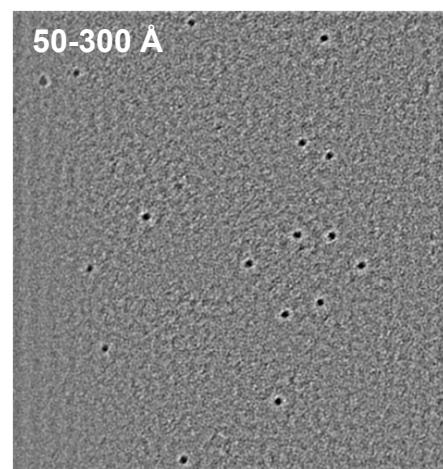
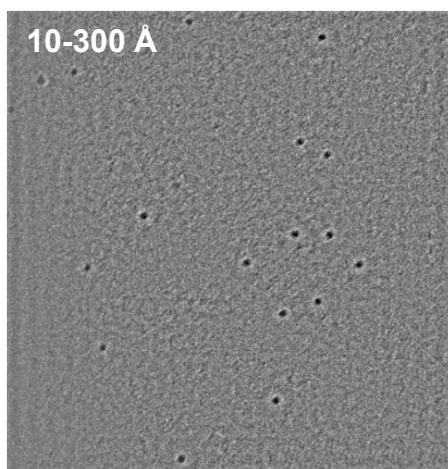
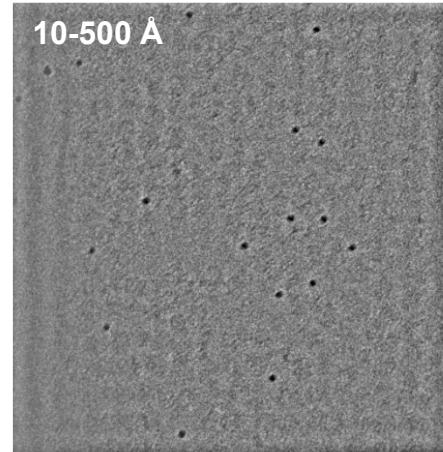
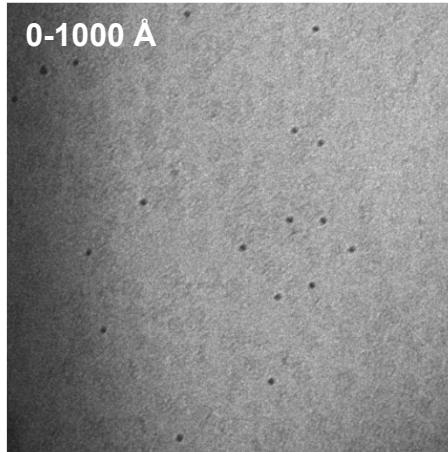


```
bnorm -ver 7 -images -rescale 127,10 -data byte -out output.star input.mrc output.pif  
btomo -v 7 -sampling 8.05 -axis 78 -tilt -60,2 -gold 5 -out output.star input.star
```

Finding fiducial markers for alignment of tilt series

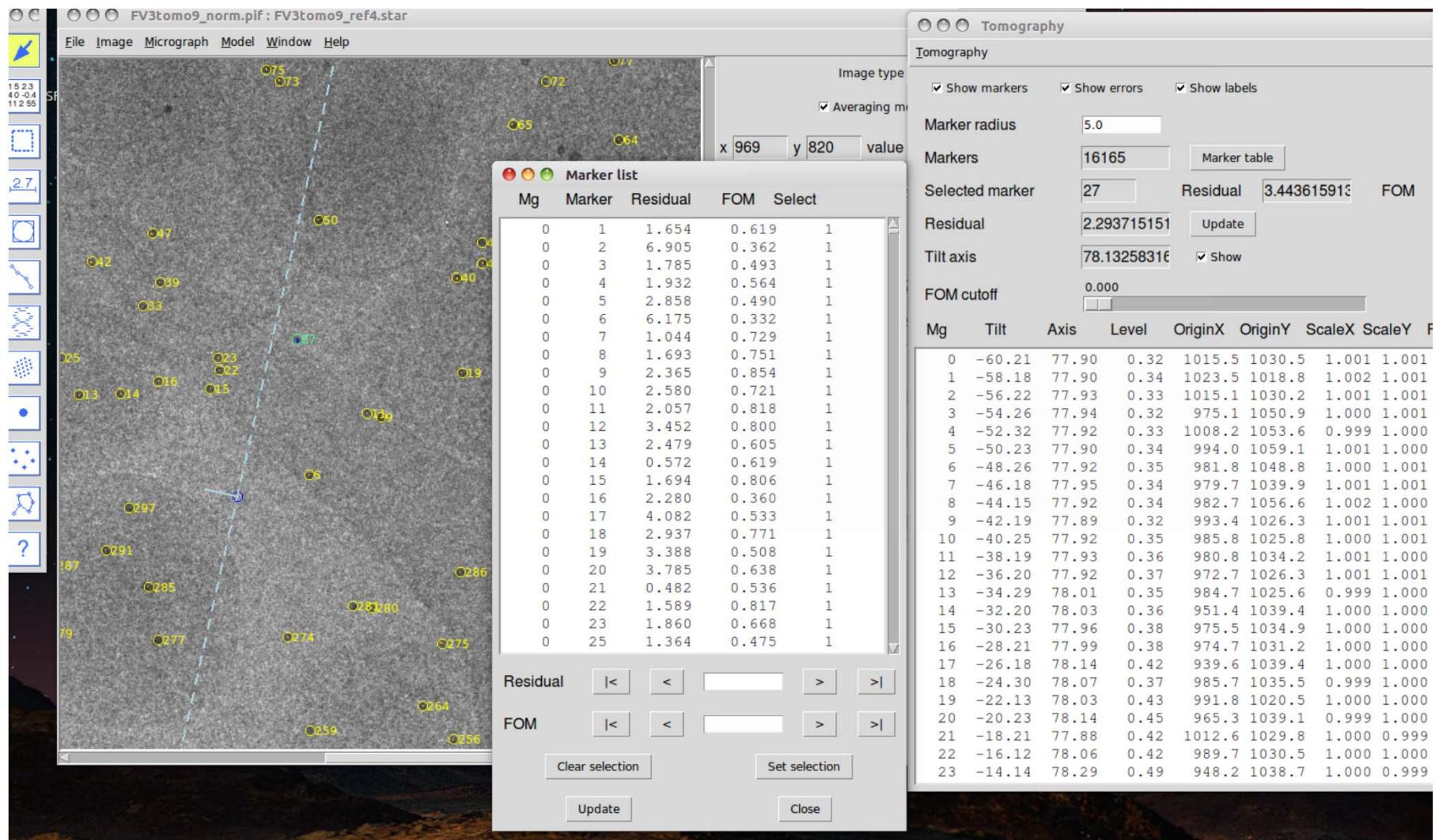


Tracking fiducial markers in all tilt images



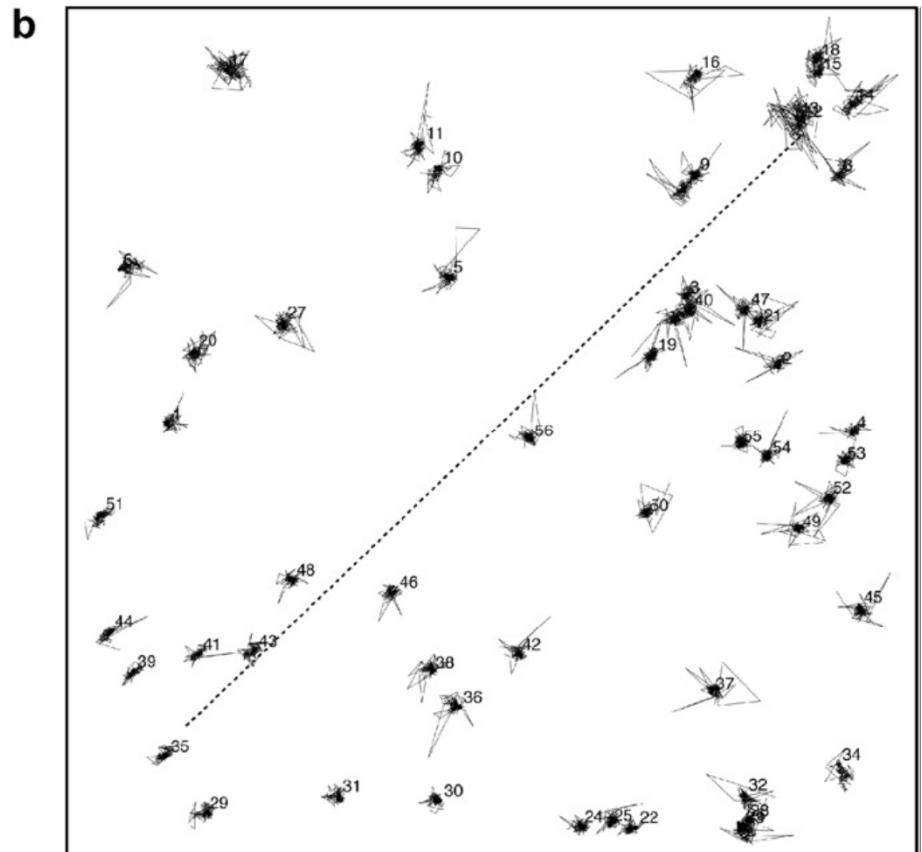
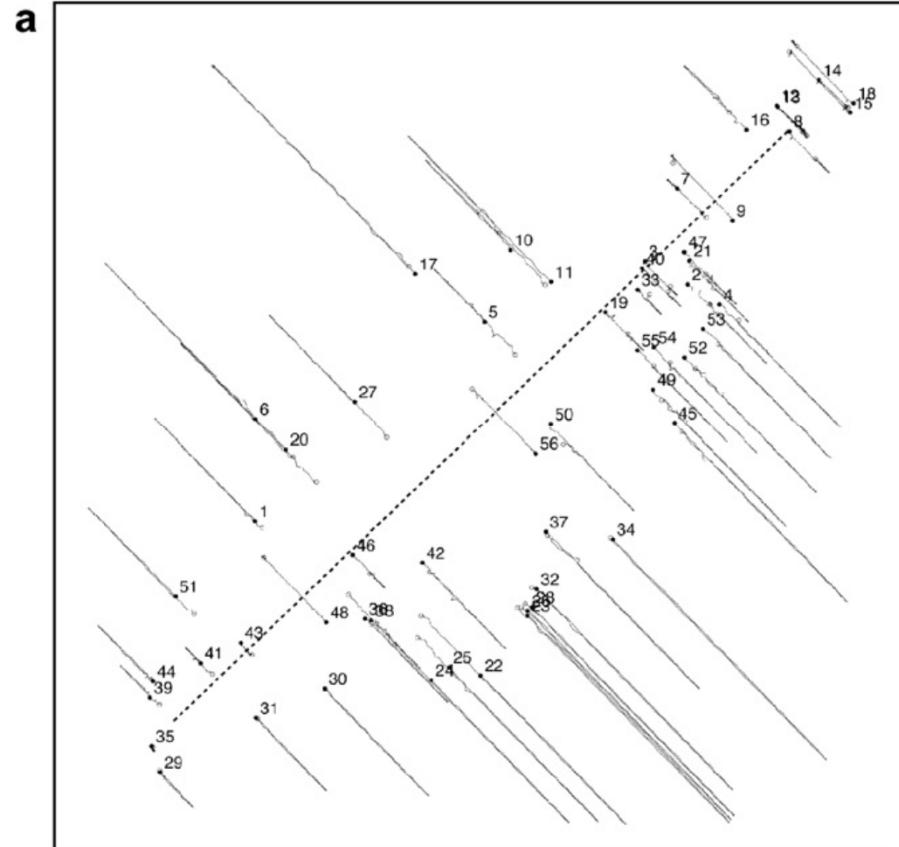
```
btrack -ver 1 -reset -axis 78 -exclude none -resol 15,300 -shift 1000 -update -track 5  
-refine markers -out FV3tomo9_trk.star FV3tomo9_seed.star >& FV3tomo9_trk.log
```

Refinement of fiducial marker positions



```
btrack -ver 1 -reset -refine 10,z,o,v -image FV3tomo9_align.pif -Post FV3tomo9_err.ps
-out FV3tomo9_ref1.star FV3tomo9_ref0.star >& FV3tomo9_ref1.log
```

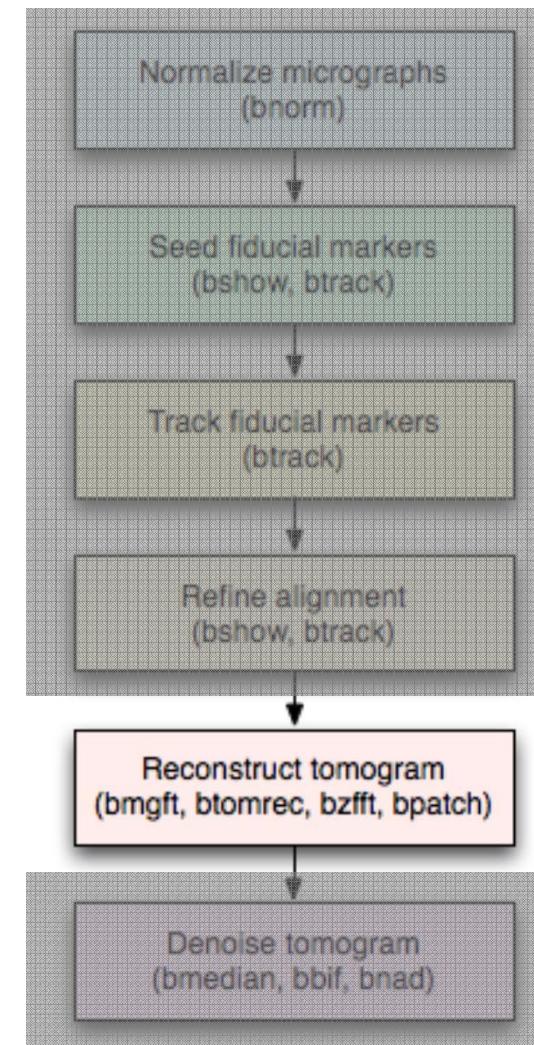
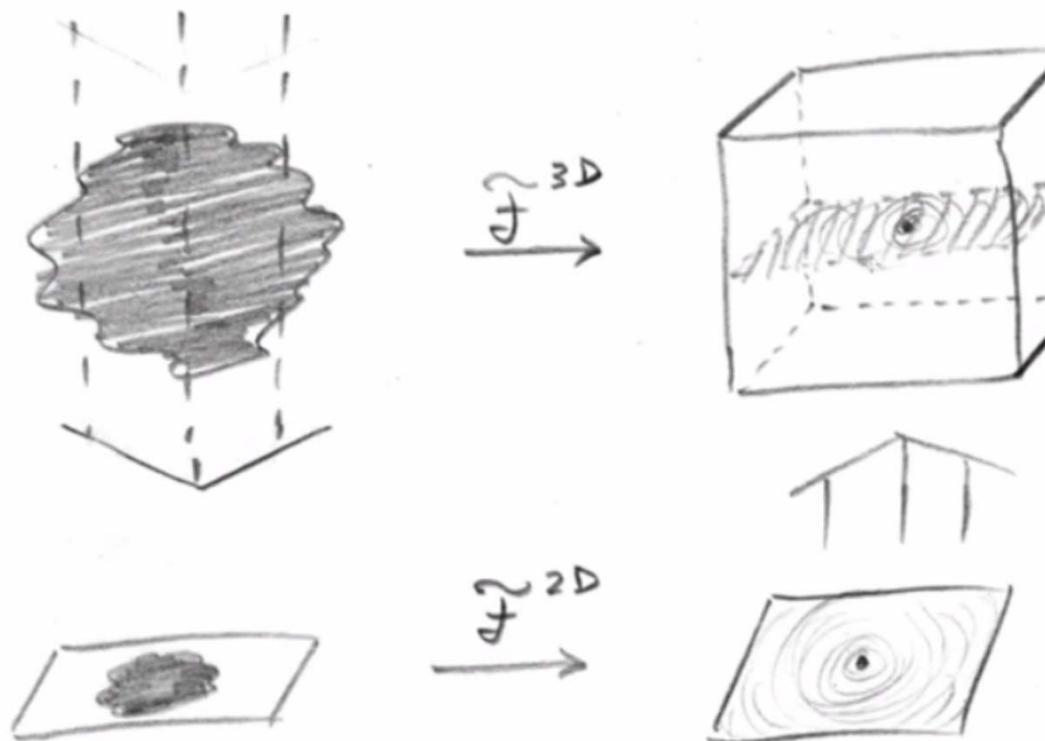
Refinement of fiducial marker positions



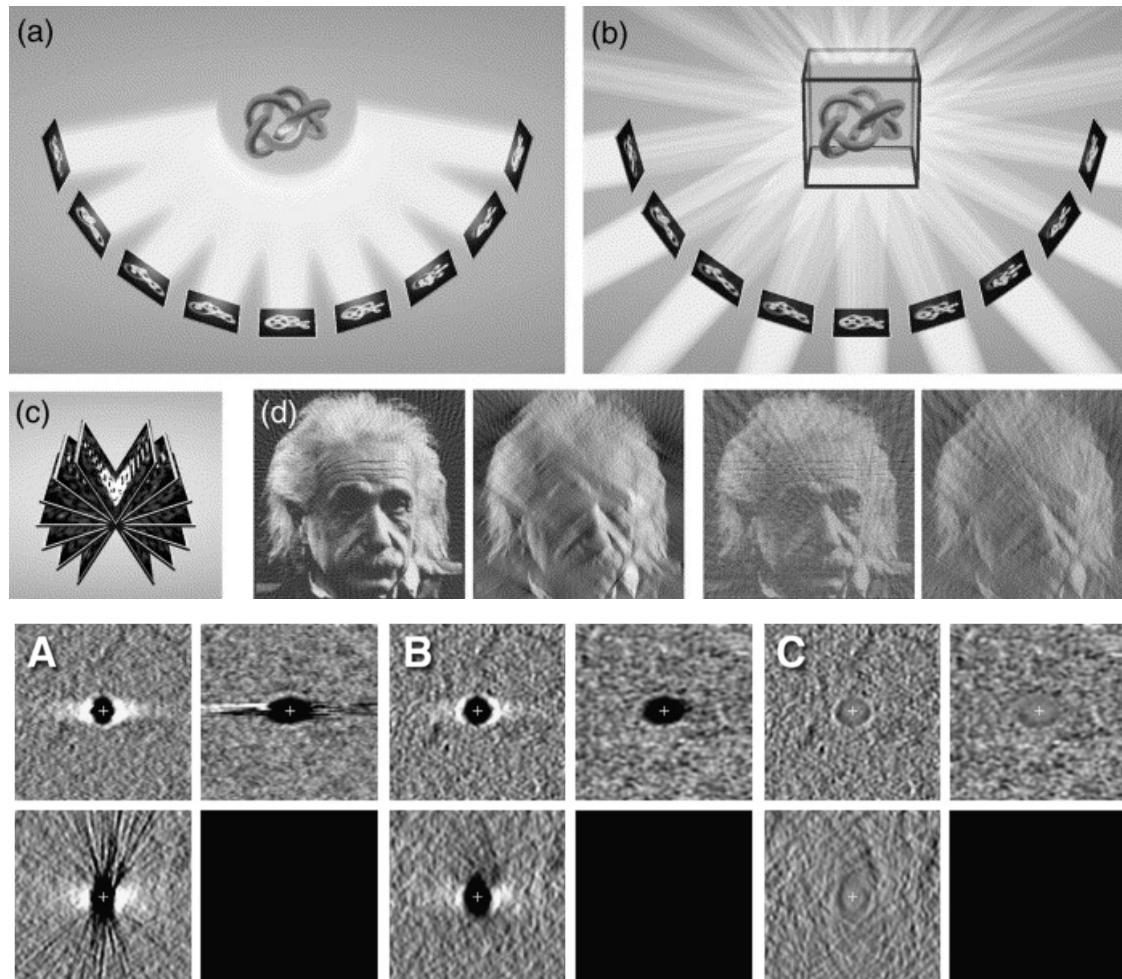
```
btrack -ver 1 -reset -refine 10,z,o,v -image FV3tomo9_align.pif -Post FV3tomo9_err.ps  
-out FV3tomo9_ref1.star FV3tomo9_ref0.star >& FV3tomo9_ref1.log
```

Tomogram reconstruction

The projection theorem

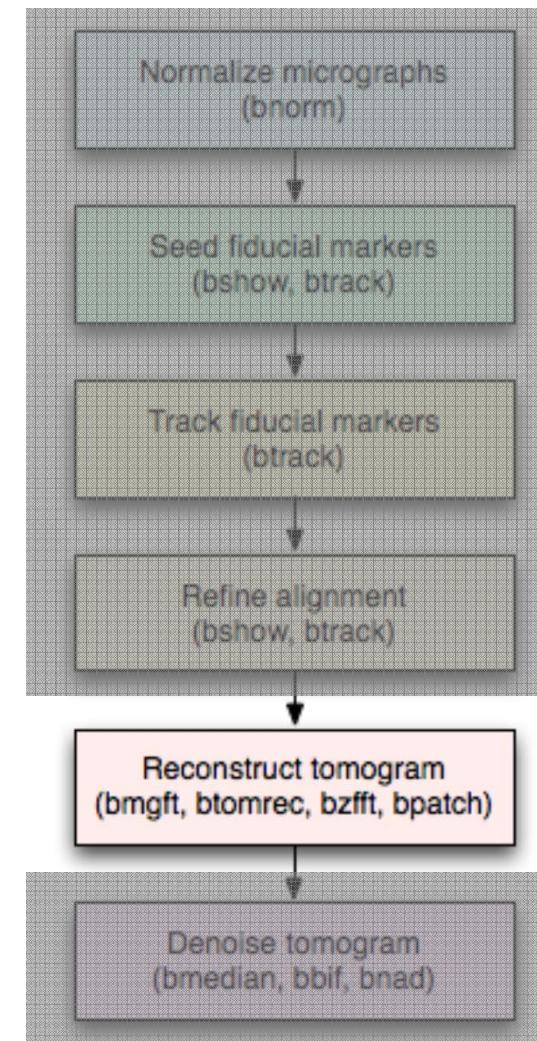


Tomogram reconstruction

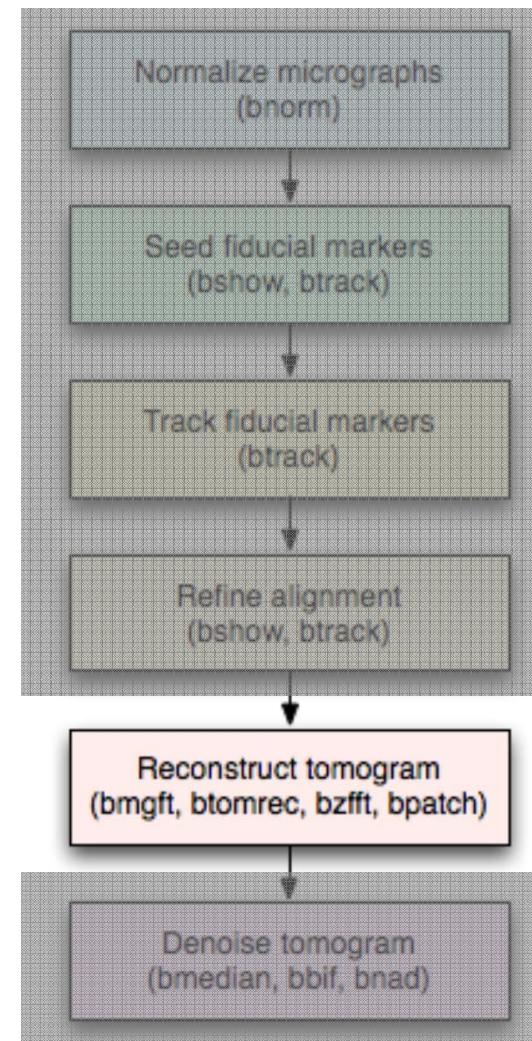
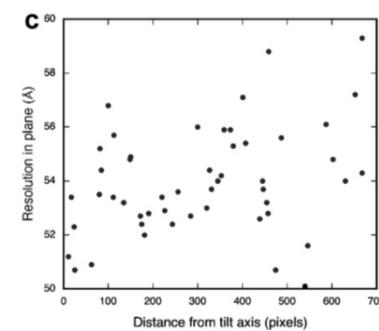
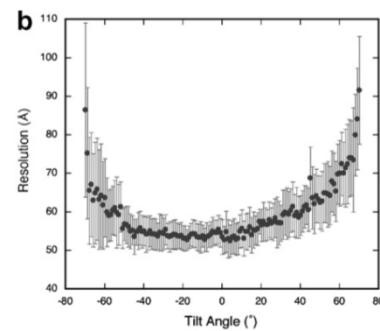
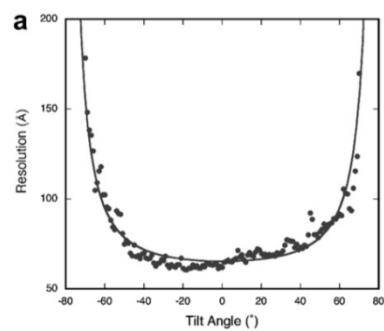
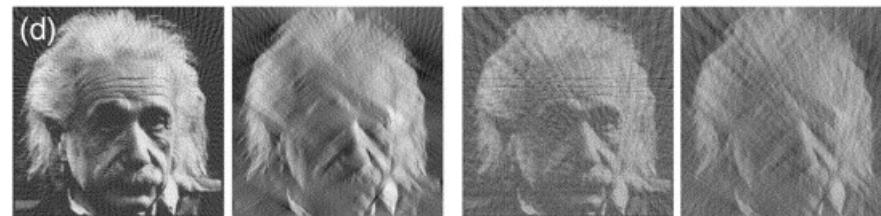
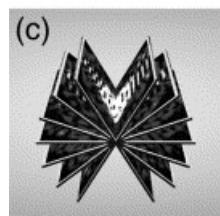
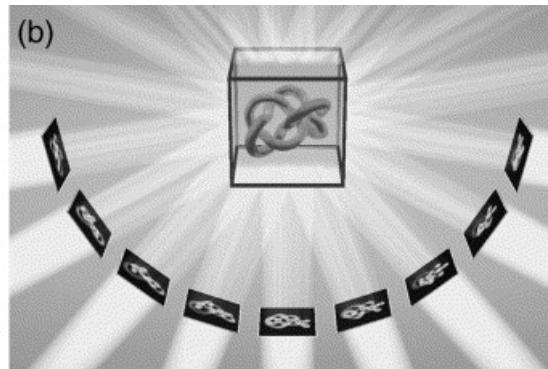
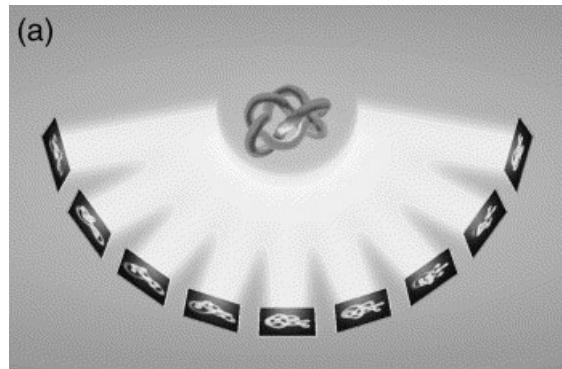


bmark -v 7 FV3tomo7_ref4.star

```
tomrec_PBS.tcsh -rec output.pif -resol 20 -size 2048,2048,550 -remove 10 -thick  
20 -scale 1 -out output.star input.star
```



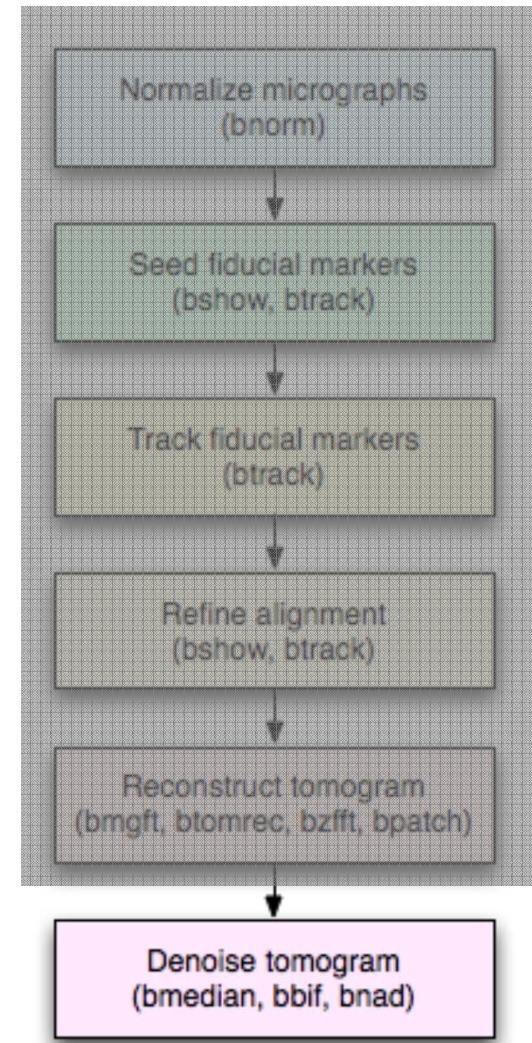
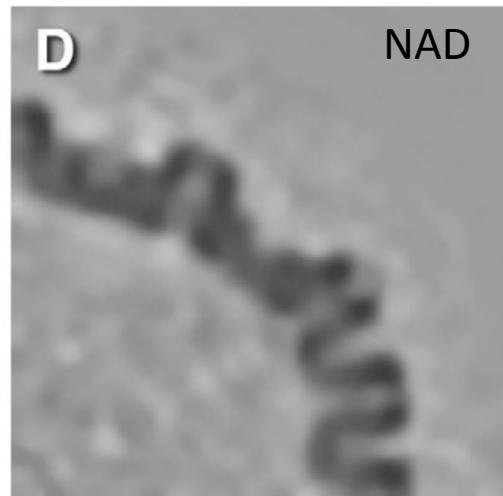
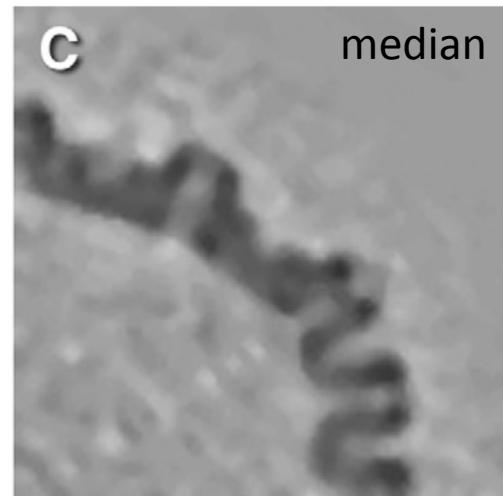
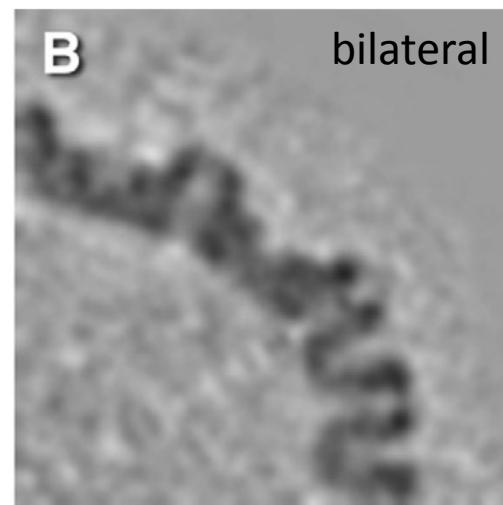
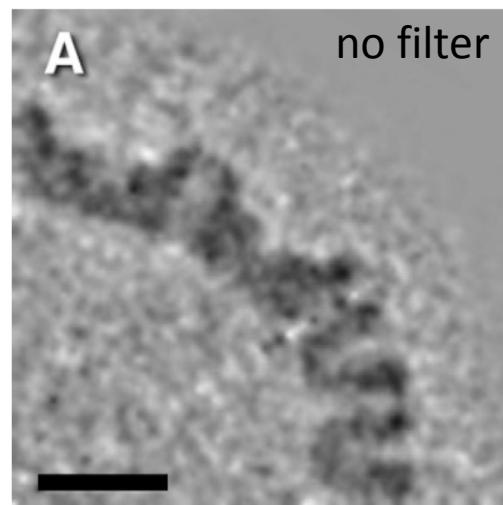
Tomogram reconstruction



bmark -v 7 FV3tomo7_ref4.star

tomrec_PBS.tcsh -rec output.pif -resol 20 -size 2048,2048,550 -remove 10 -thick 20 -scale 1 -out output.star input.star

Denoising of reconstructed tomograms



tomnad_PBS.tcsh -size 300,300,550 -overlap 100,100,0 -iterations 30 input.pif output.pif