ITERATIVE METHODS IN LARGE FIELD ELECTRON MICROSCOPE TOMOGRAPHY

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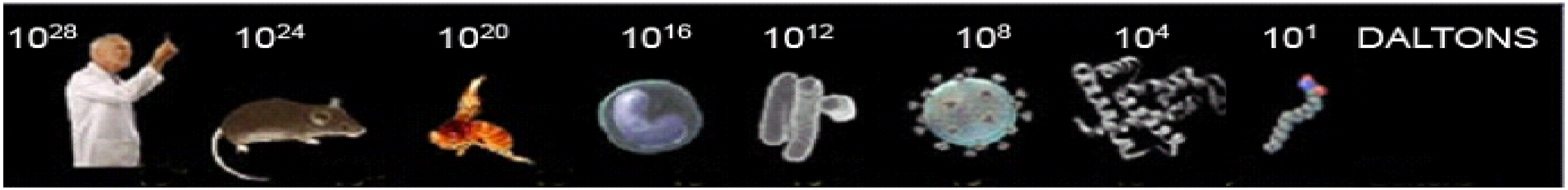
Outline

- Background
- Problem
- Our work
- Future work

Microscopy and Scale

Background



amino acid/nucleotide →

protein and nuclei acid →

protein complexes →

organelle →

cell →

tissue →

1m **1mm** **1um** **1nm**

→ Computed Tomography (CT)

→ Optical Microscopy

→ Confocal Microscopy

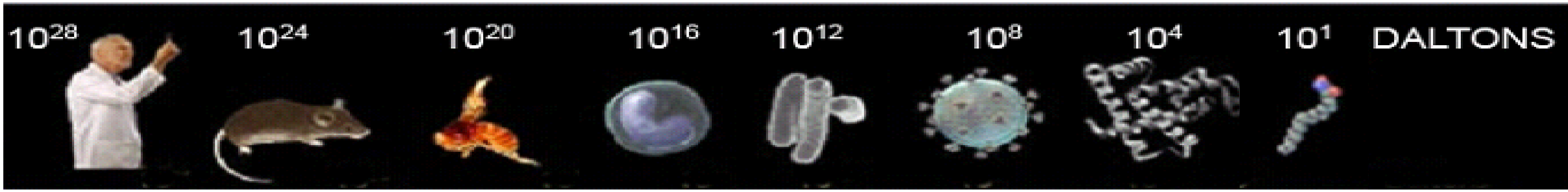
→ STED Microscopy

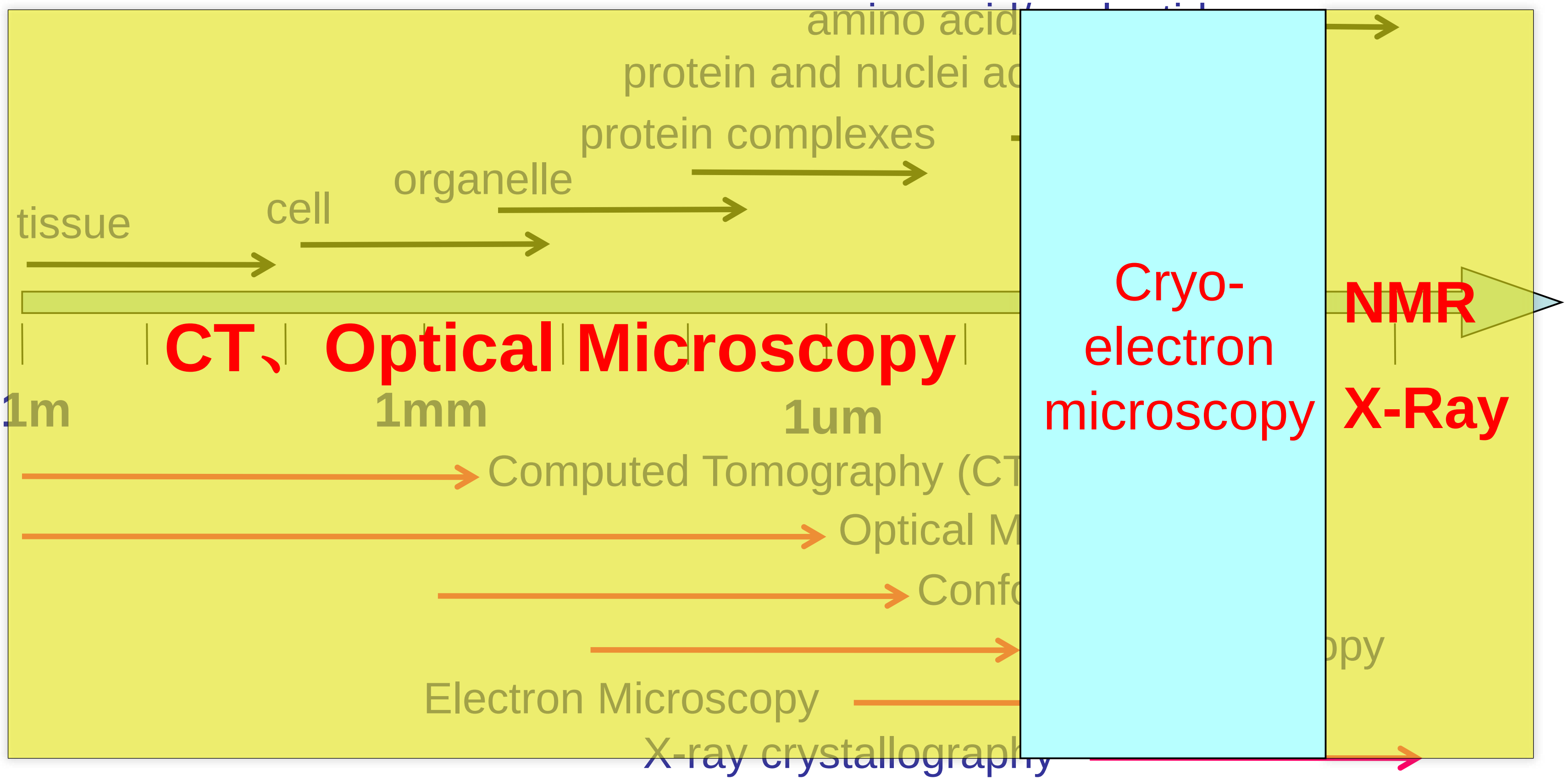
Electron Microscopy →

X-ray crystallography →

Microscopy and Scale

Background

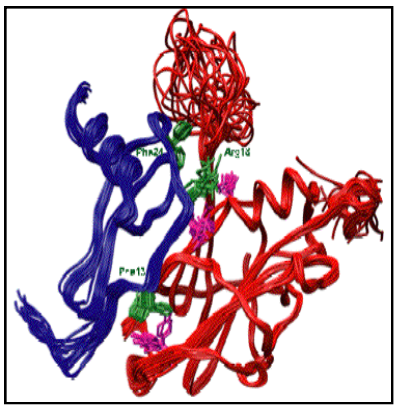
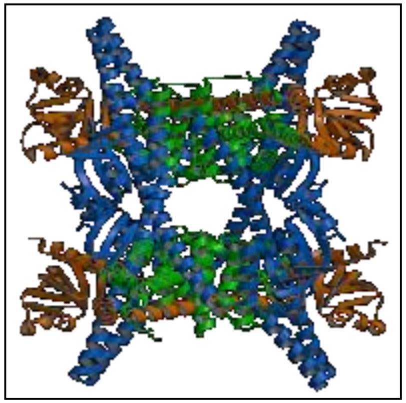
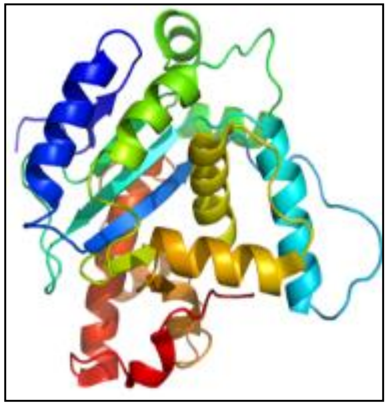
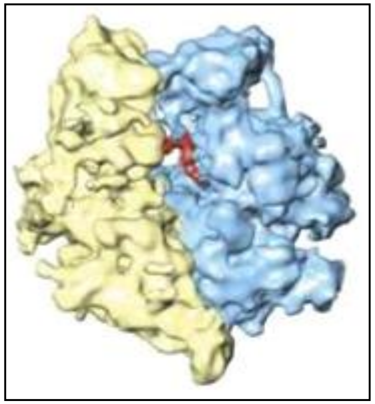




Methods for protein structures

Background

Protein Structures

NMR	X-ray crystallography	Structure Prediction	Electron Microscopy
			
20kD	virus	20kD	200kD

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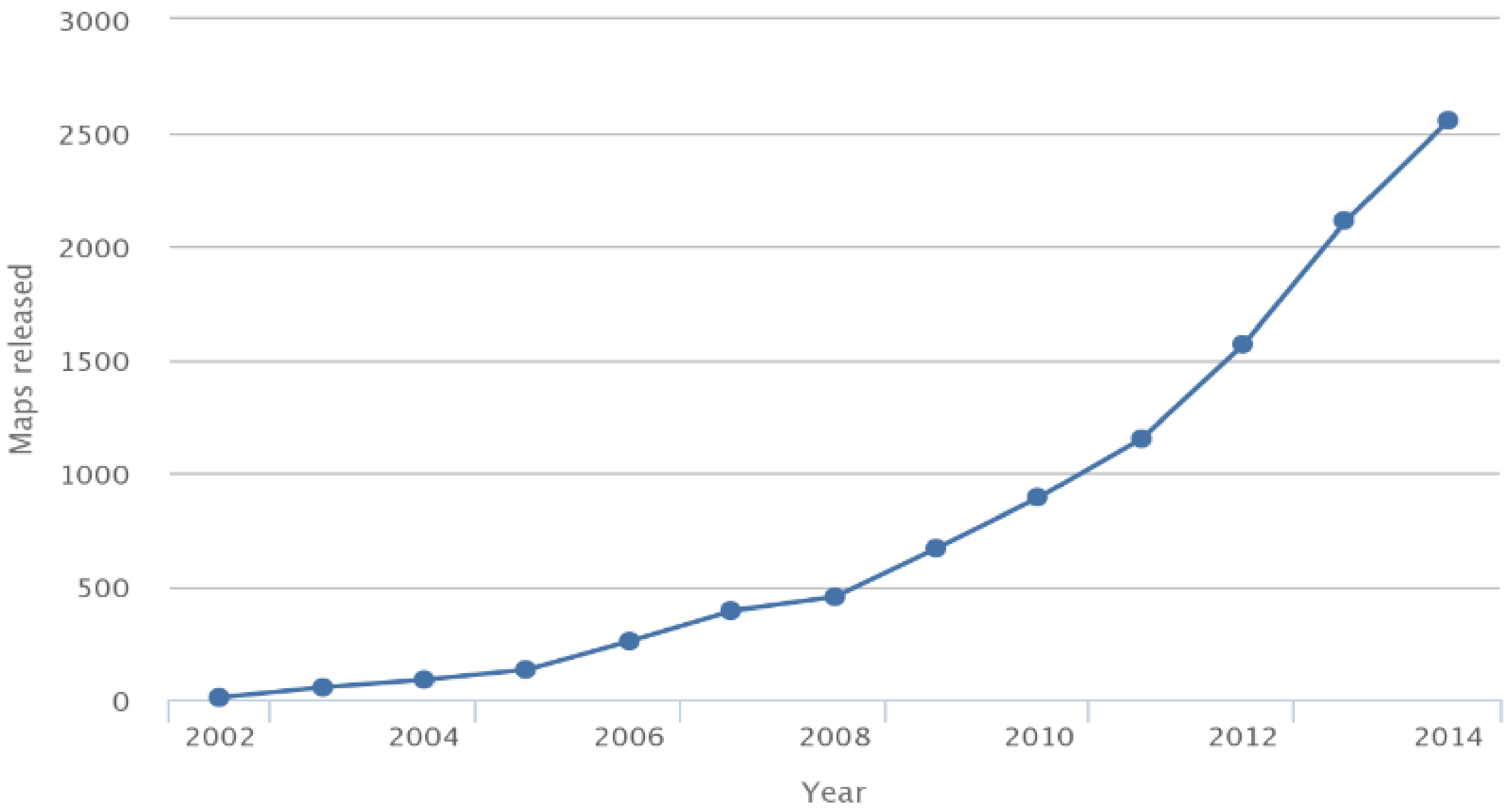
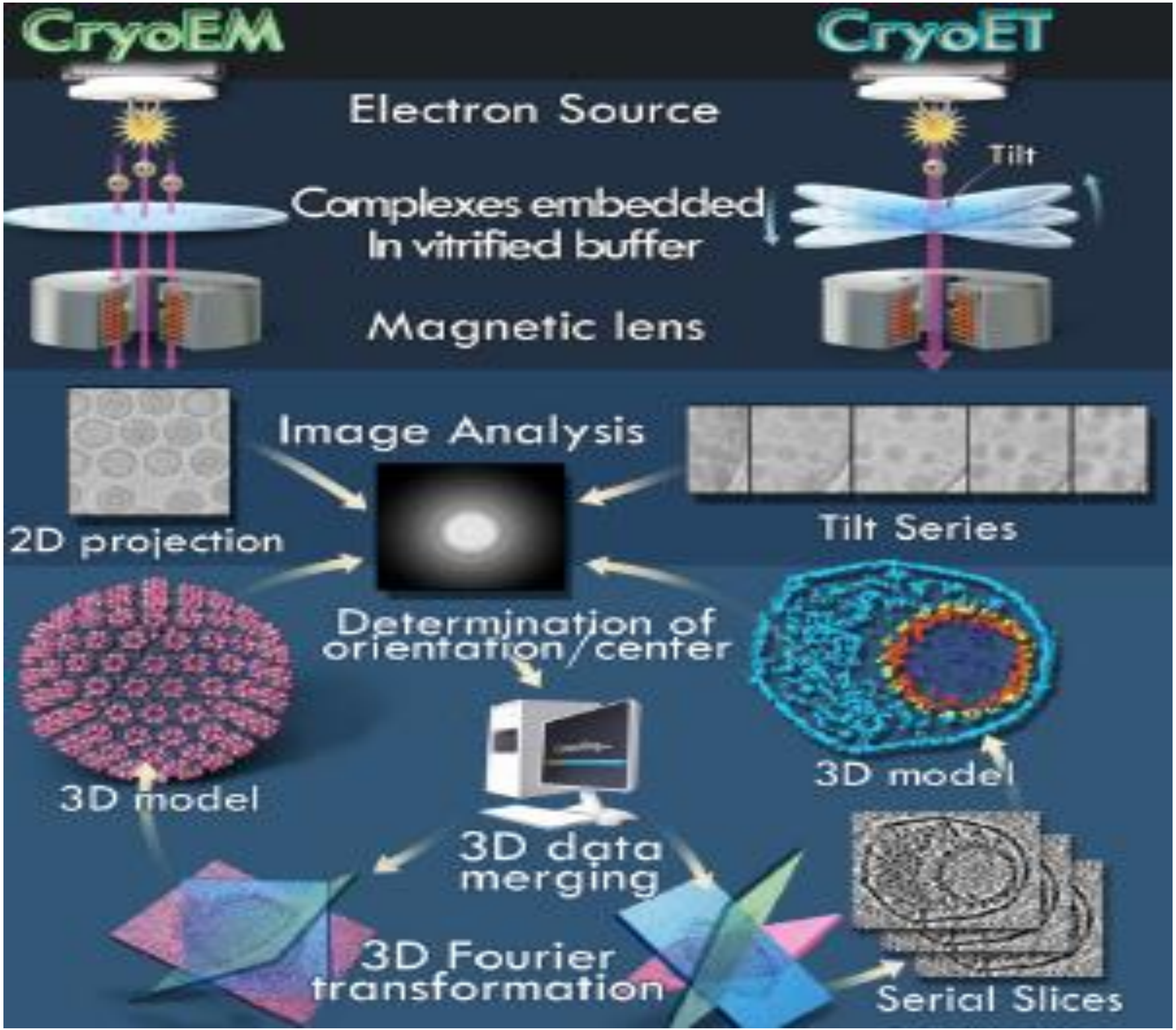
3D-EM Structures



http://www.ebi.ac.uk/pdbe/emdb/index.html

Electron Microscopy

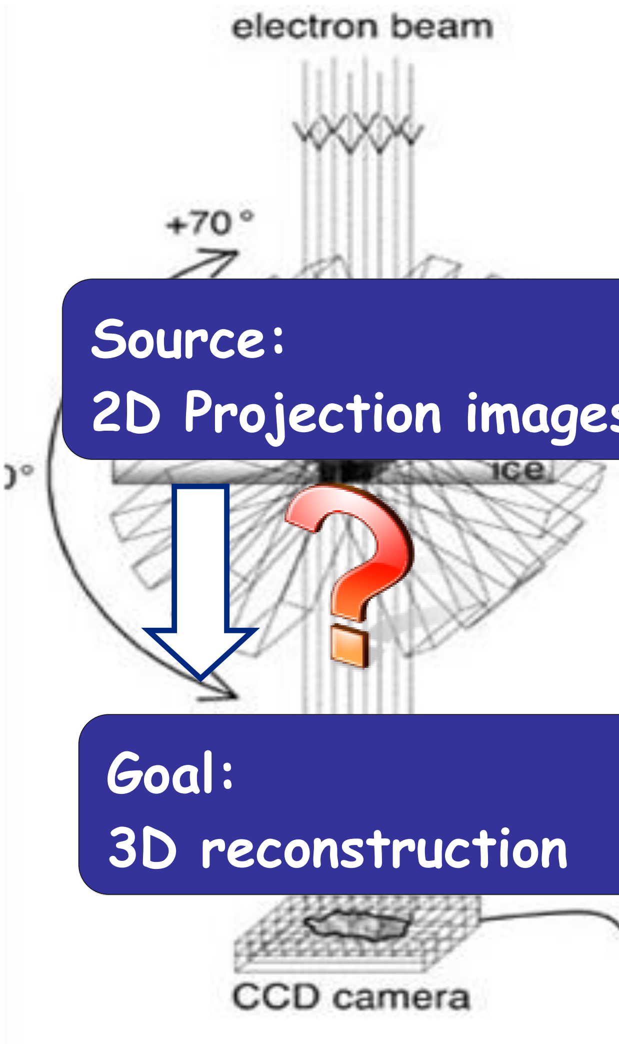
Single Particle



Electron Tomography

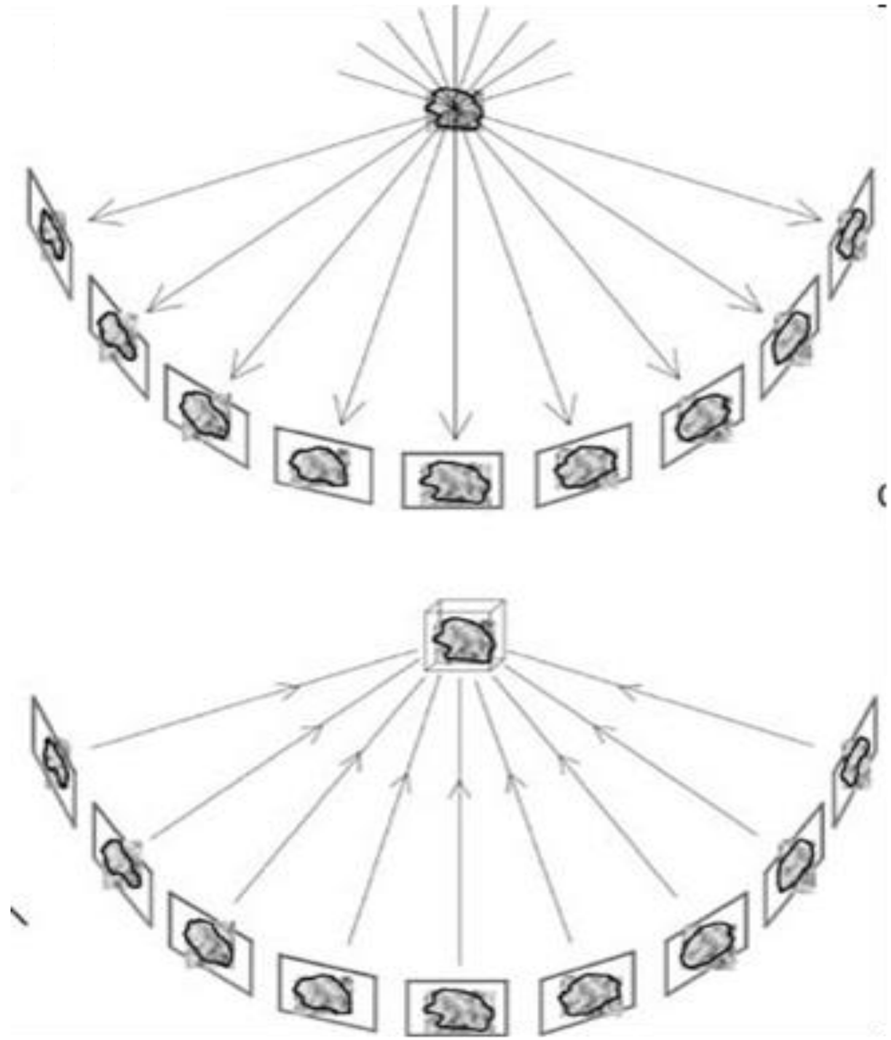
Electron Tomography (ET)

Background



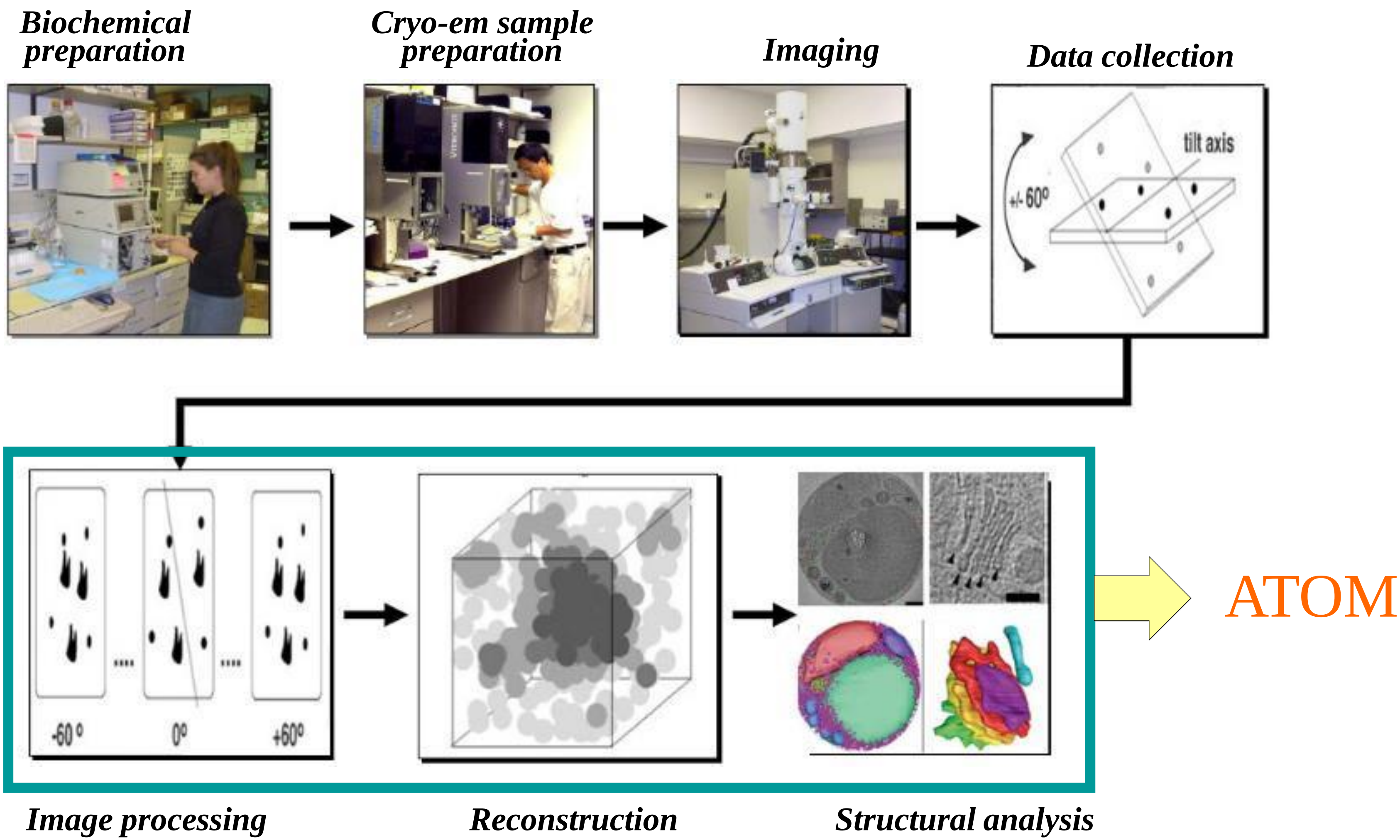
Source:
2D Projection images

Goal:
3D reconstruction



Electron Tomography (ET)

Background



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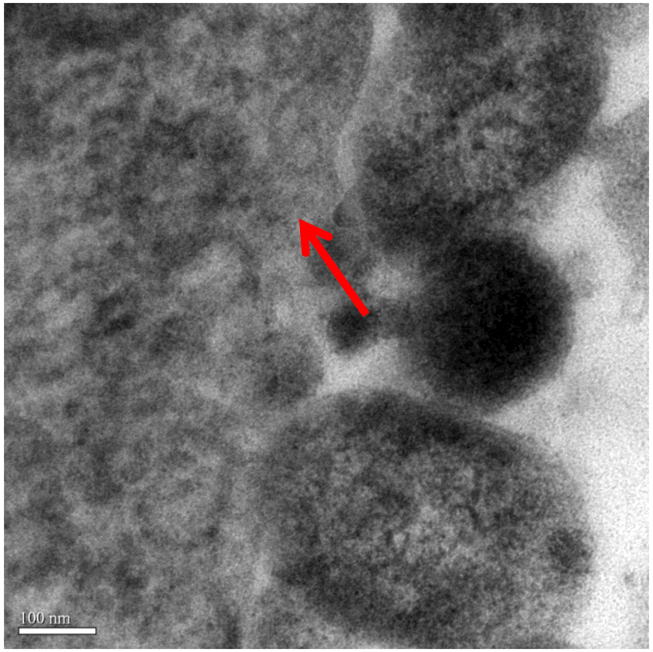
Technical Problems in ET

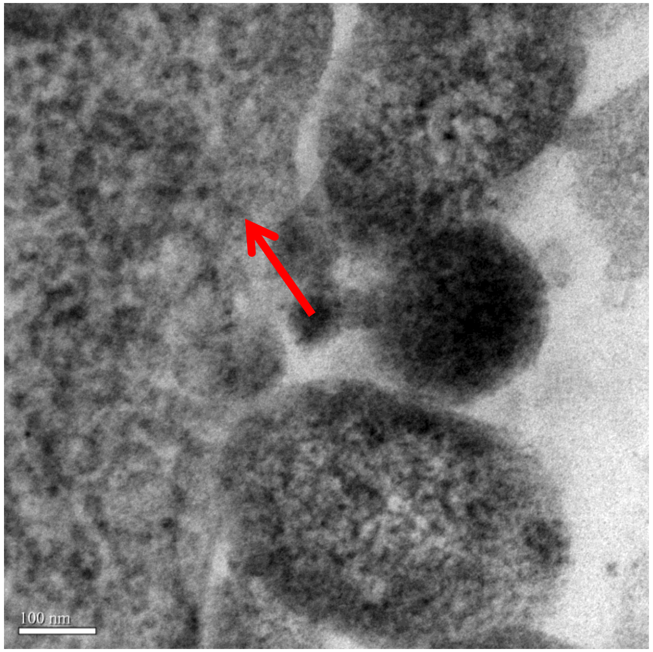
Problem

- **Noise (SNR <0.1)**

Caveolae of PAE cell



-60 °

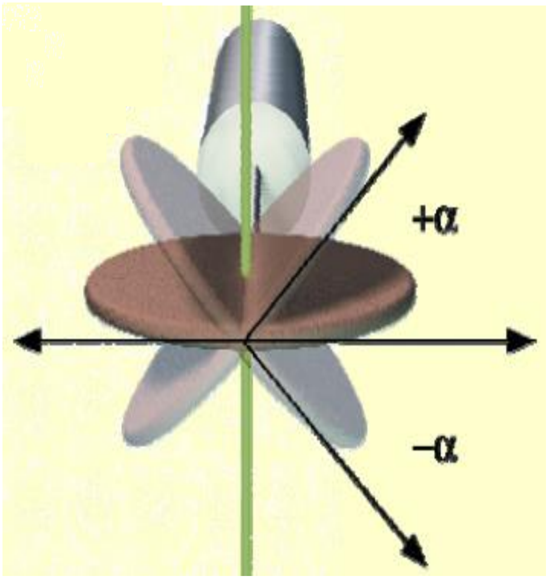


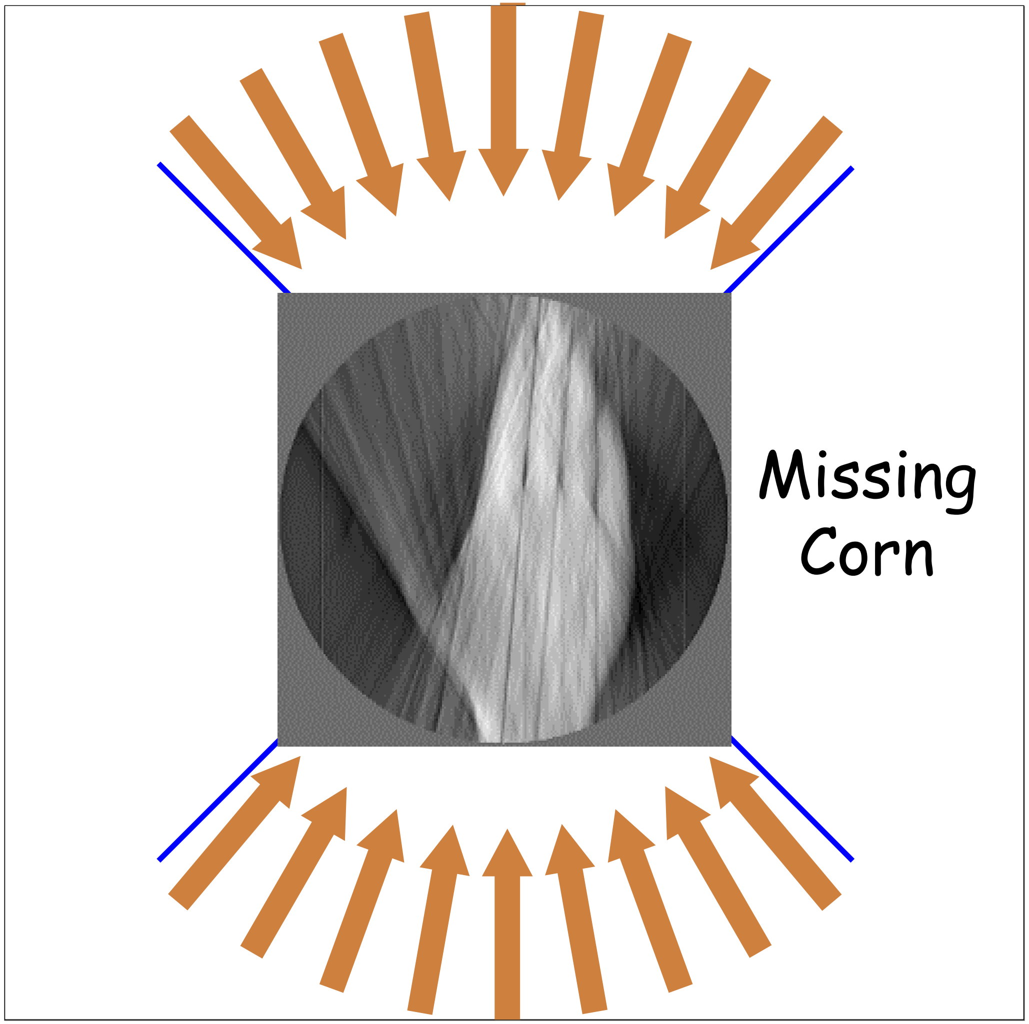
-50 °

Technical Problems in ET

Problem

- **Noise**
- **Incomplete Data**

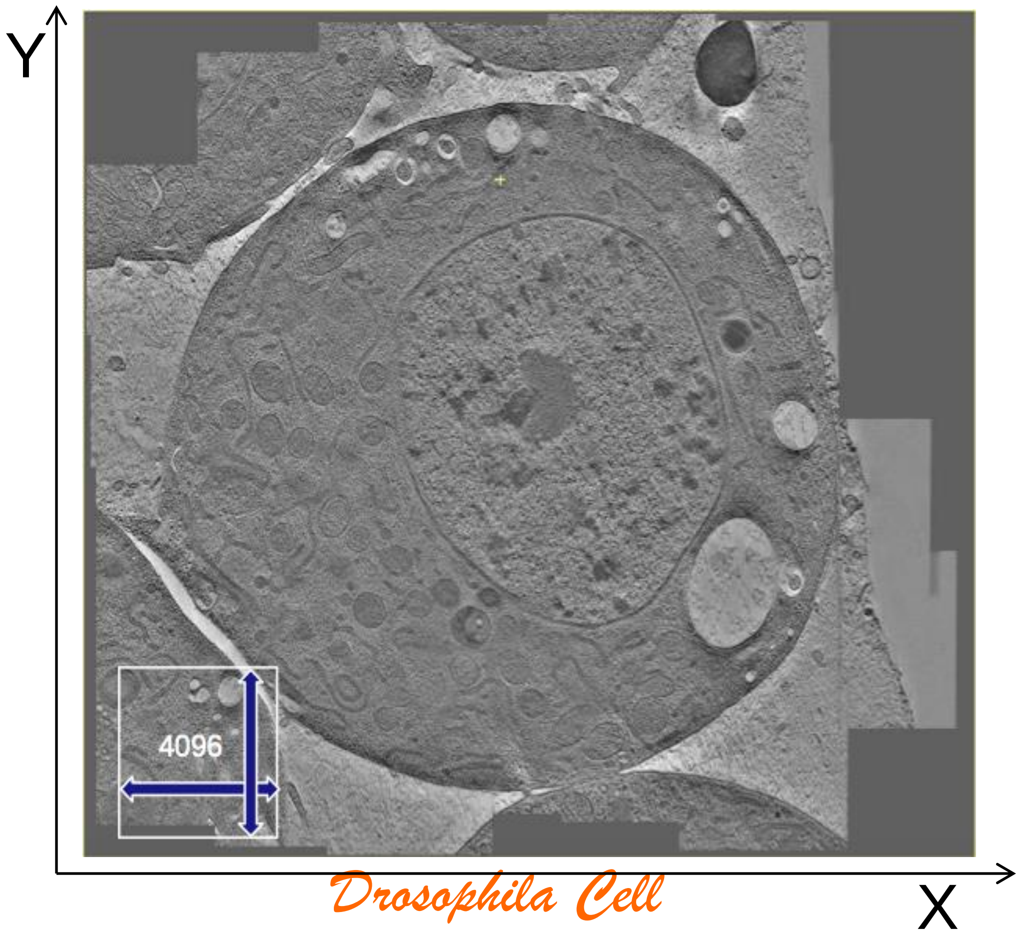


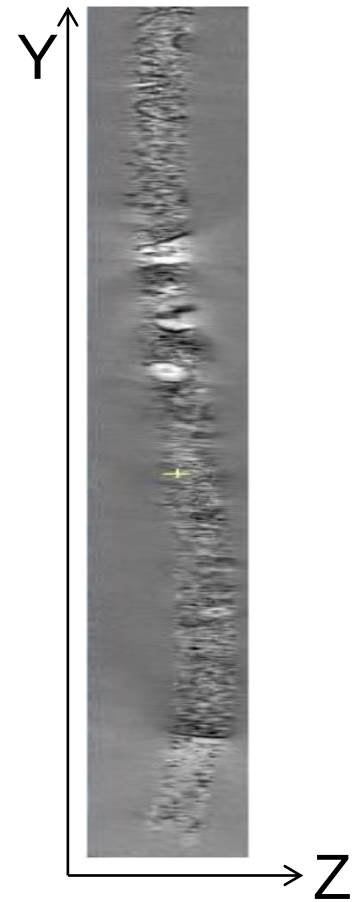


Technical Problems in ET

Problem

- **Noise**
- **Incomplete Data**
- **Distortions in large-scale reconstruction**





Technical Problems in ET

Problem

- **Noise**
- **Incomplete Data**
- **Distortions in large-scale reconstruction**
- **Large computational resources and processing time**
  - **8K*8K，TB**
  - **several months**
  - **an exascale computing problem**

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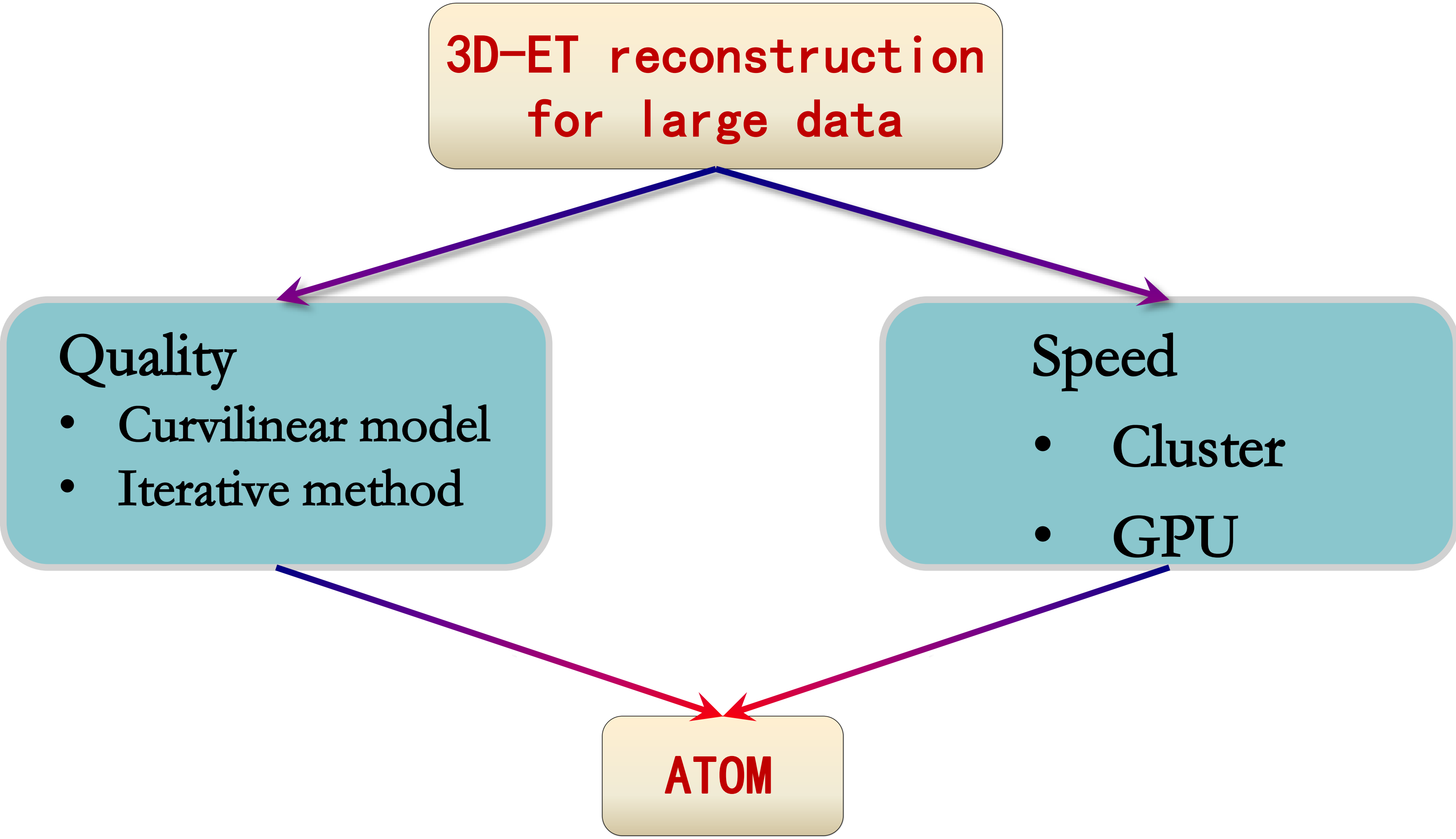
Our research



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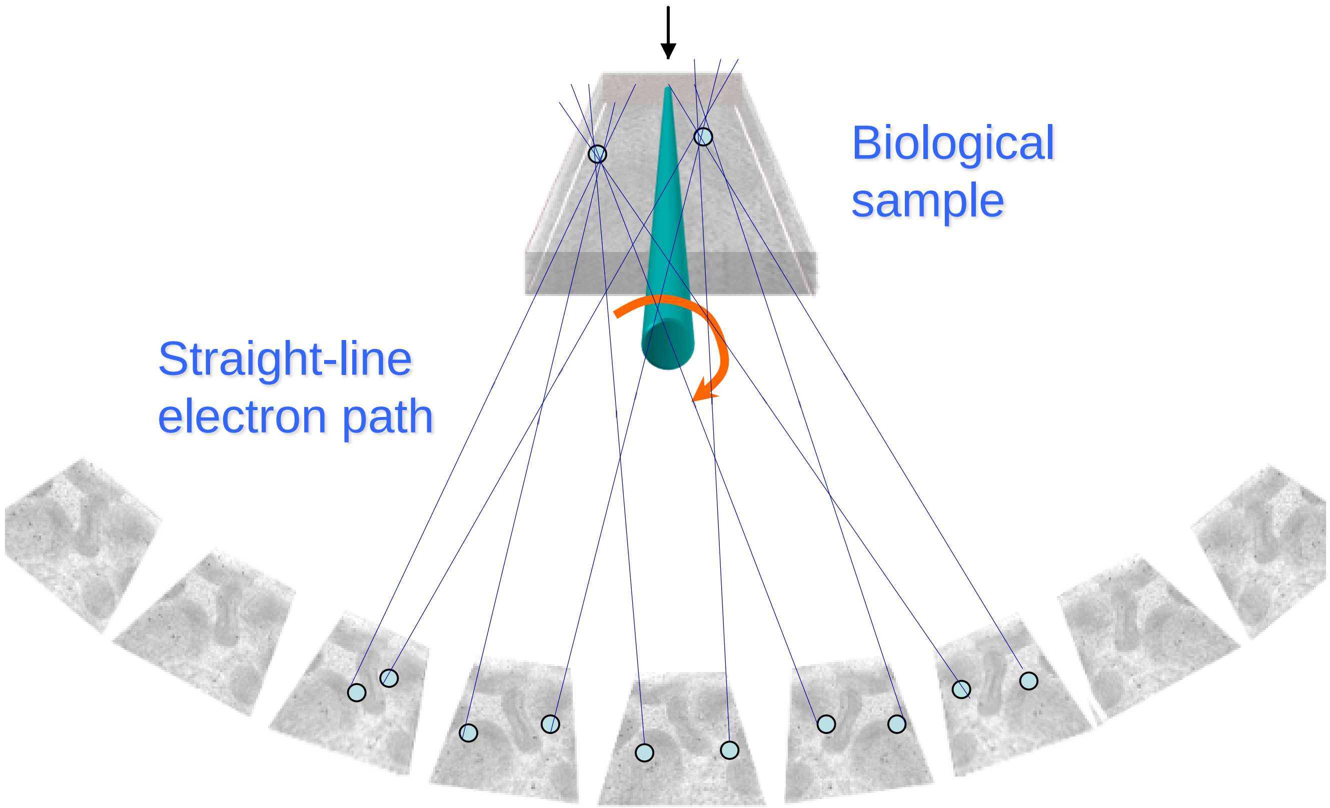
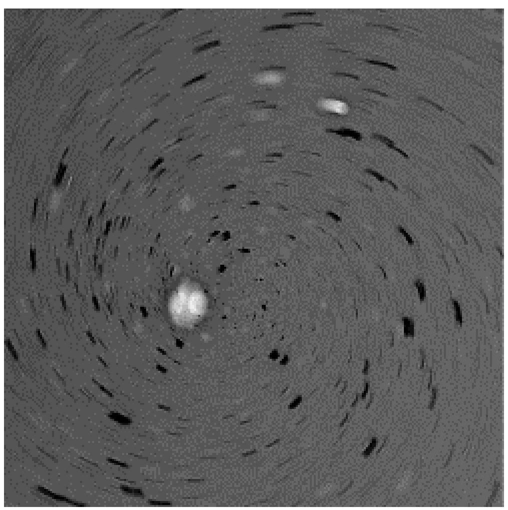
Our methods

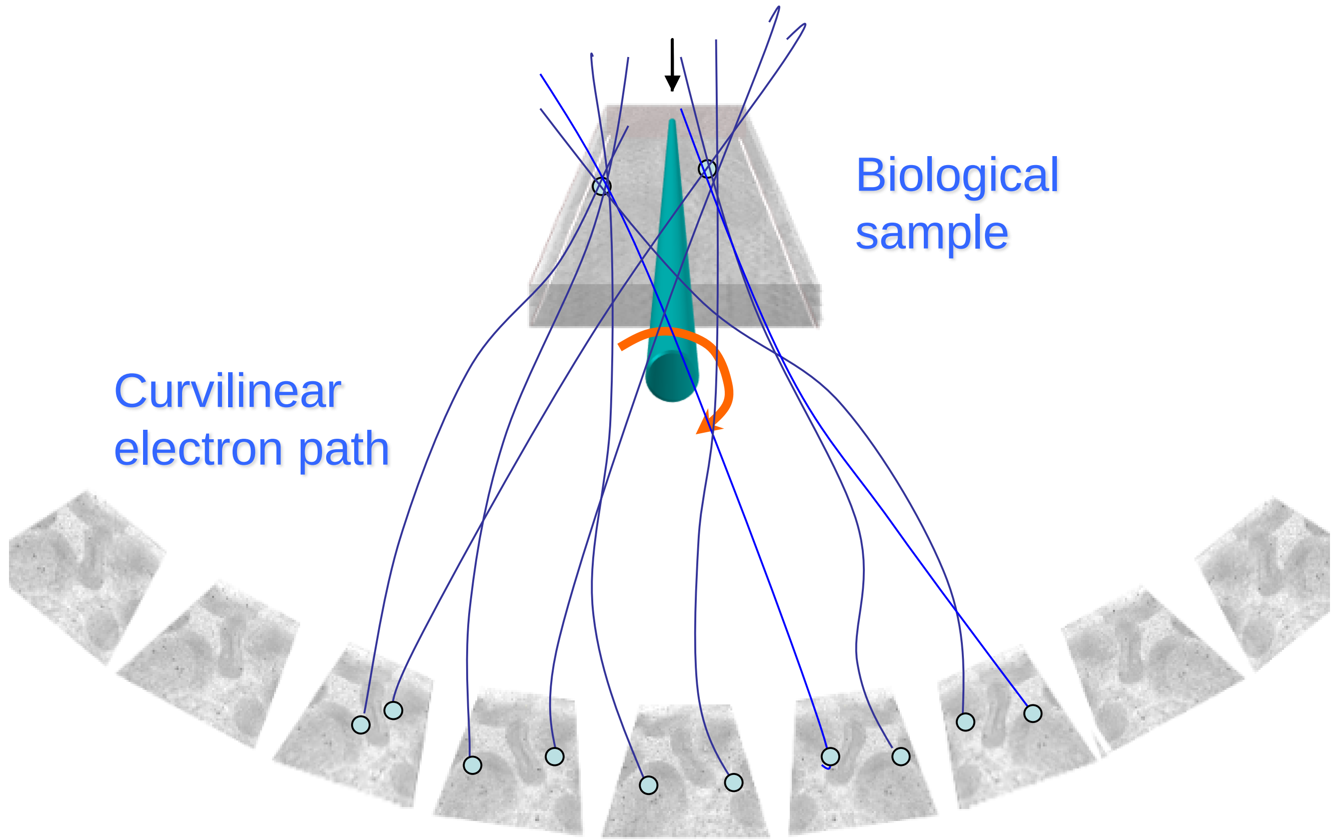
- Straight-line projection model



Our methods

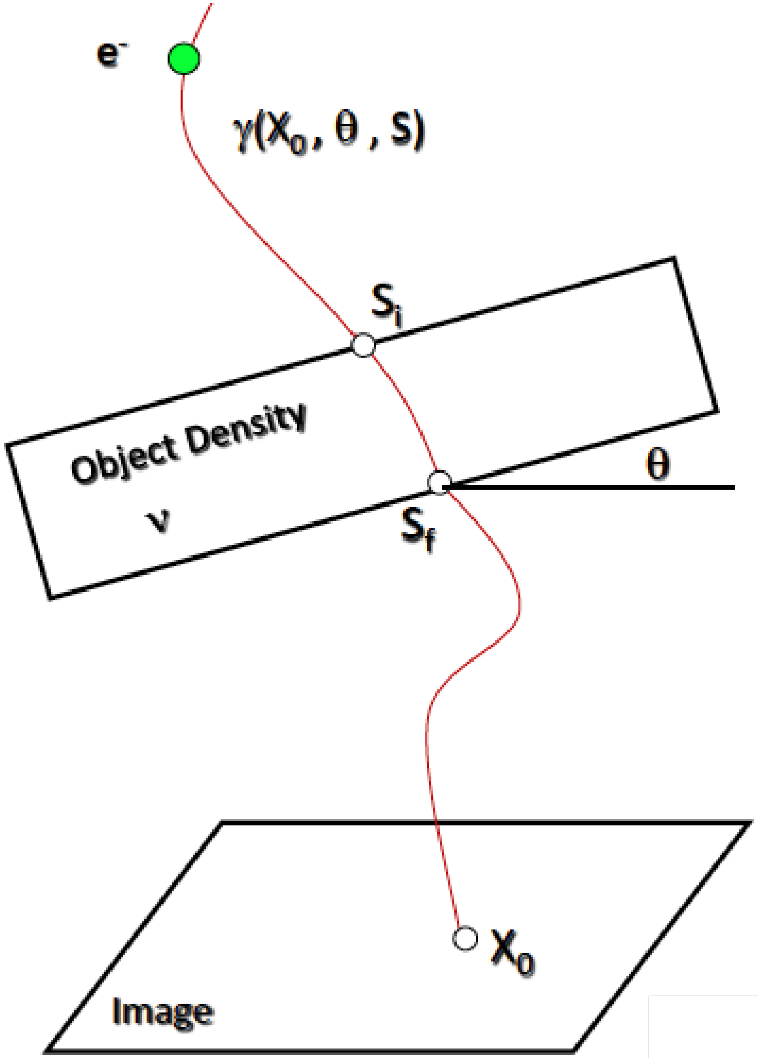
- Curvilinear projection model





Our methods

- Curvilinear projection model



$$\Gamma = \{\gamma_{\mathbf{x},\omega}(t) | t_0 \leq t \leq t_1\}$$

$$I = I_0 e^{-\int_{t_0}^{t_1} u[\gamma_{\mathbf{x},\omega}(t)]dt}$$

Our methods

- Generalized radon transform

$$R_\Gamma u(\mathbf{x},\omega) \equiv v(\mathbf{x},\omega) = \int_{t_0}^{t_1} u[\gamma_{\mathbf{x},\omega}(t)]dt$$

- Determination of the curves $\gamma_{\mathbf{x},\omega}(t)$

Projection map:

$$P_\omega(\gamma^1_{\mathbf{x},\omega}(t), \gamma^2_{\mathbf{x},\omega}(t), \gamma^3_{\mathbf{x},\omega}(t)) = (x_1, x_2)$$

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Our methods

- Reconstruction

$$R_{\Gamma}u(\Phi,\theta) \equiv v(\Phi,\theta) = \int_{t_0}^{t_1} u[\gamma_{\Phi,\theta}(t)]dt \quad \Longrightarrow \quad u(X) = R_{\Gamma}^{-1}v(\mathbf{x})$$

- Two reconstruction methods:
  - Filter Backprojection (FBP) (easy)
  - Iterative methods (noisy+incomplete data)

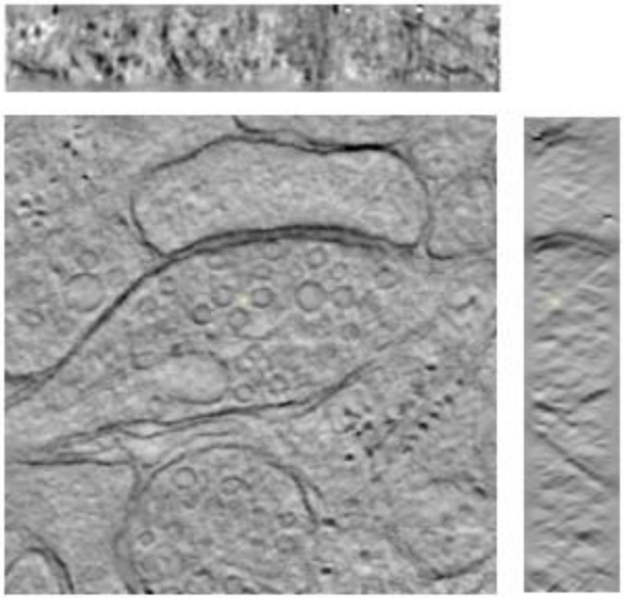
Our methods

- ASART based on a curvilinear projection map
  - Initial value (BPT and FBP)
  - Modified multilevel scheme for data access
  - Adaptive adjustment for relaxation parameters
  - Curvilinear projection map

$$\begin{cases} u_j^{(0)} = \frac{\sum_{i=1}^{M} w_{ij} v_i(P_b(j))}{\sum_{i=1}^{M} w_{ij}} \\ u_j^{(k+1)} = u_j^k + \sum_{s=1}^{S} \frac{\lambda w_{ij} u_j^{(k)}}{\sum_{s=1}^{S} w_{ij} \sum_{h=1}^{N} w_{ih} u_h^{(k)}} (v_i(P_b(j)) - \sum_{h=1}^{N} w_{ih} u_h^{(k)}) \end{cases}$$

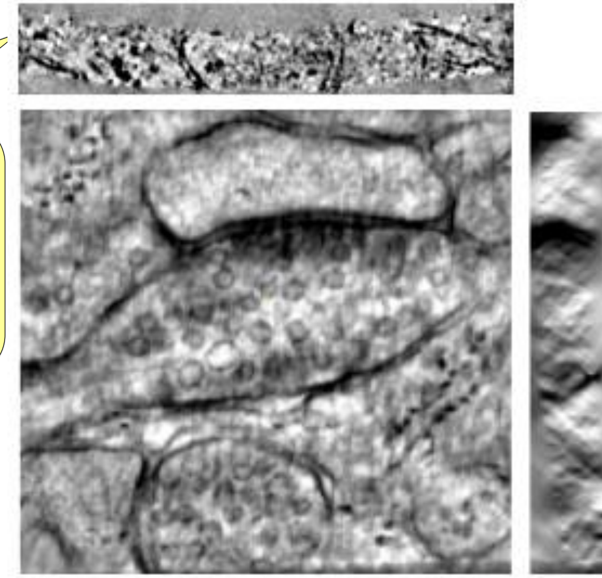
XH Wan, et. al. J. Struct. Biolo. 2011

Results

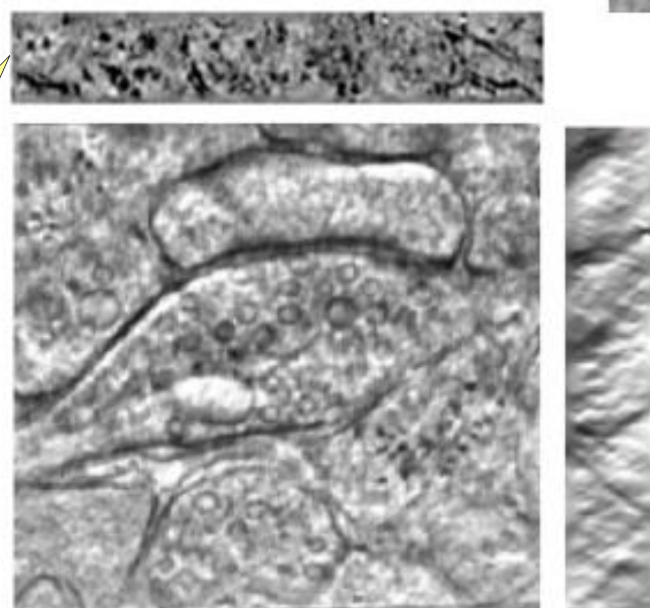


FBP + curvilinear projection map

There is a distortion because of the straight-line projection model.



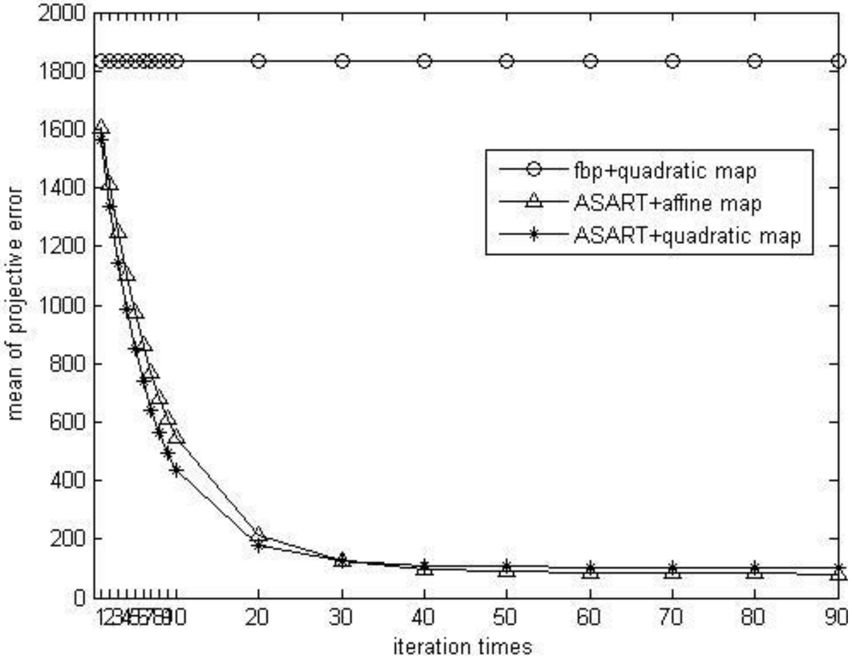
ASART + straight projection map



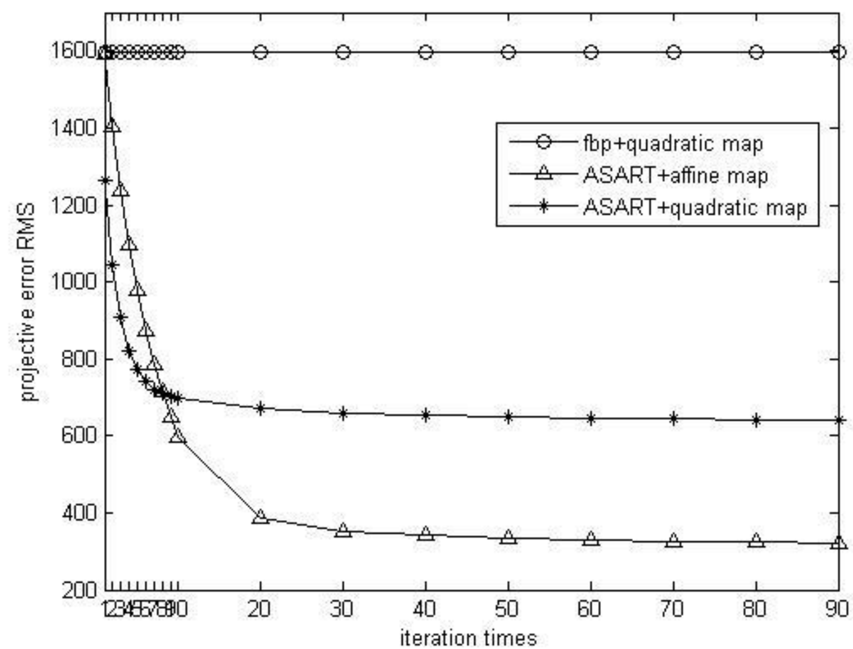
There is no distortion because of the curvilinear projection model.

ASART + curvilinear projection map

Results



Mean of projection error

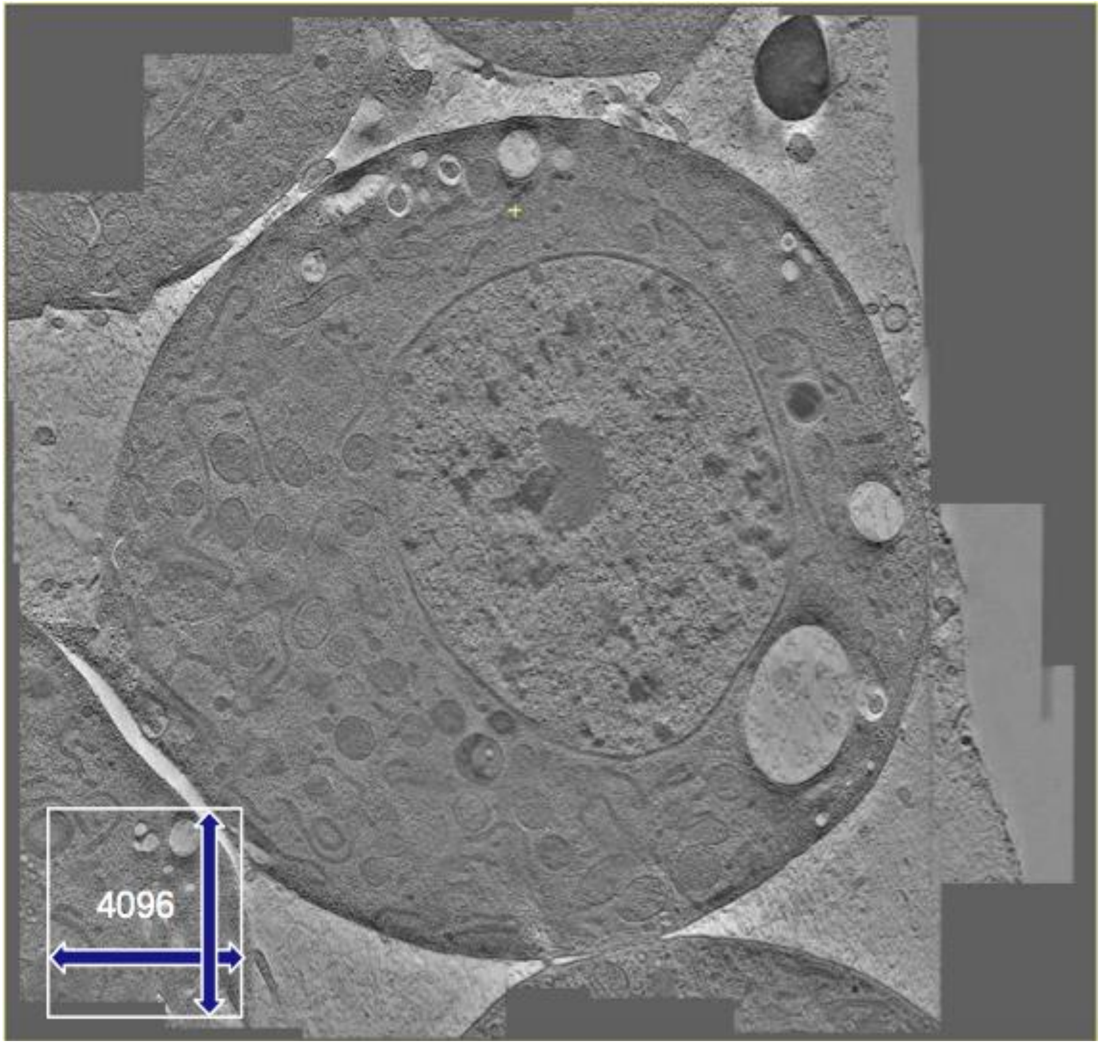


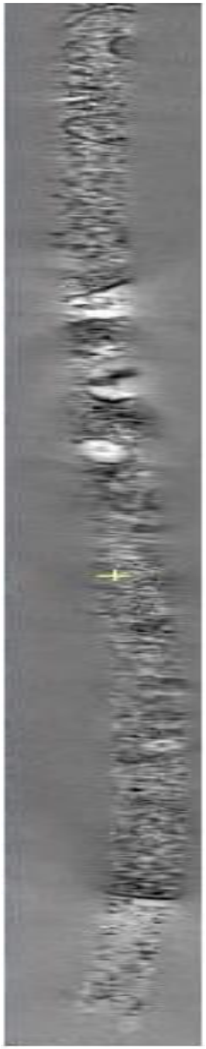
RMS of projection error

Xiaohua Wan, Sebastien Phan, Albert Lawrence, Fa Zhang, Renmin Han, Zhiyong Liu, Mark Ellisman. "Iterative Methods in Large Field Electron Microscope Tomography". **SIAM Journal on Scientific Computing, 35(5).**

Results

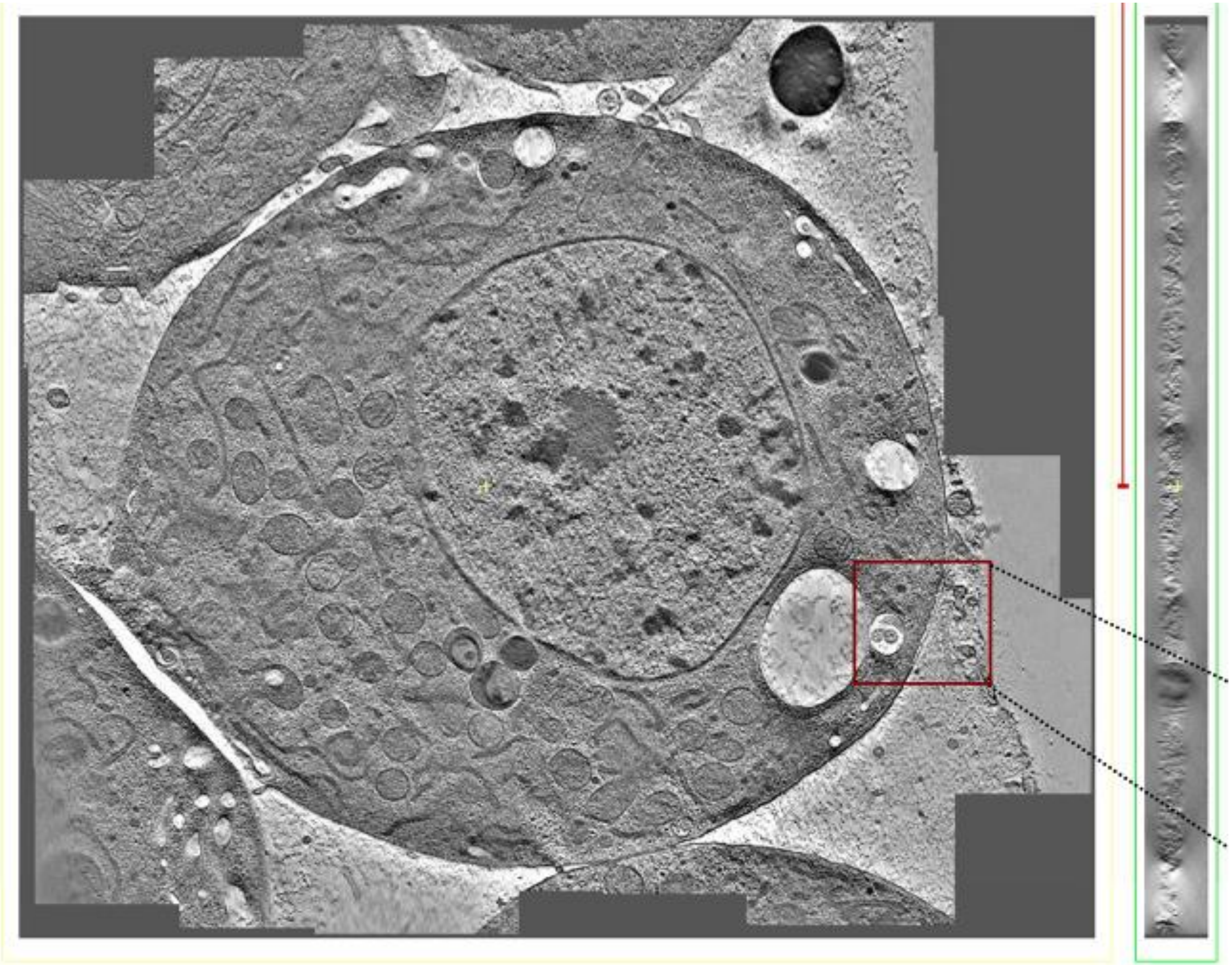
- **Straight-line projection model+FBP**





Results

- **Curvilinear projection model+ASART**

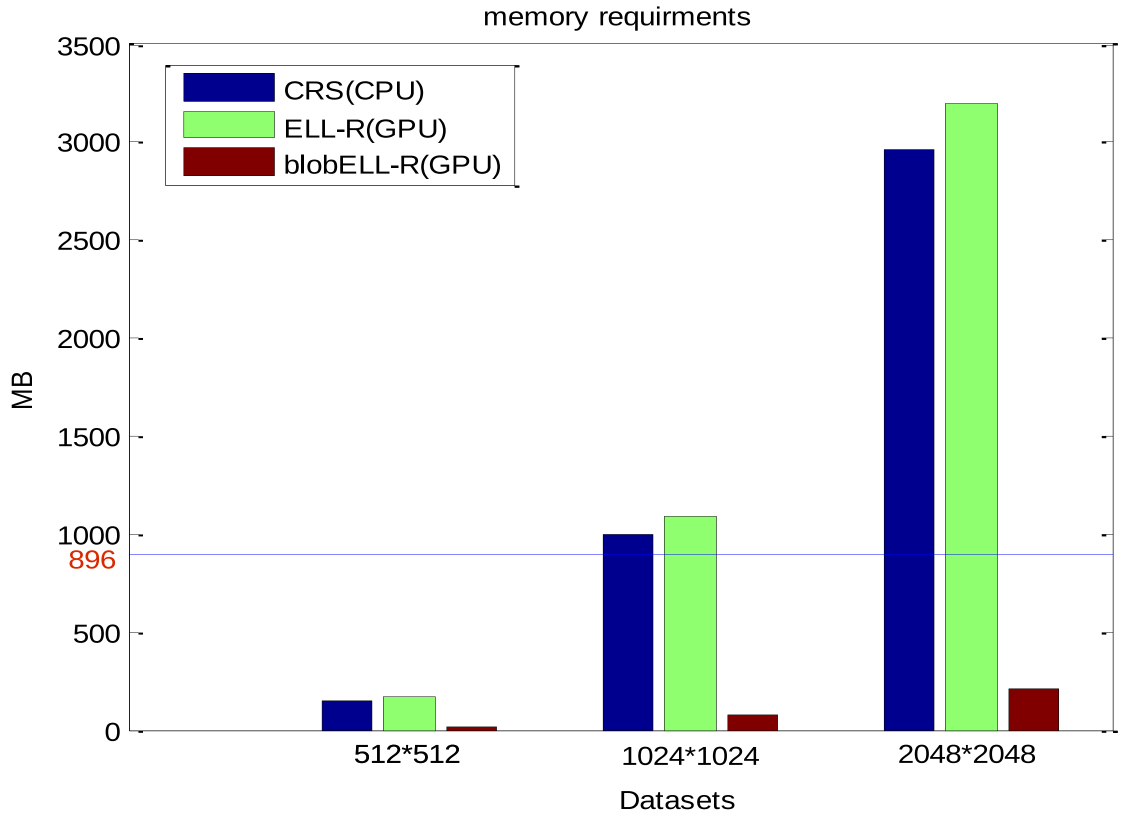


Our methods

- Parallel strategy for iterative reconstructions
  - Decomposition of reconstruction into independent slabs along Z-axis
  - Computing the polynomials of each X-line in parallel
  - Blob-ELLR

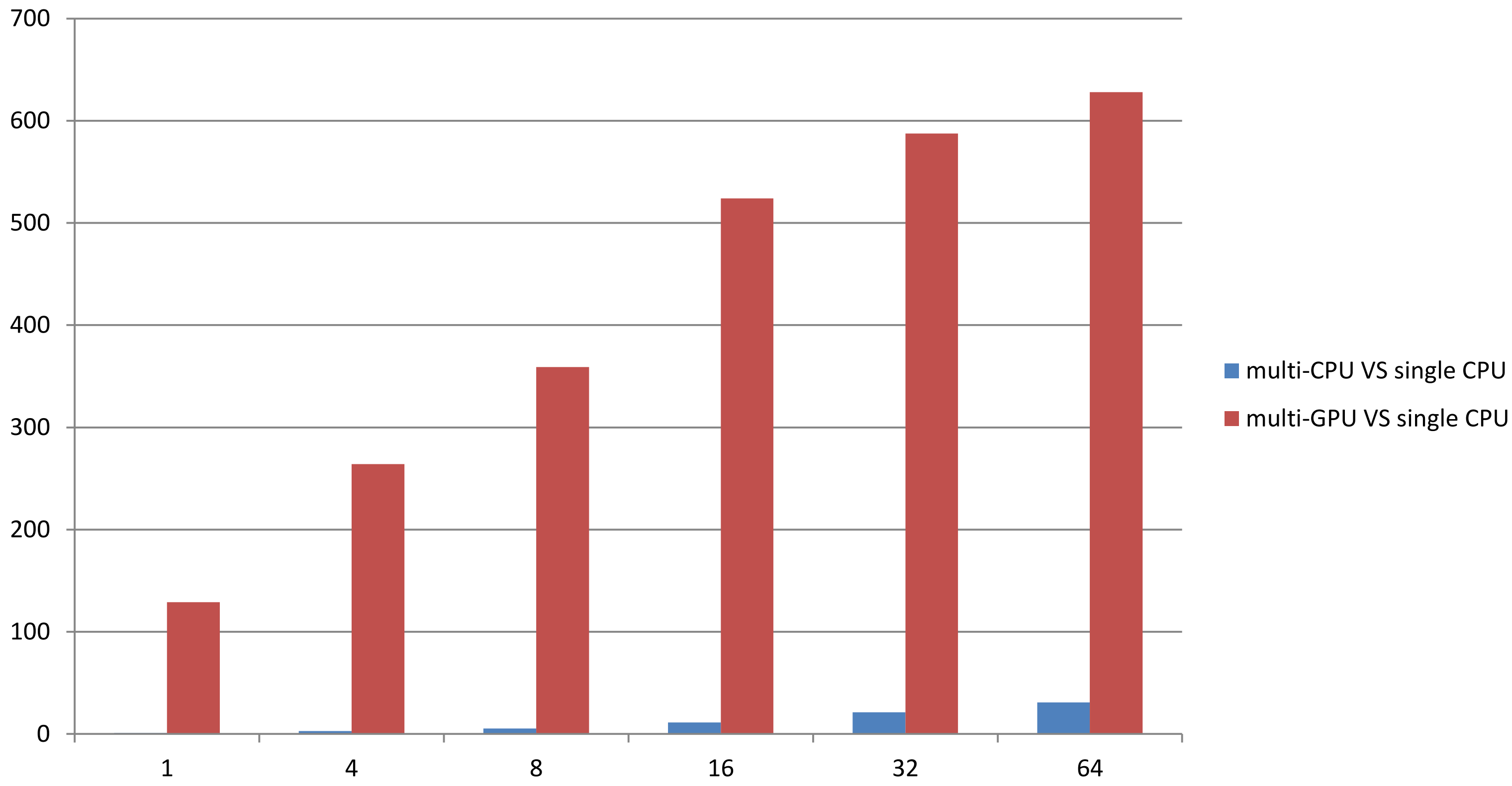
Results

➢ Blob-ELLR



XH Wan, et. al. BMC Bioinformatics. 2012

Results



node num	1	4	8	16	32	64
multi-CPU	1	2.8	5.5	11.2	21.2	30.9
multi-GPU	128.9	264	359	524	587.6	627.9

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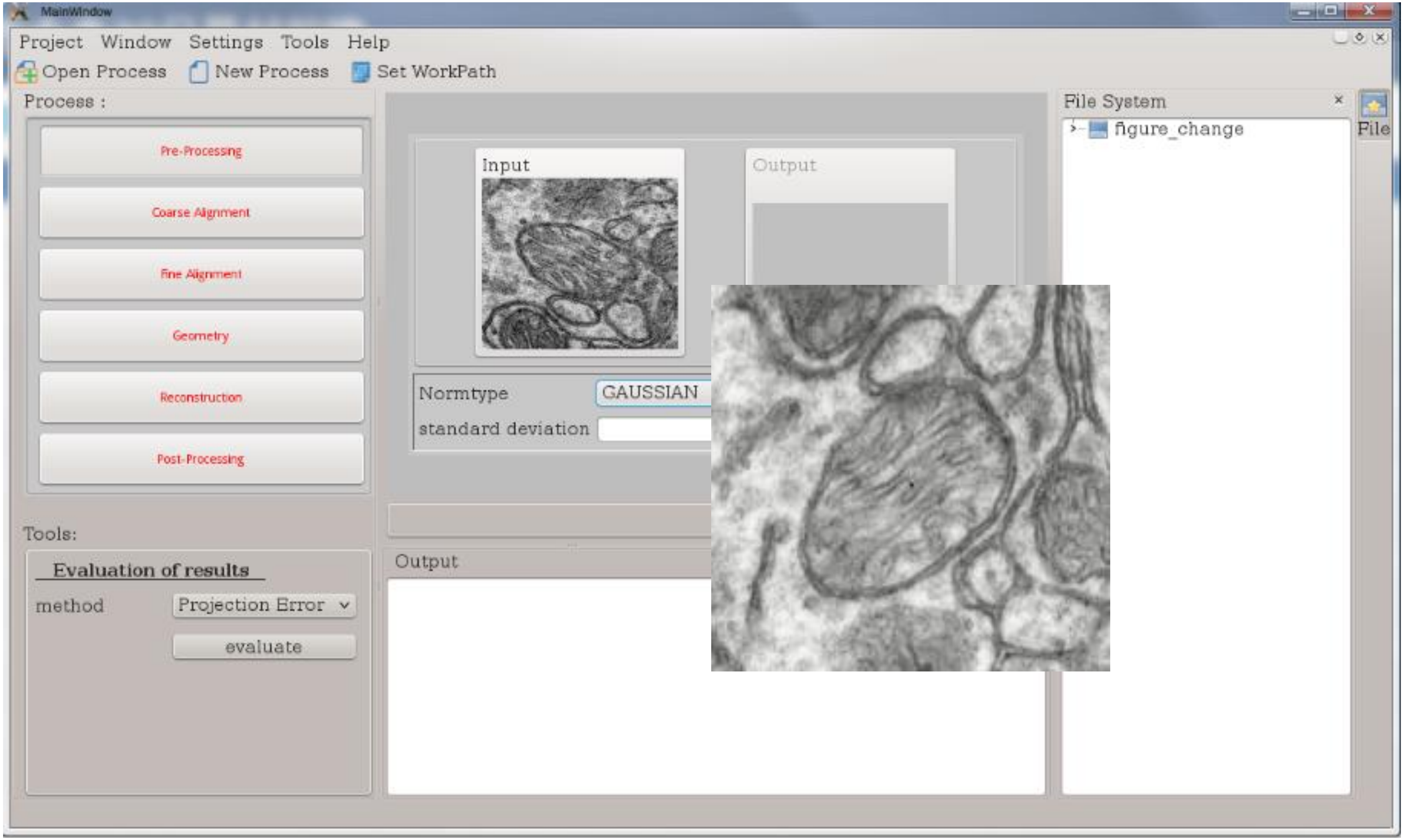
Results – ATOM



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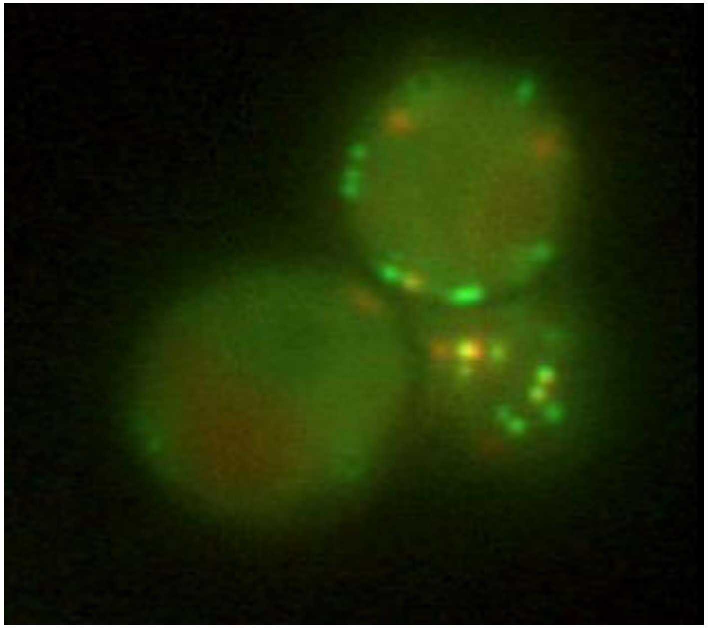
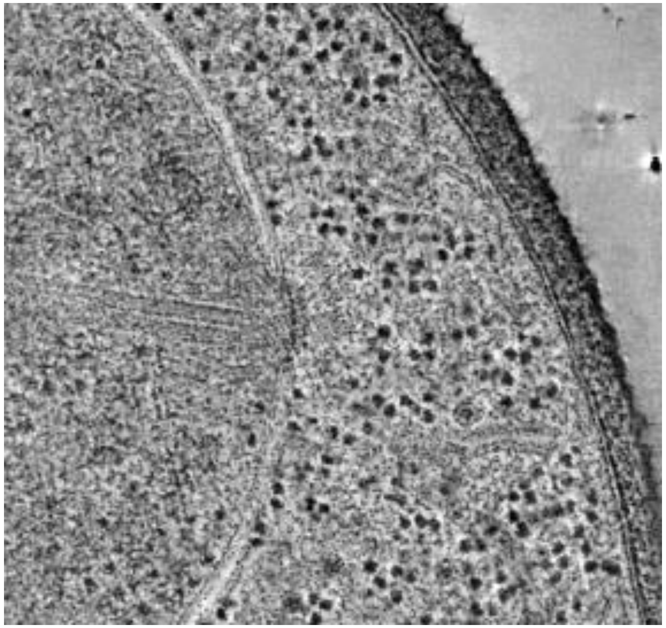
Future work

- Large-scale Electron Tomography
- How to combine light microscopy and electron microscopy
  - New techniques in fluorescence microscopy allow us to label specific biological molecules for light microscopy and then stain for electron microscopy.



Fluorescence Microscopy



Electron Microscopy

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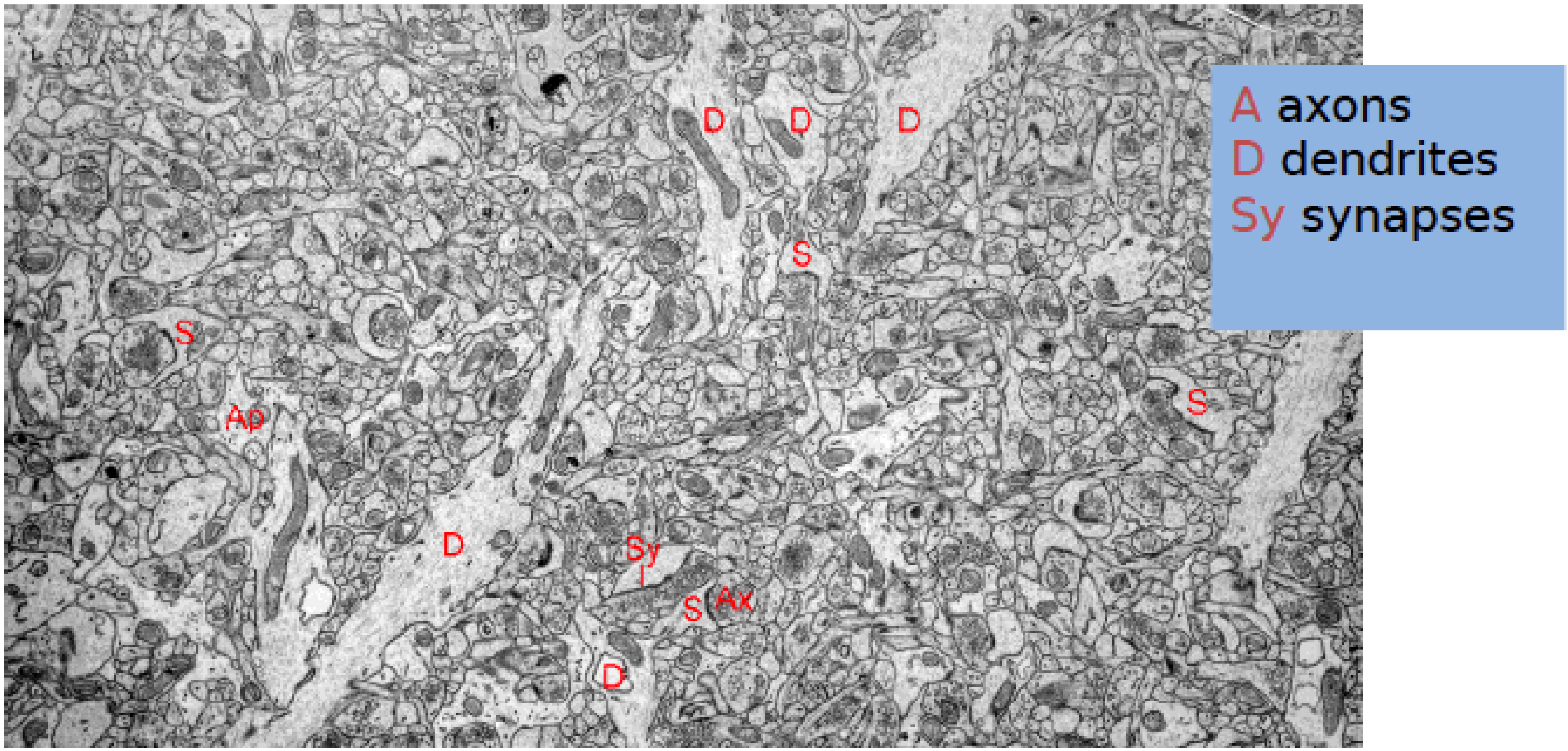
Future work

- Large-scale Electron Tomography



Thin section of neuropil
(How we look at the brain)

Achnowledgements

ICT-CAS

- Prof. Zhiyong Liu
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- Yu Chen

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