Transmission Electron Microscopy 3D Construction by IPET Method

TCBG GPU Workshop

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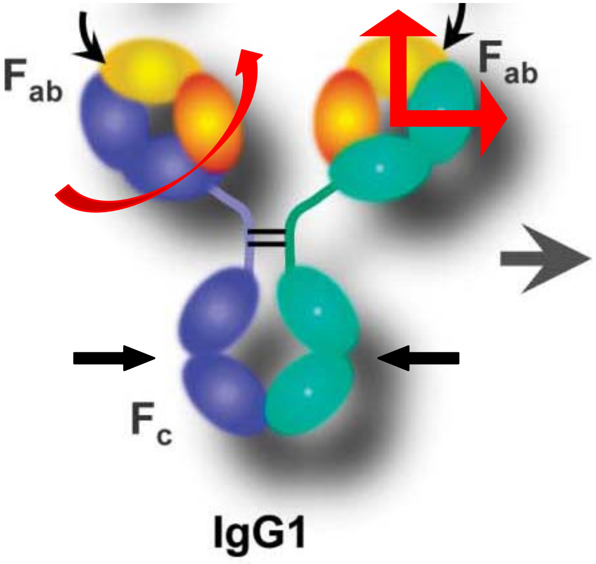
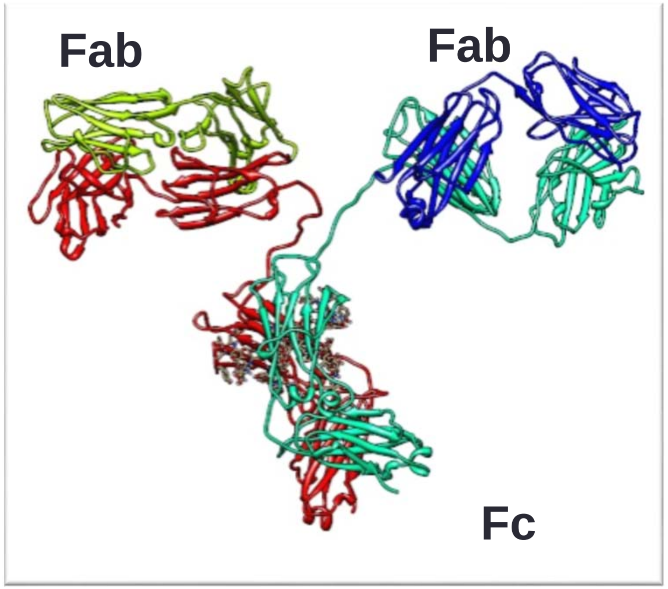
Out line

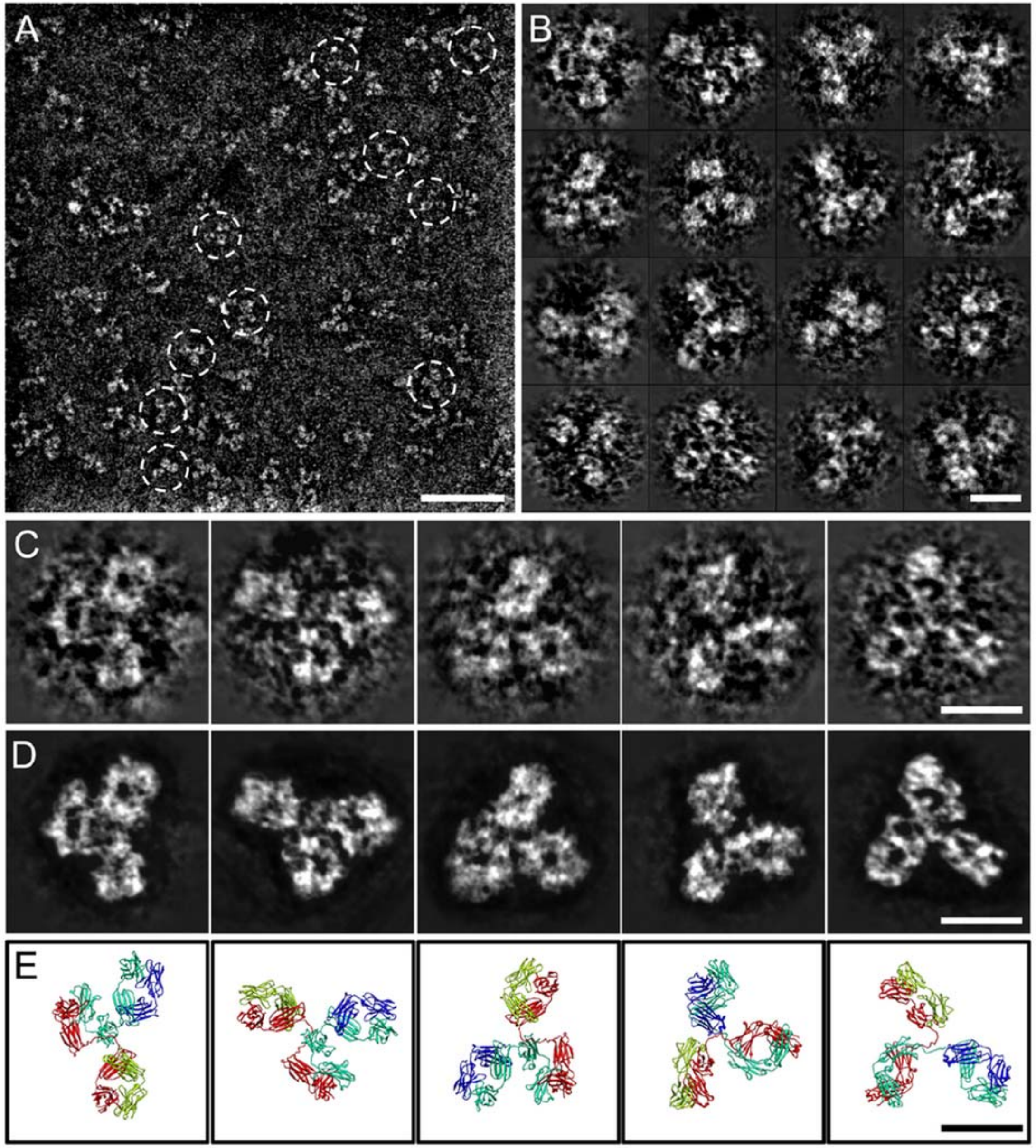
- Protein dynamic and TEM
- Electron Microscopy Cryo-Tomography
- Individual-particle Electron Tomography method
- Goals for GPU implementation

Protein Dynamics

- The dynamic nature and structural heterogeneity of proteins is essential for their functions.
- Dynamic proteins, like antibody, have a big conformation space.







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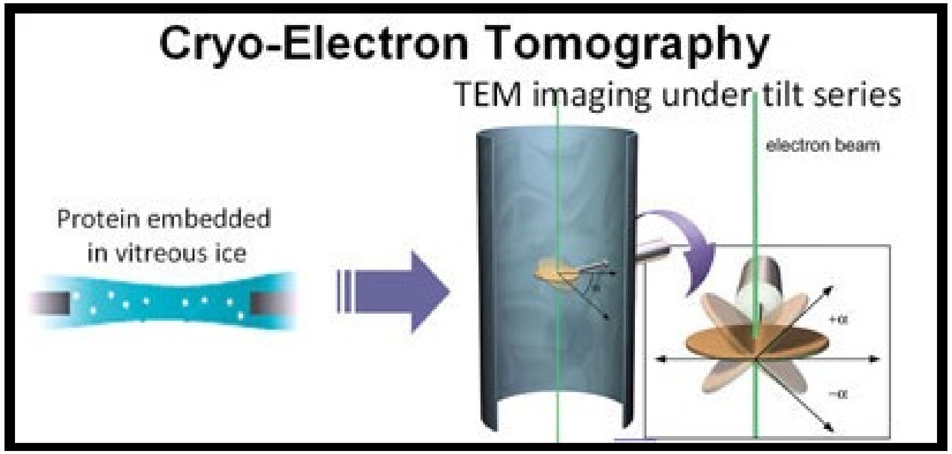
However, conventional structural determination technologies, such as X-ray, NMR and single-particle electron cryo-microscopy (cryo-EM) are limited by structural heterogeneity because they all involved in averaging process of hundreds to thousands of different particles.

Electron Microscopy Cryo-Tomography (ET)



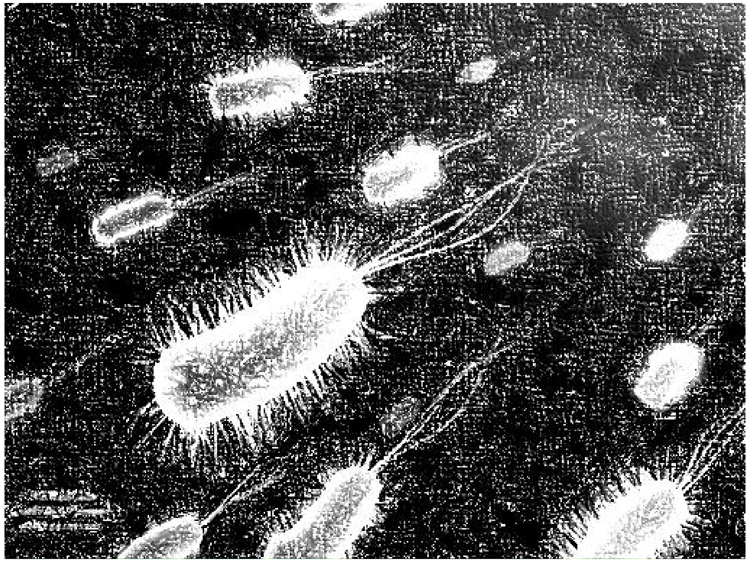
Negative stain and Cryo-EM

View unaltered macromolecular assemblies by freezing them

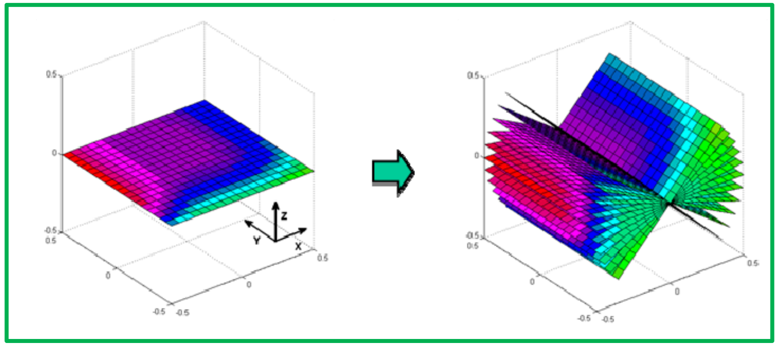
Sample is studied at cryogenic temperatures

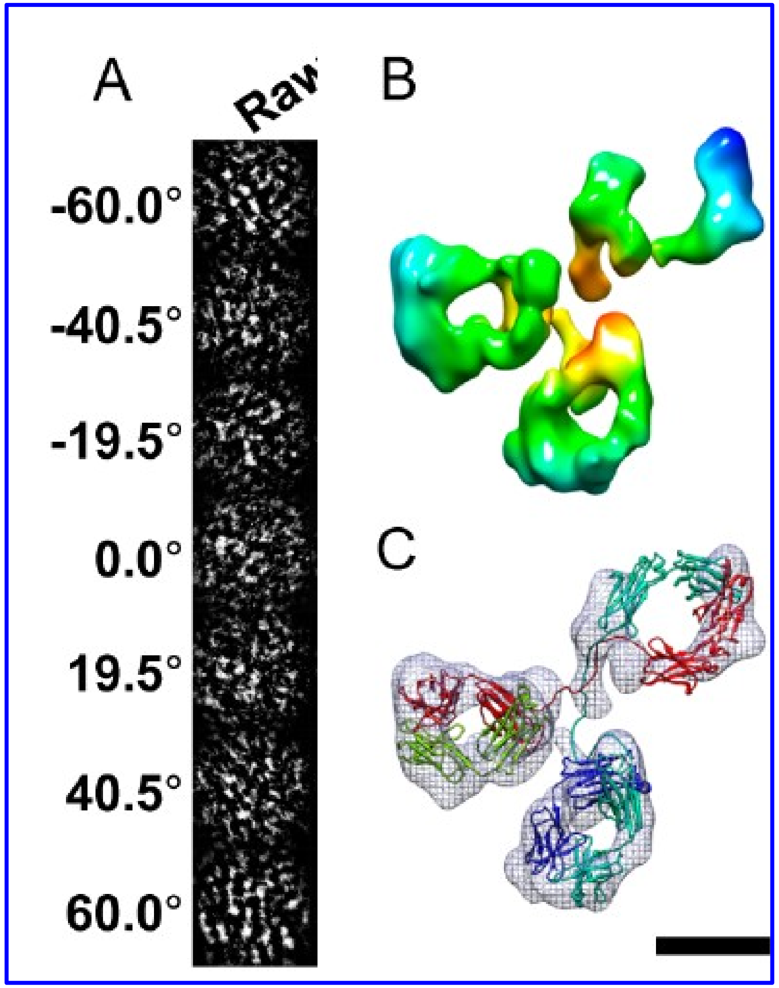
Show biological specimen in their native environment

Improving steadily since vitreous ice can be produced



Tomography 3D Reconstruction





- 3D reconstruction is a challenge with Cryo-TEM data for small protein

  Low dose, low contrast

  High noise ratio 0.05

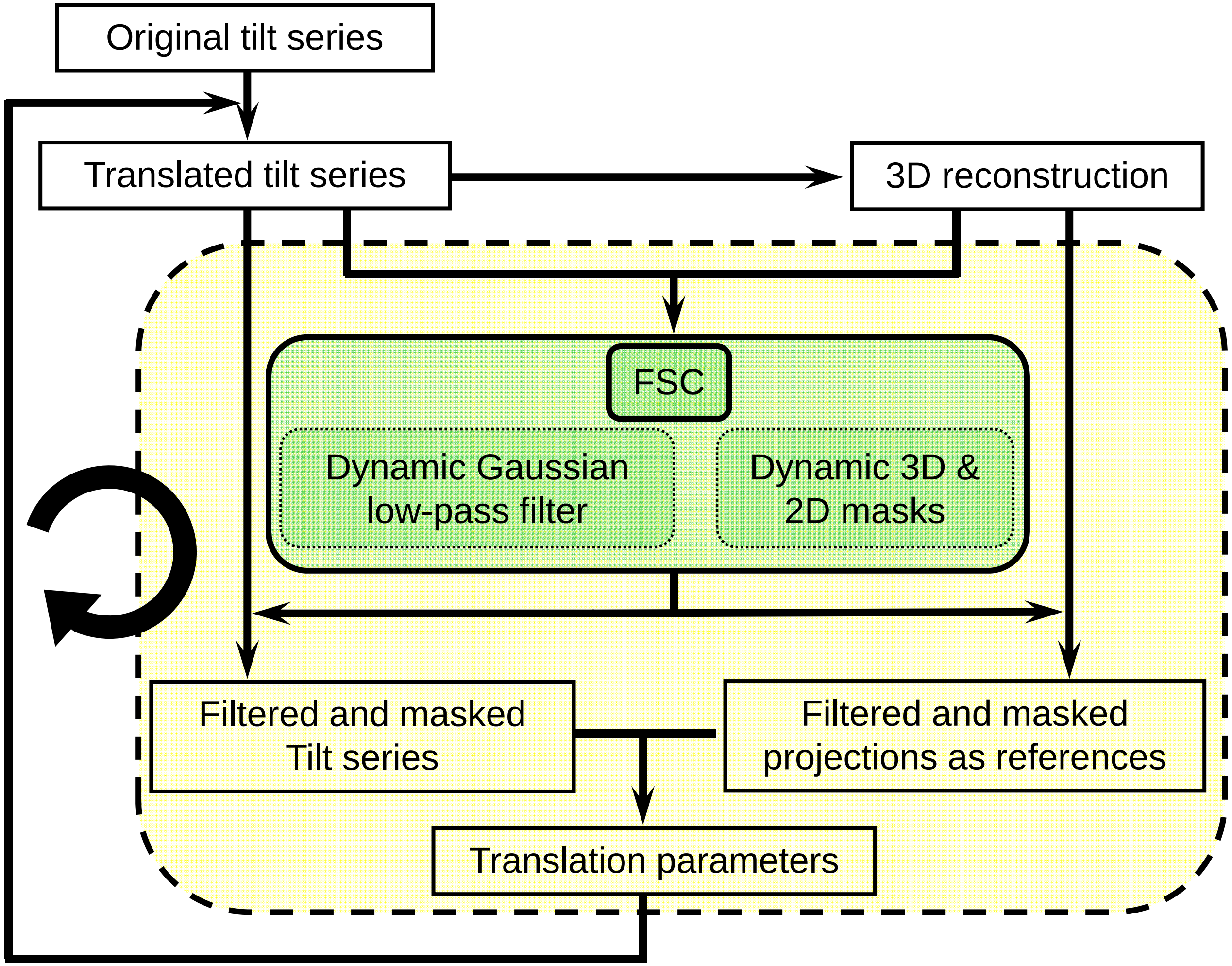
  Distortion in large area

- How to make good alignment and reduce noise lever?

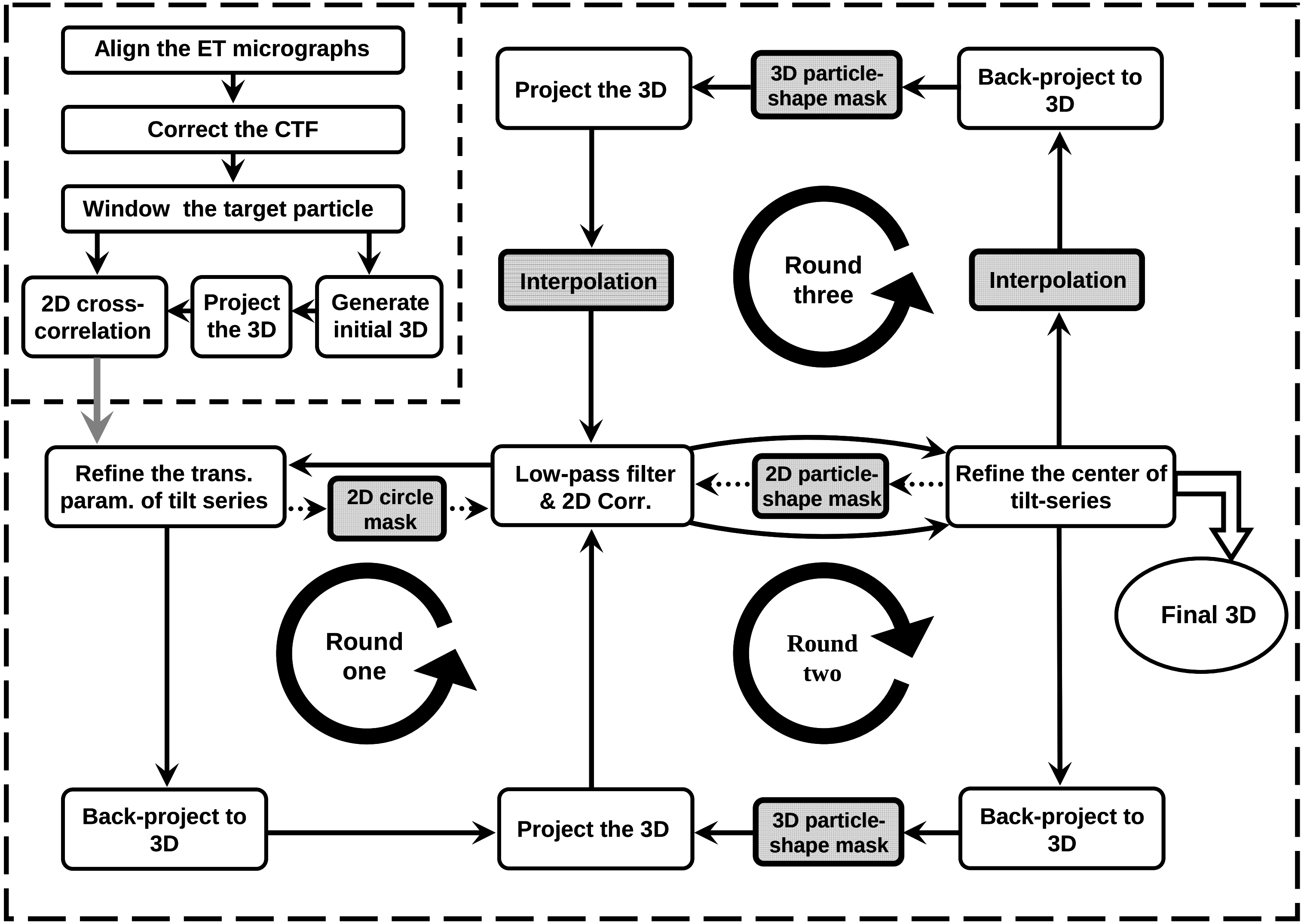
Individual-particle Electron Tomography (IPET)

Lei Zhang, Gang Ren PLoS ONE January 2012 | Volume 7 | Issue 1 | e30249

The Core Algorithm
of the Local Refinement Program



The Flow Diagram of Our Local Refinement Program



Align the ET micrographs

Correct the CTF

Window the target particle

2D cross-correlation

Project the 3D

Generate initial 3D

Project the 3D

3D particle-shape mask

Back-project to 3D

Interpolation

Round three

Interpolation

Refine the trans. param. of tilt series

2D circle mask

Low-pass filter & 2D Corr.

2D particle-shape mask

Refine the center of tilt-series

Final 3D

Round one

Round two

Back-project to 3D

Project the 3D

3D particle-shape mask

Back-project to 3D

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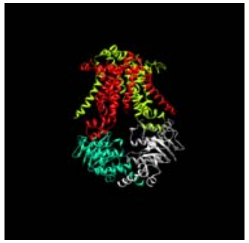
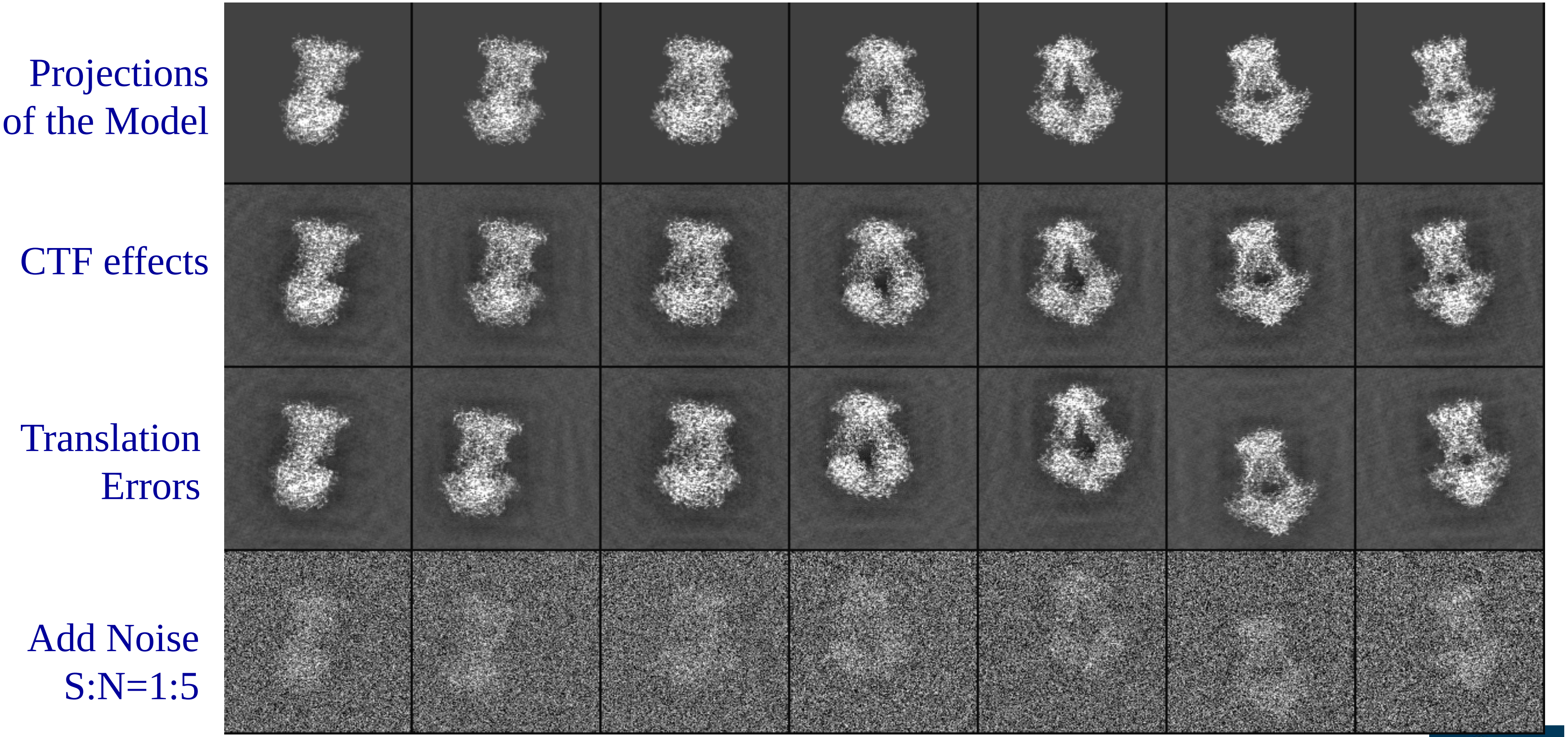
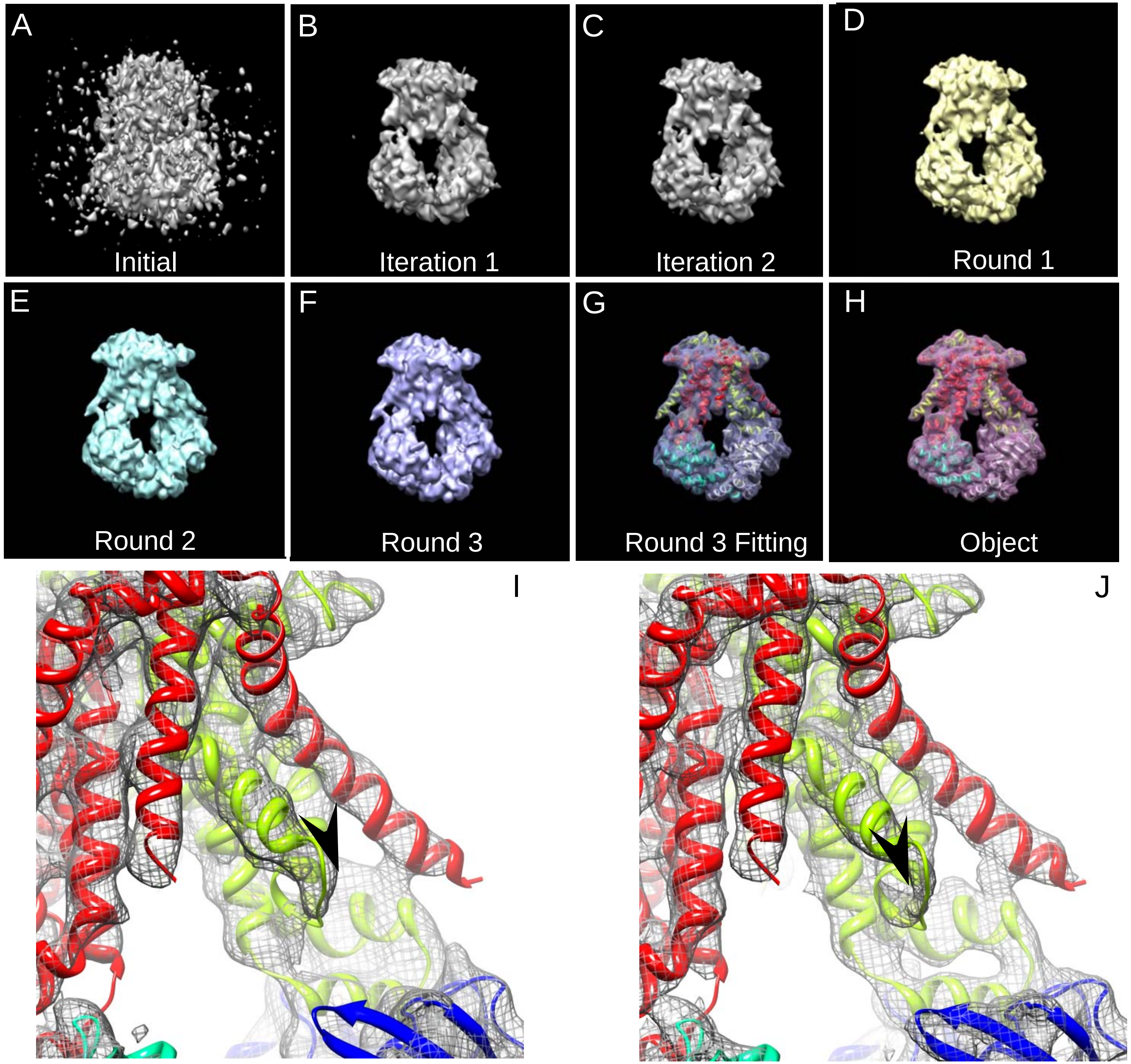
Creating a Series of Simulating Cryo-ET Tilt Images of One Individual Particle - A 100kDa Transporter

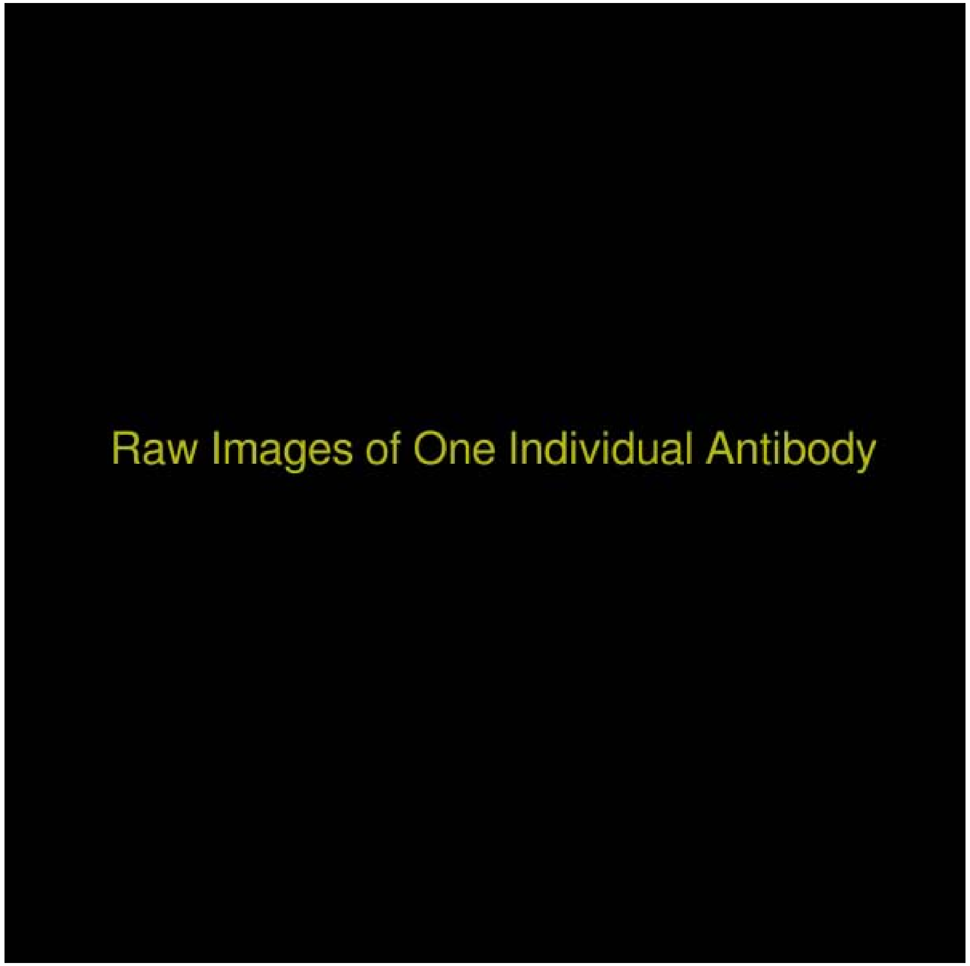




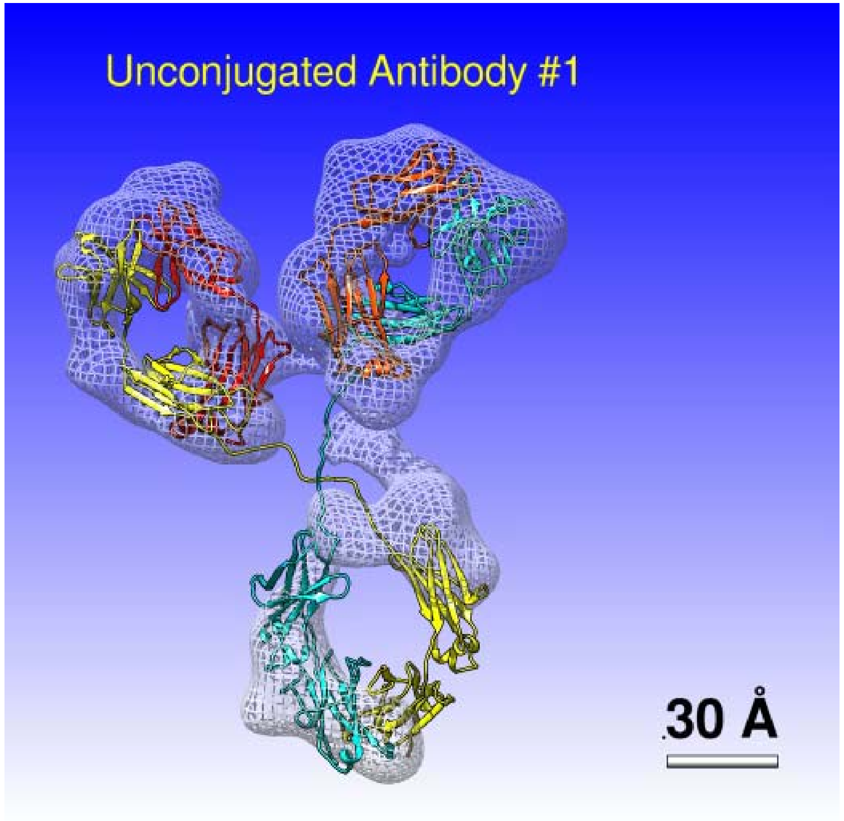
The 3D reconstruction by IPET method



Antibody 3D reconstruction


Raw Images of One Individual Antibody

Antibody Dynamic



GPU implementation?

- The 3D reconstruction is very time consuming

  To finish one 3D construction by IPET method need hundreds of iterations which means more than 5 hours, just for 120 tilted images (400*400 pixel)

- Key algorithm(s) involved in traditional CPU approach

  Pixel by pixel matrix operations, Fourier transform, Cross-Correlation calculation, interpolation and function fitting calculation

- GPU acceleration

  Imaging processing is very suit for GPU implementation, because their internal parallel property

Goals

- Increase calculation speed by verify SPIDER code and apply GPU accelerate
- The speed limiting steps: 3D volume rotation, FFT, Cross-Correlation calculation, Fourier space interpolation

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