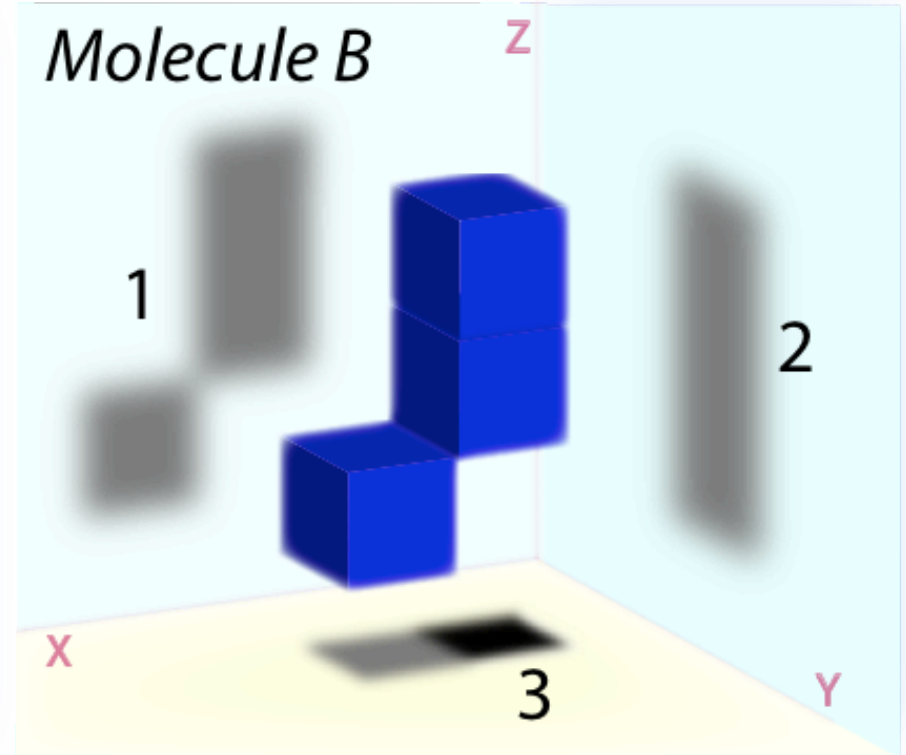
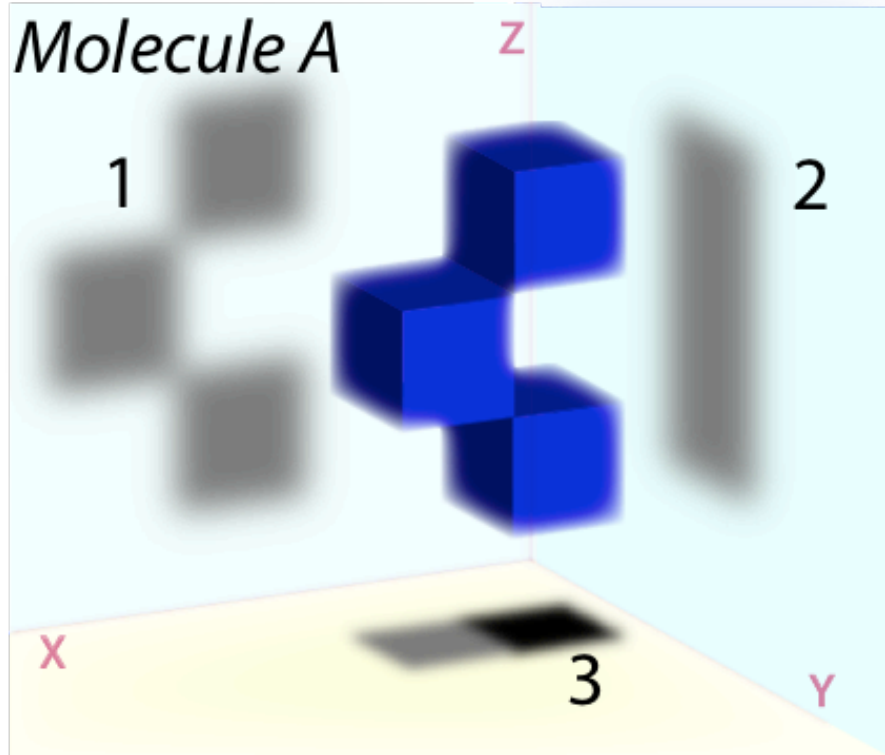
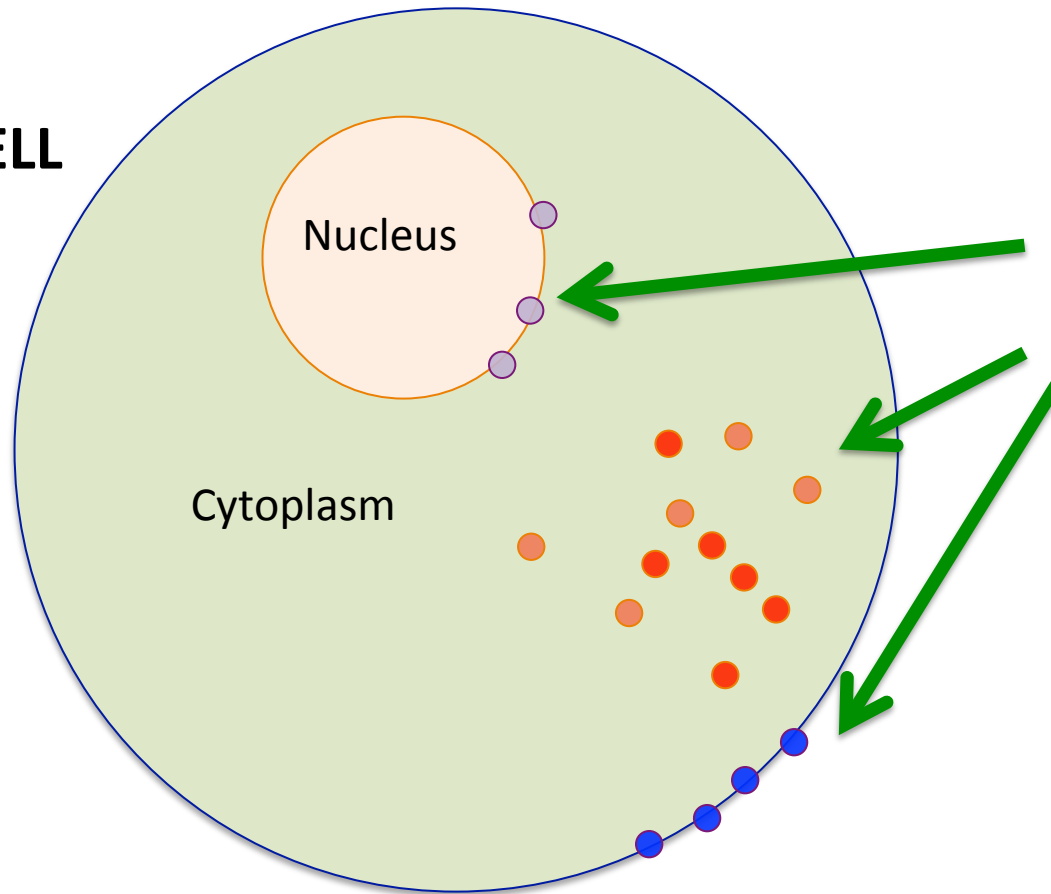


- **WHY Single Particle Tomography?**
- **Background**
- **Tasks**

TOMOGRAPHY vs 2D cryoEM (SPA)



CELL



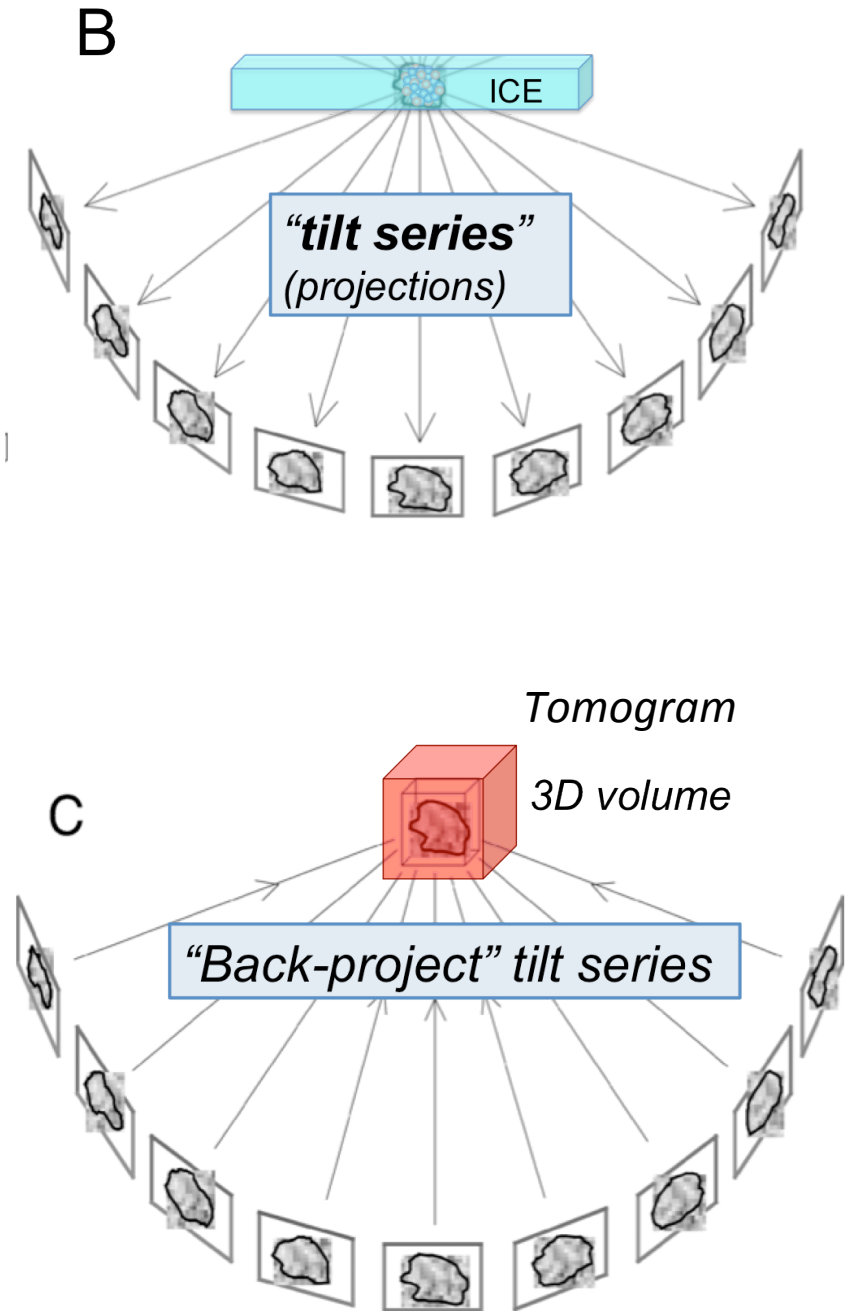
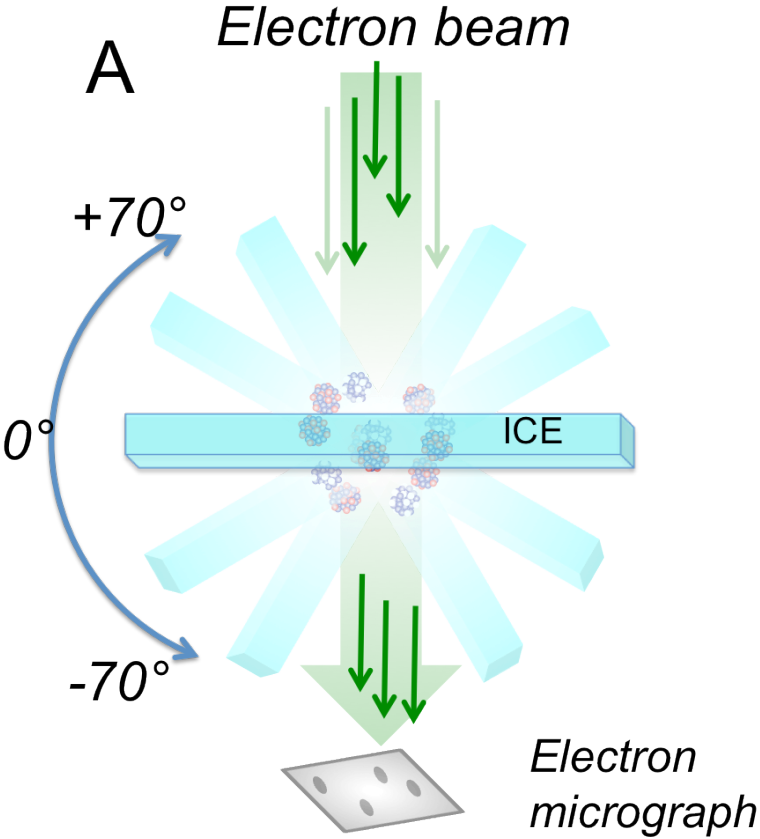
Nucleus

Cytoplasm

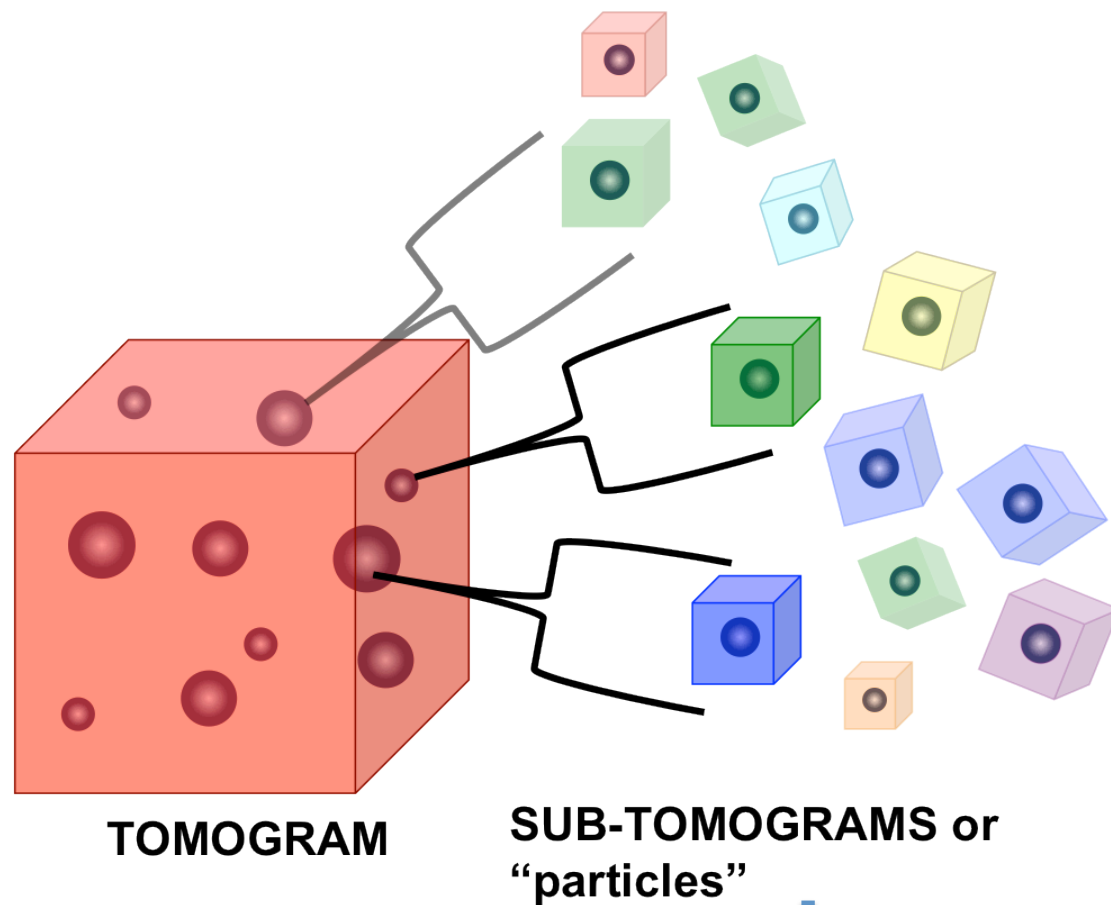
SPTable STUFF

- Ribosomes
- Viruses
- NPC
- Etc...

Cryo Electron Tomography (cryoET)

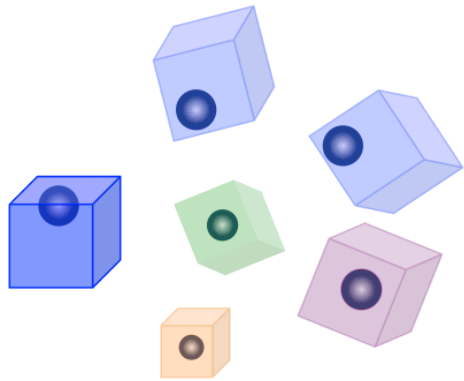


SUBTOMOGRAM EXTRACTION



Preparation, alignment, (classification), averaging

REFERENCE BASED ALIGNMENT

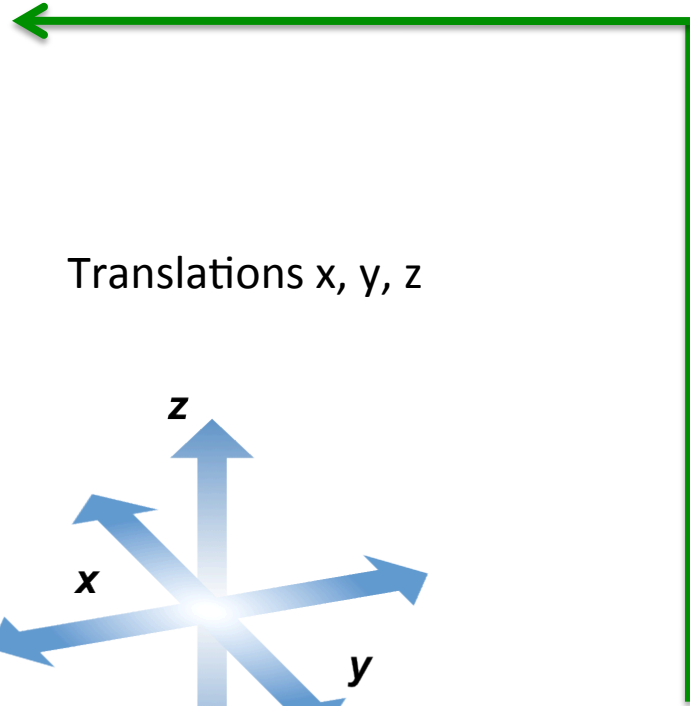


VS

model

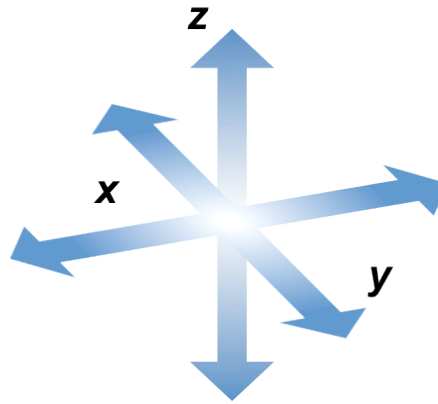
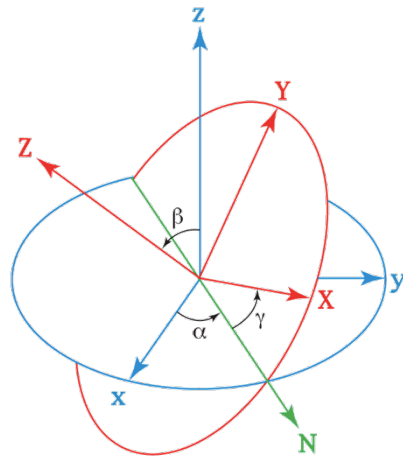


REFINEMENT

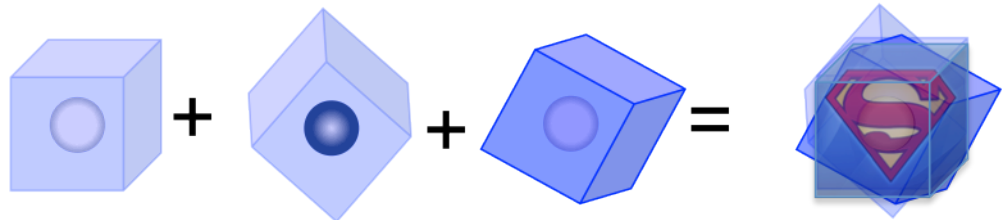


Rotations az, alt, phi

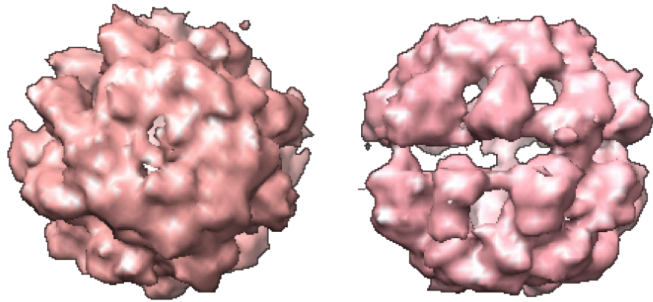
Translations x, y, z



Average

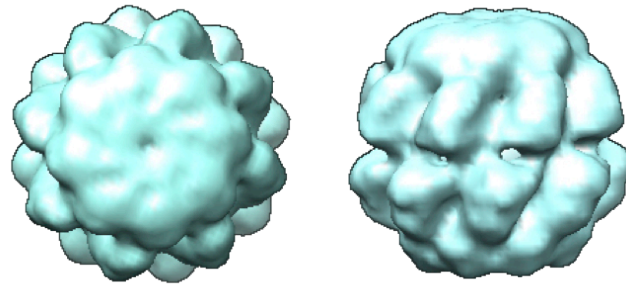


310 closed-TRiC particles
Asymmetric average



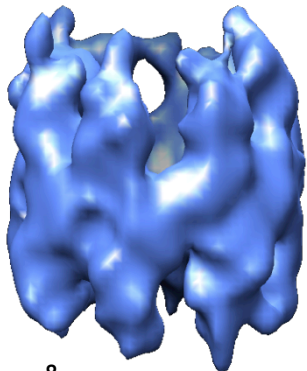
~35Å resolution (FSC 0.5)

C8 symmetric average



~26Å resolution

ASYMMETRIC average
102 open-TRiC particles



7-refinements

~26Å resolution

- **New** code (needs optimization; i.e. memory usage)
- Suggested memory: **8+ GB** of (Workshop machines have only 3GB of ram)
- **CUDA** support, **10x-100x faster** (compile EMAN2 yourself).

