

# Aligning and Averaging 3-D Subvolumes from Electron Cryo-Tomograms

Michael F. Schmid



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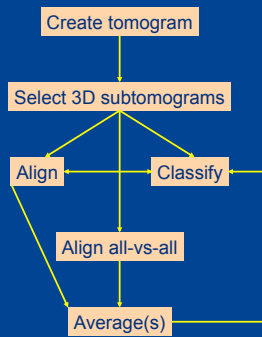
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Flow Chart for processing subtomograms



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## Key Points/Concepts

Effect of the Missing Wedge

Image considerations

filtering, masking

All-vs-all alignment as an option

Optimizing search parameters for efficiency

Examples

carboxysome,  $\epsilon$ 15, herpes pentonless capsid, trypanosome flagella

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### Effect of the missing wedge

- Tomographic data is limited to  $\pm 70^\circ$  max tilts
- Distorts the reconstructions
- Makes mutual alignment difficult

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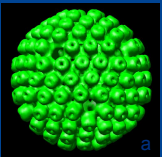
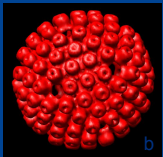
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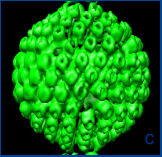
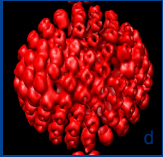
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### Demonstration of the effect of the missing wedge

No missing wedge

40% missing wedge  
(Equivalent to  $\pm 54^\circ$  tilt)

5-fold map
3-fold map

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### The missing wedge in Fourier space during orientation cross-correlation search

data





The number of zeros in the complex product changes with orientation, and the more zeros, the lower the cross-correlation peak

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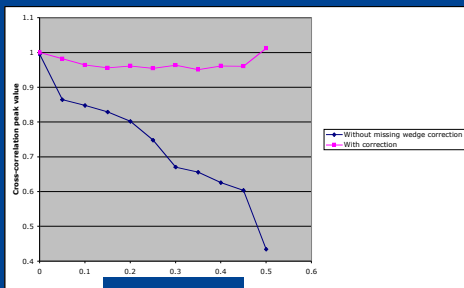
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Effect of the zeros in complex product on cross-correlation peak height



One solution is to scale the cross-correlation peak by the reciprocal of the number of non-zeros in the complex product for that orientation

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Another more recent option

•At each orientation, normalize the cross-correlation map

- In real space, this makes the mean=0 and s.d.=1, so peak value is the # times s.d. by which the peak exceeds the average for that orientation
- In Fourier space this makes total power of the complex product equal for all orientations, which compensates for the missing wedge

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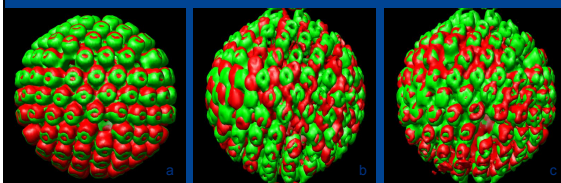
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Mutual alignment of a 3-fold oriented map to the 5-fold for a ±54° tilt series

(exact correct answer = 37.72°, 18°, -18°)



- Alignment (5° step size) of 3-fold maps to 5-fold maps
- a- No Missing wedge (40°, 20°, -20° - RIGHT (to within 5° step size))
  - b- Missing wedge without compensation (5°, 15°, -15° - WRONG)
  - c- Missing wedge with compensation (40°, 20°, -20° - RIGHT)

This figure is intended to illustrate the need for tilt series compensation. It is not intended to be used as a guide for tilt series compensation. However, it is a good starting point for the correct orientation.

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### Improvement of alignment by accounting for the missing wedge in cross-correlation search

(Right answer = (37, 72), 10, -18 or 3-fold related\*)

Fraction missing	Tilt series equivalent	Ignoring effect of missing wedge	Accounting for missing wedge
.00	$\pm 90^\circ$	40, 20, -20	40, 20, -20
.05	$\pm 85.5^\circ$	40, 20, -20	40, 20, -20
.10	$\pm 81.0^\circ$	40, 20, -20	40, 20, -20
.15	$\pm 76.5^\circ$	40, 20, -20	40, 20, -20
.20	$\pm 72.0^\circ$	40, 20, -20	35, -105, 125*
.25	$\pm 67.5^\circ$	5, 20, -20	40, 15, -15
.30	$\pm 63.0^\circ$	5, 15, -15	35, 20, -20
.35	$\pm 58.5^\circ$	5, 15, -15	35, 20, -20
.40	$\pm 54.0^\circ$	5, 15, -15	40, 20, -20
.45	$\pm 49.5^\circ$	5, 15, -15	15, 75, -90
.50	$\pm 45.0^\circ$	5, 15, -15	10, -60, 50

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### Image Preparation Considerations

- Contrast-flipping, initial rotation and hand-choice
  - Reconstruction is usually contrast-reversed
  - Some reconstructions do not have missing wedge along z
  - Some reconstructions have hand-flip
- Filtering
  - Subtomograms are inherently low-res and high-noise, so alignment should not be overly optimistic (~40Å lowpass is appropriate)
  - Large-scale features of the object may allow even more aggressive filtering for initial alignment
- Normalization
  - Useful for classification based on cross-correlation peak values
- Masking
  - Spherical Zero mask insures correct "fill-in" function for rotated volumes
- Always carry out resulting operations (rotation and translation) on the ORIGINAL files, not the low-passed, etc. versions!
- Ultimate goal is to keep track of all transformations to be able to re-insert the average into the tomogram at the orientation of each instance of the structure

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### Carboxysome

- Found in photosynthetic and chemoautotrophic bacteria
- "Polyhedral" bodies - ~100 nm diameter, thin angular shell, granular interior
- Contain RuBisCO - fixes CO<sub>2</sub>
- Regulated
- Size, shape, symmetry of carboxysome and arrangement of RuBisCO unknown
- What if we want to inventory macromolecular machines in the cell if we don't know much about them *a priori*

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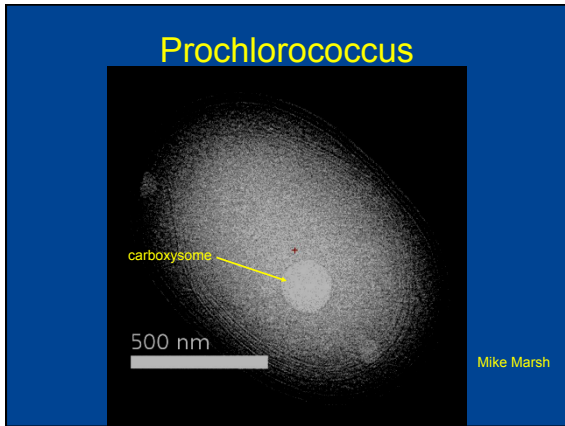
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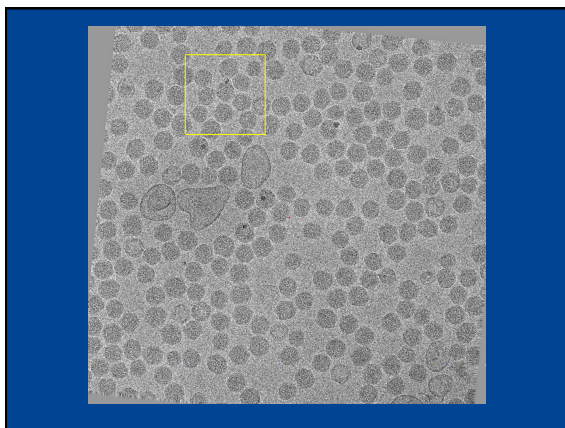
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### Approach

- Conventional single particle processing with icosahedral symmetry using common lines did not work
- Our approach - averaging 3D subvolumes extracted from tomograms (subtomograms)
  - but subtomograms have a missing wedge in Fourier space the same shape as the missing wedge of the entire tomogram
- In the literature of post-tomographic averaging, subtomograms have been aligned against a 3D model template which does not have a missing wedge
- Size heterogeneity and unknown symmetry make it difficult to choose a starting model
- Therefore we chose to mutually align subtomograms to each other

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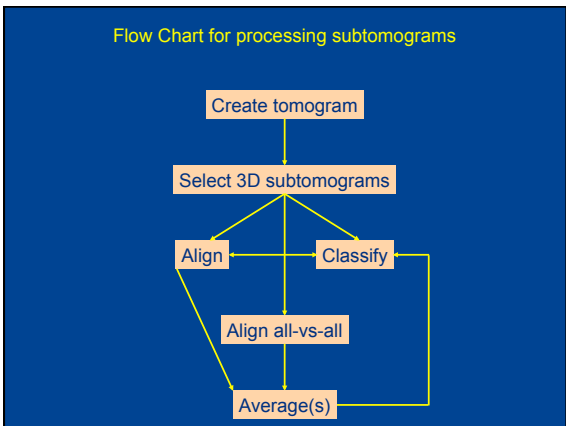
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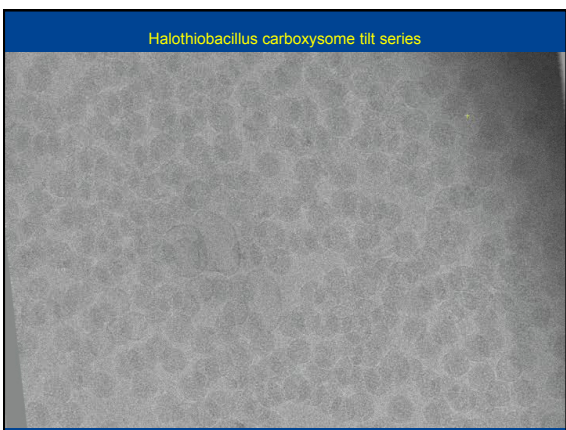
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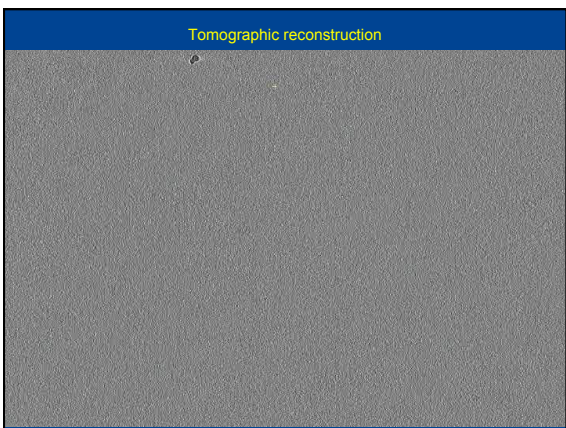
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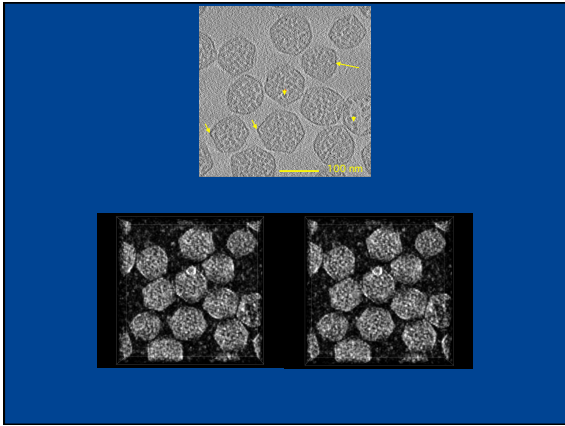
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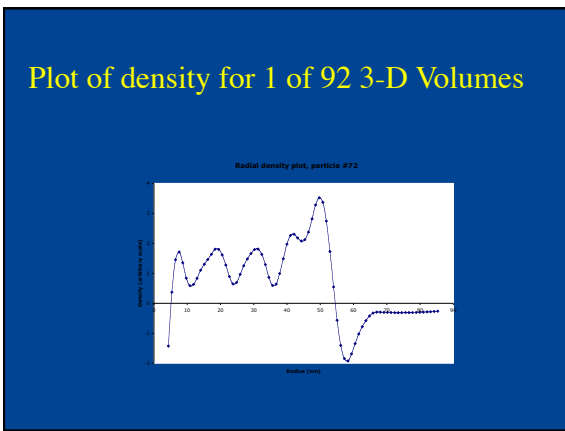
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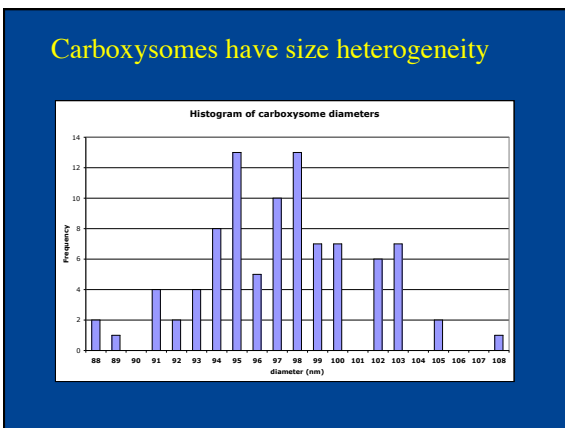
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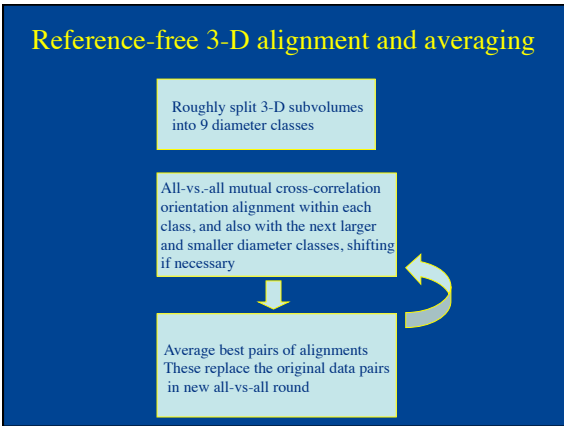
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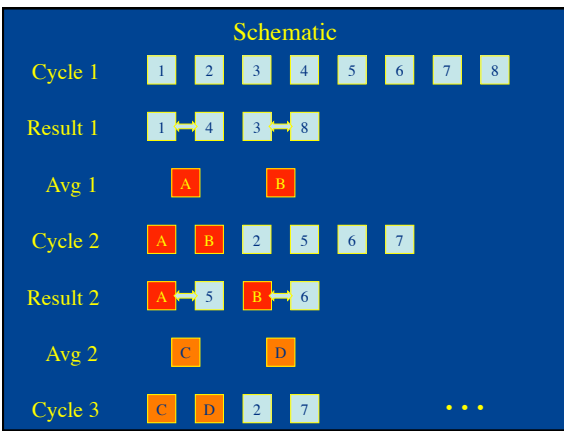
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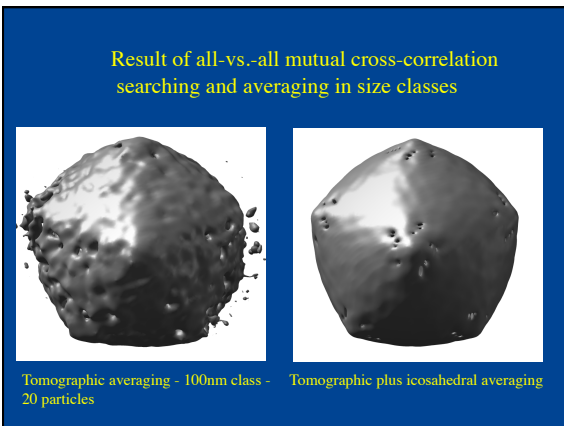
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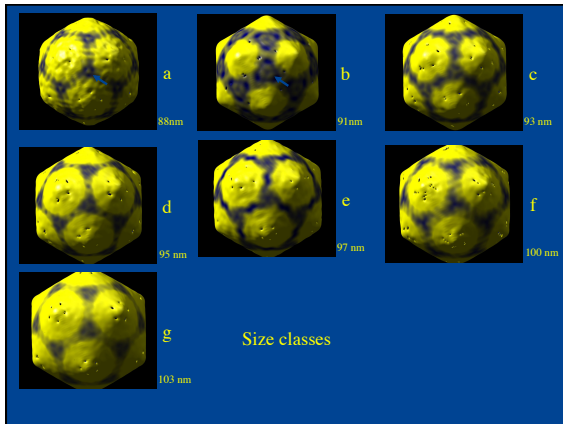
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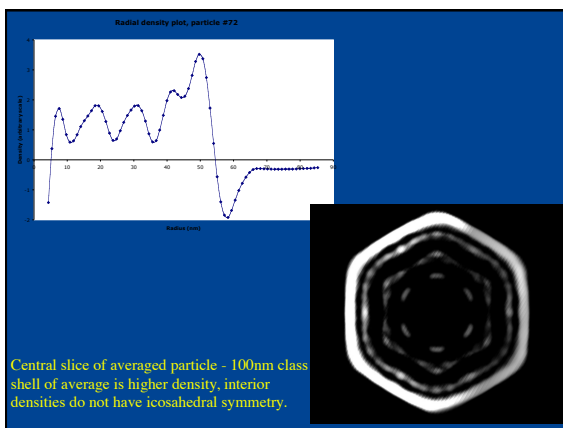
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## Conclusions

- Shell symmetry is icosahedral
- Size of carboxysome varies from 88 to 103nm - unusual for an icosahedral particle
- Shell protein arrangement varies with size
- RuBisCO organization in layers inside, but not regular, nor constant amount per particle
  
- Specialized processing needed for determining mutual orientation and for averaging of particles with missing wedge
  
- Schmid et al. (2006) J. Mol. Biol. (in press, online 09/14/06 )

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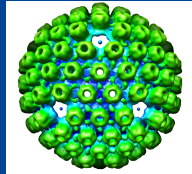
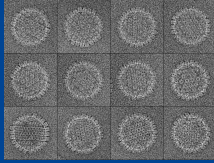
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### HSV pentonless capsids

Produced by chemical treatment of capsids with urea - removes pentons, but not portal



Icosahedral single particle reconstruction -  
Portal averaged away

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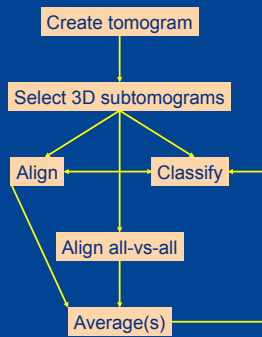
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### Flow Chart for processing subtomograms



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### Tilt Series of Herpes Pentonless capsid



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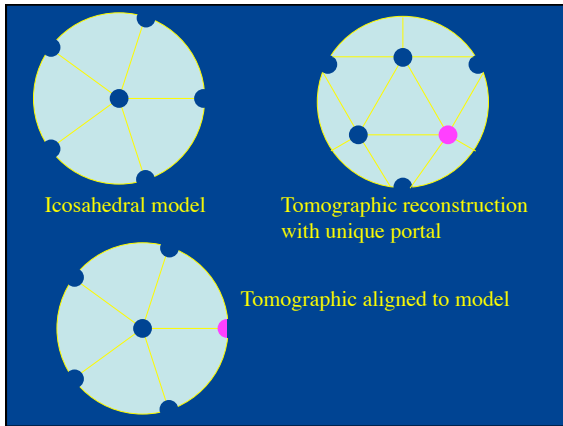
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**Alignment problem**

- The missing wedge causes densities to be different in different directions (from part 1)
- However, opposite vertices are affected equally by the missing wedge, so our solution was to compare the densities at opposite vertices; the one with the biggest *difference* in density was the portal vertex.

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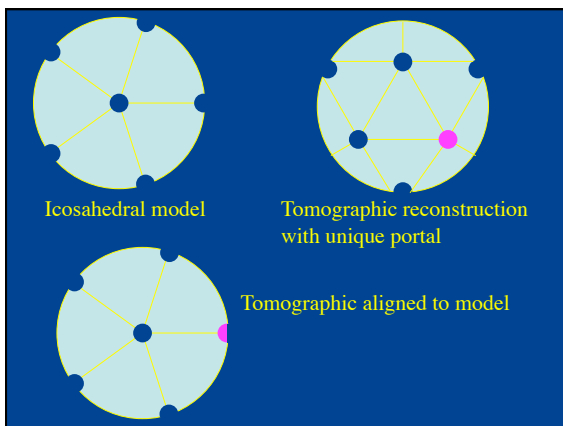
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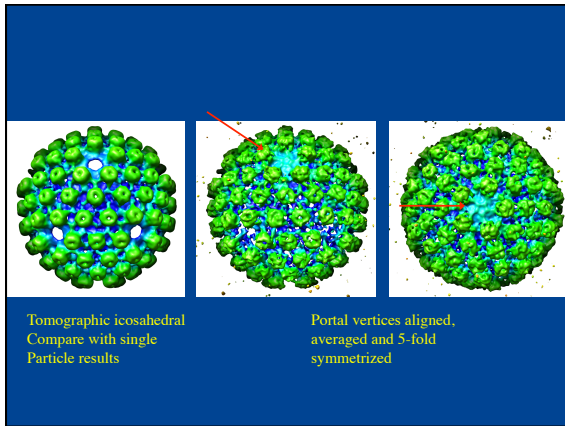
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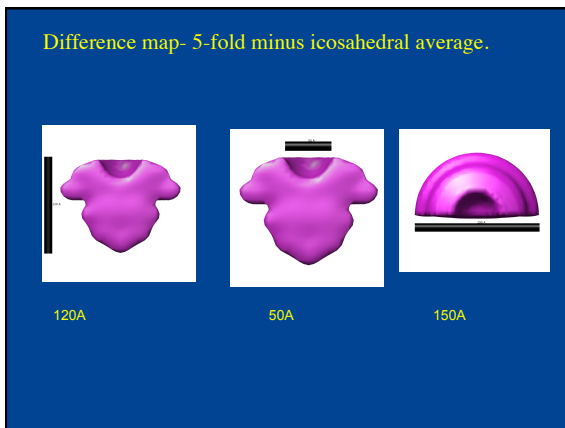
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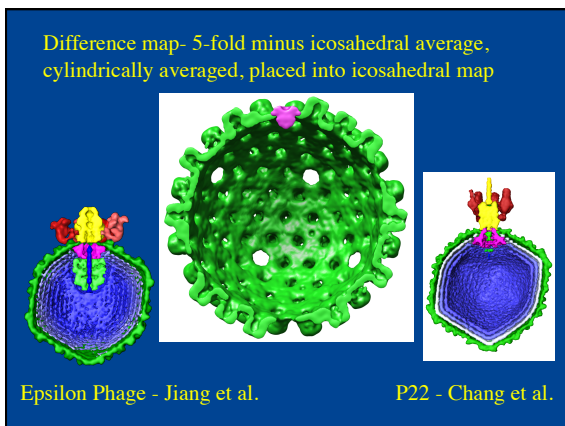
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### Epsilon 15 tomographic averages

1. Align tomographic subvolumes to icosahedrally averaged model from single particle (after this, no model used)
2. Put each vertex in turn along z, average it c19 (cylindrical)
3. Put unique vertex along +z. (6 tail spikes still not aligned)
4. All-vs-all cross-correlation with 5 search orientations
5. Average best-correlating pairs, etc.

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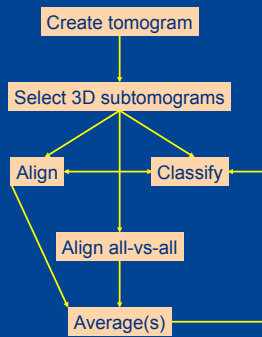
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Flow Chart for processing subtomograms



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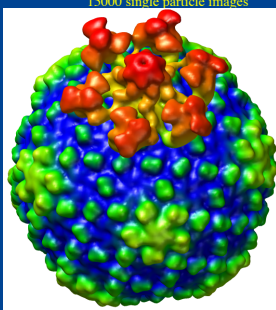
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15000 single particle images



Jiang et al. (2006) Nature 439:612

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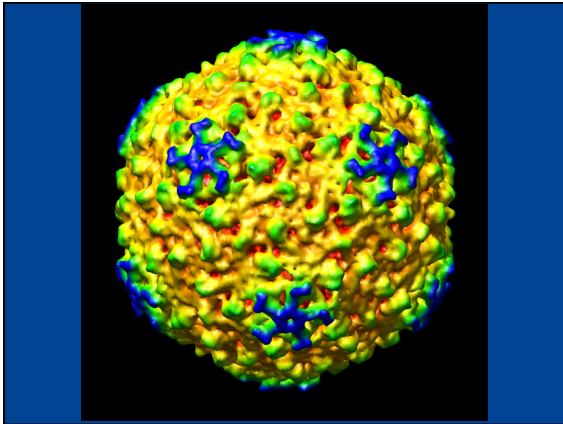
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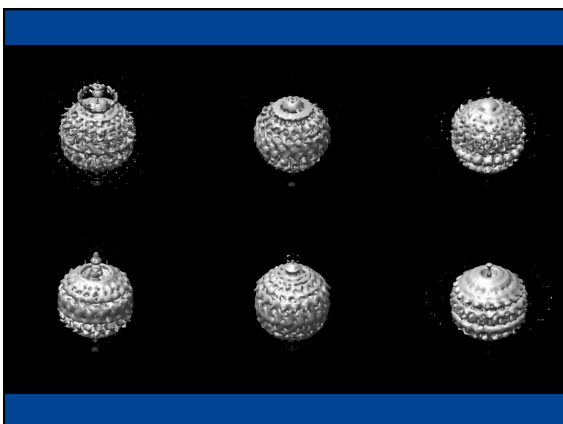
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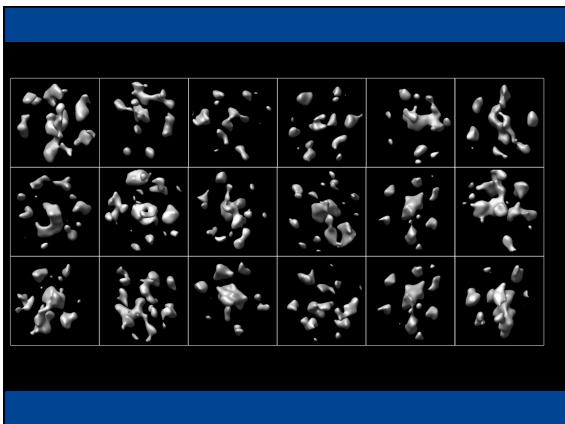
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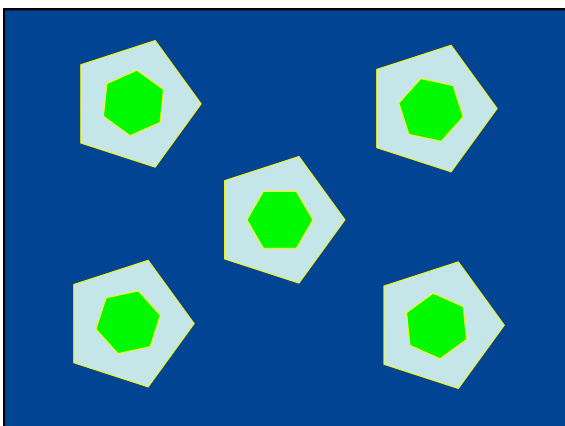
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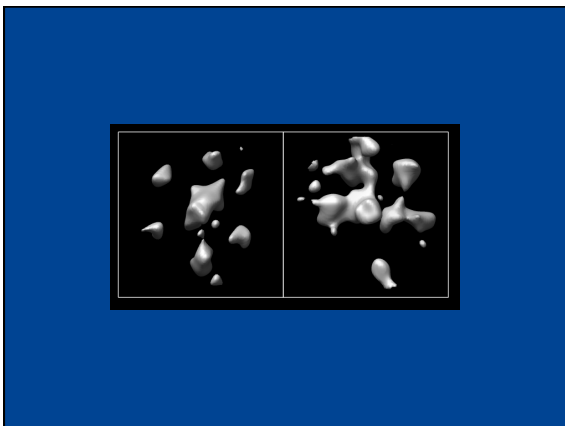
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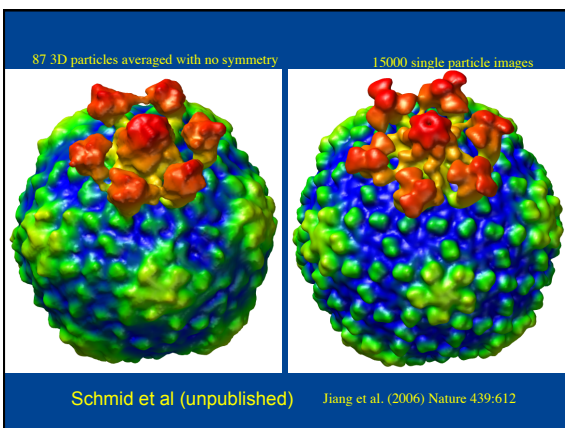
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