

Canonical SPA in EMAN

- Image Acquisition
- Particle Picking
- @ 2-D Analysis
- Symmetry/Low Resolution Model
- Determine CTF Parameters
- High Resolution Refinement
- Post-processing
- Dynamics Analysis

Image Aquisition

- Pick your defocus range
 - Envelope function related to defocus even on modern FEG scopes

 - Focal Pairs?
- @ CCD
 - Adequate sampling. For low symmetry, 2/5 Nyquist is a good rule of thumb (res=5*A/pix)
- @ Film
 - Scanner is important. Bit depth less important than scanner envelope function (e2scannereval.py)

Image Aquisition

- Avoid continuous carbon substrate
 - Decreases contrast
 - Difficult to separate c-film CTF from specimen
 - Makes CTF correction difficult

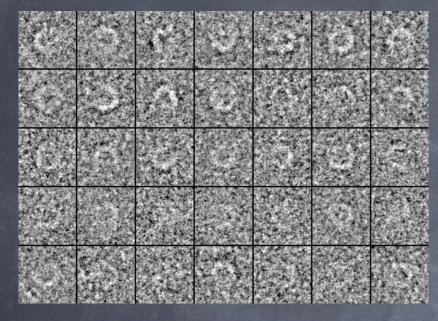
Particle Picking

- boxer, batchboxer, helixboxer, e2boxer.py
- Outside software ?
- manual or semi-automated process
- False positives are very dangerous, but also beware of excluding views you weren't expecting
- Mixing microscopes possible, but rarely worthwhile (tomorrow)

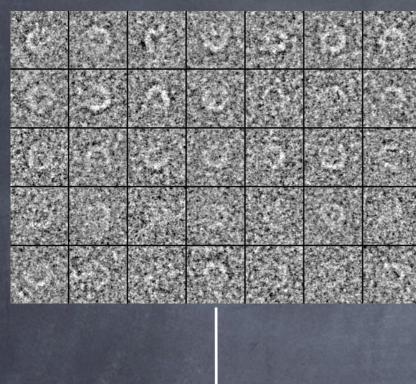
2-D Analysis

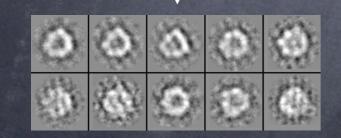
- Even if you know the quaternary structure, still worthwhile. May be surprises.
- At least 1000-2000 particles with uniform orientation distribution, perhaps fewer if symmetry or preferred orientation
- Look for dynamics or degradation
- o 'shrink' particles for speed
- # classes ≤ # particles/20
- refine2d.py not startnrclasses

Particles

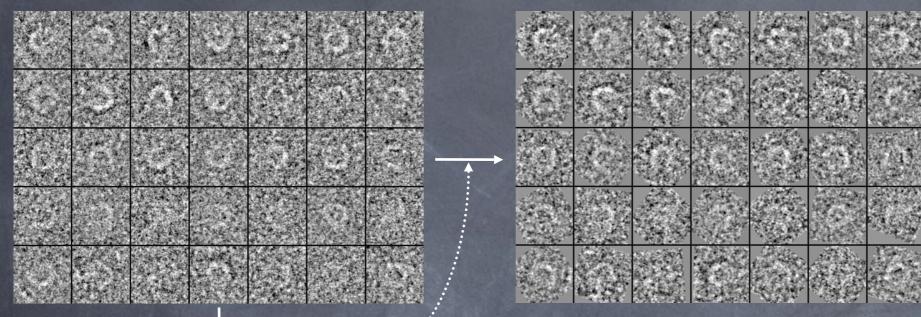


Particles

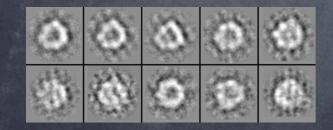




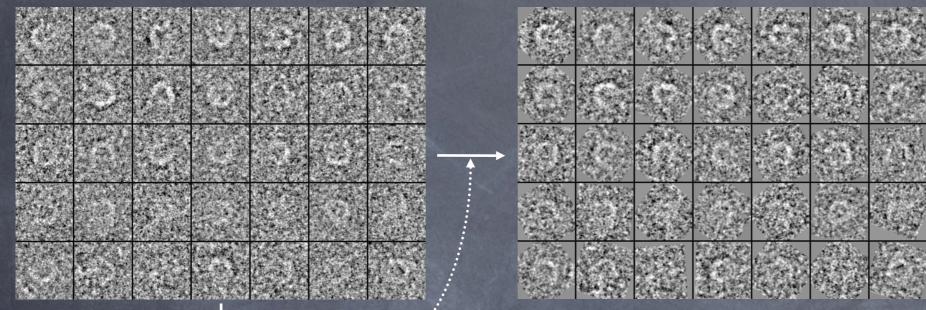
Particles



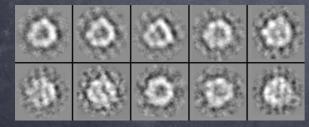
Align Particles

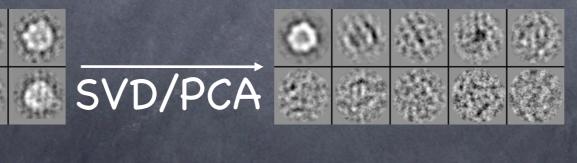




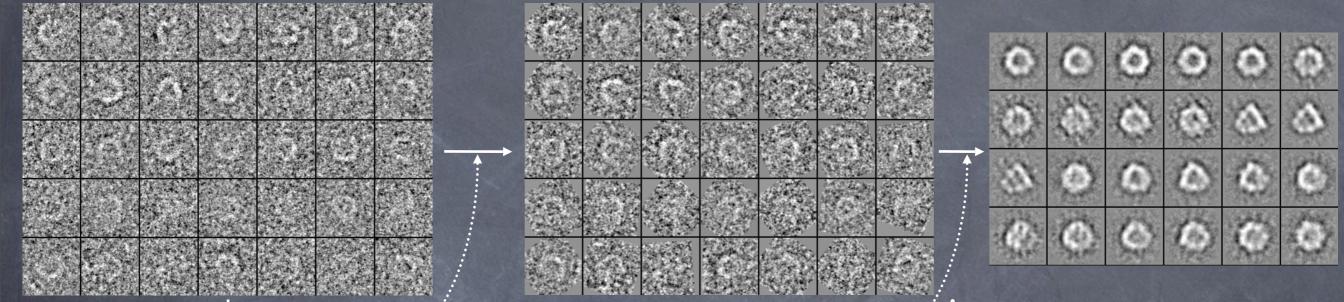


Align Particles

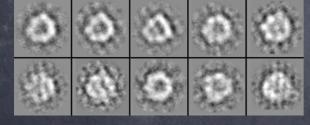




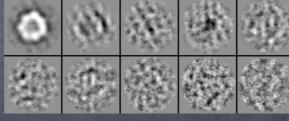


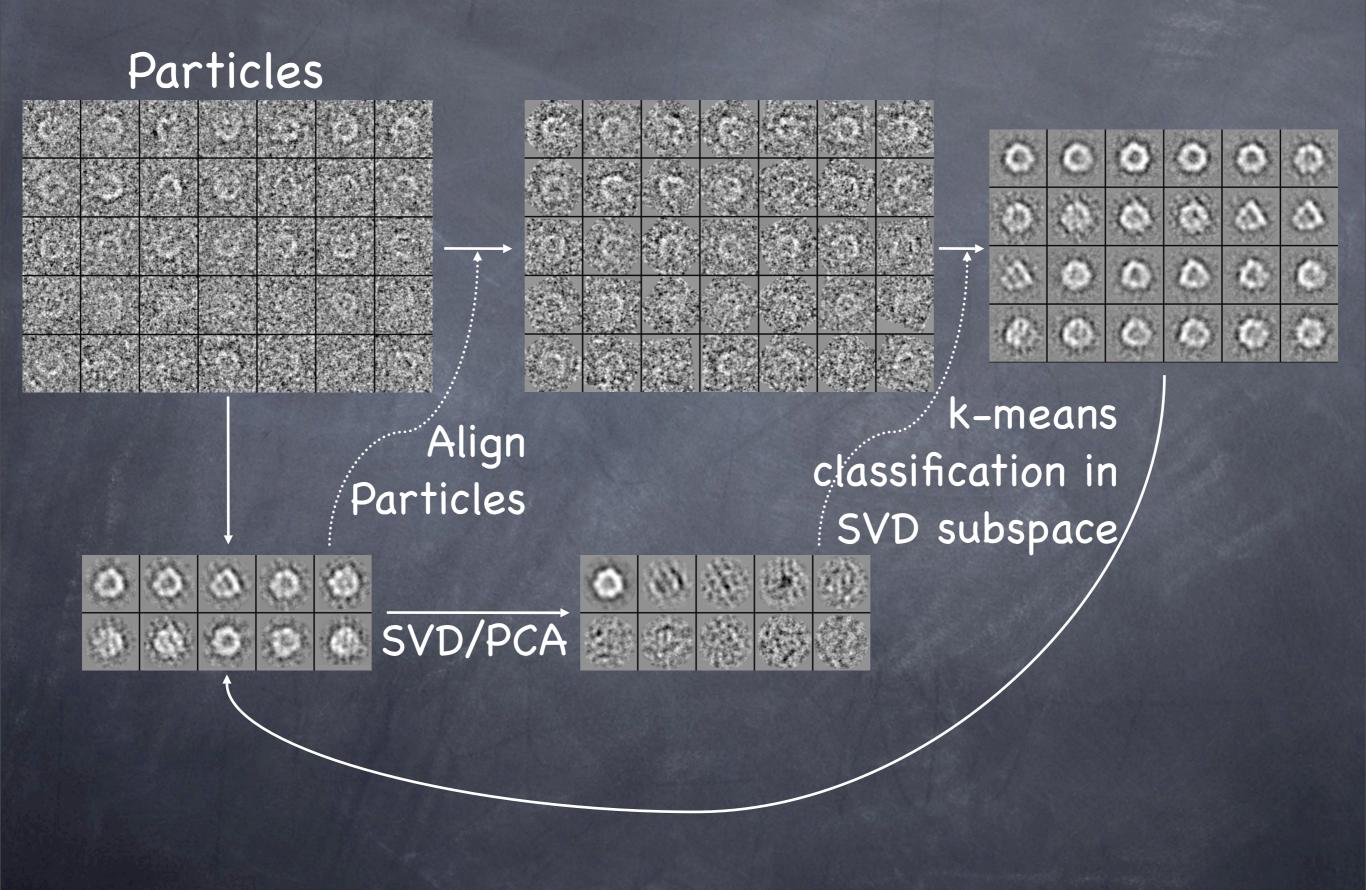


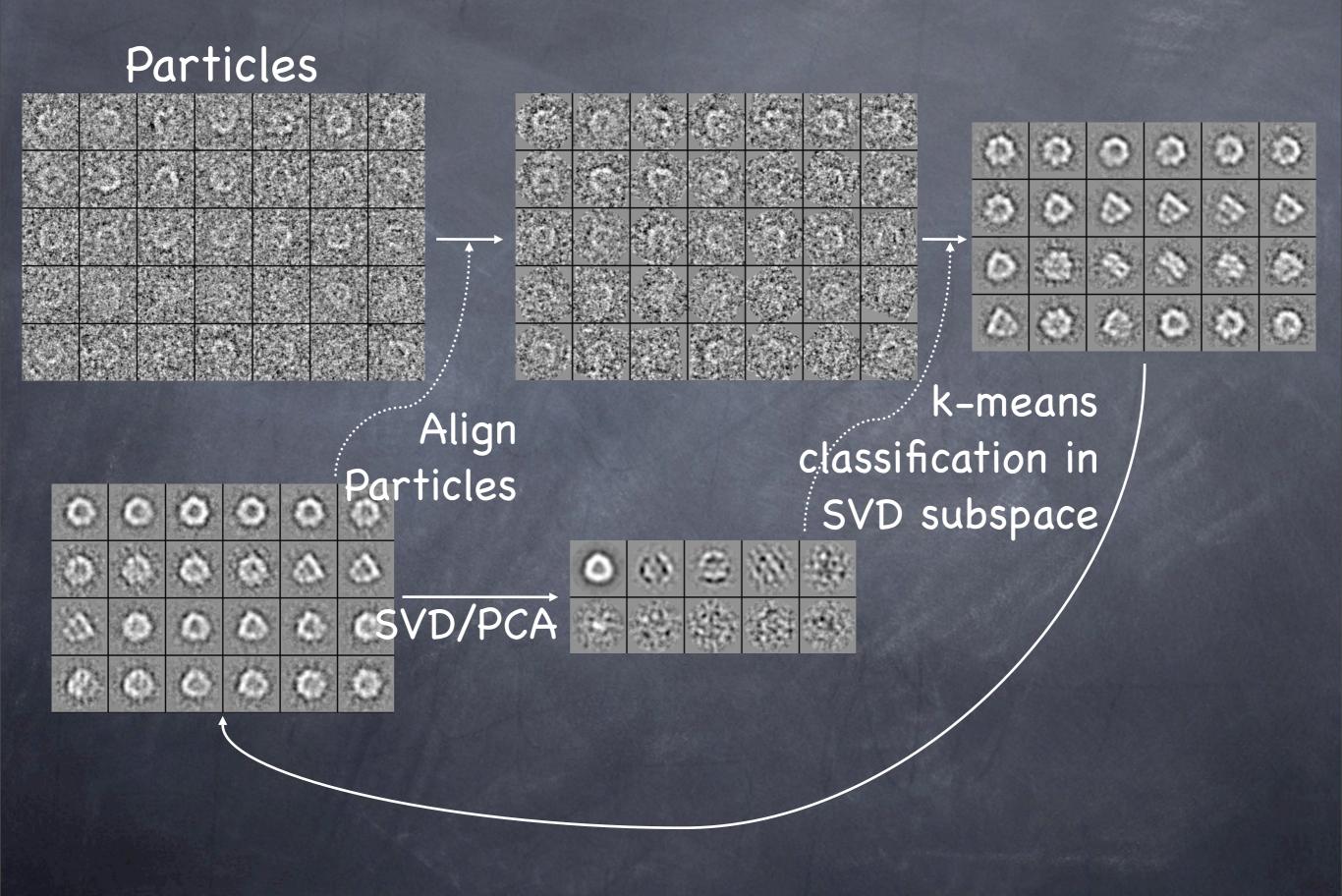
Align Particles k-means classification in SVD subspace

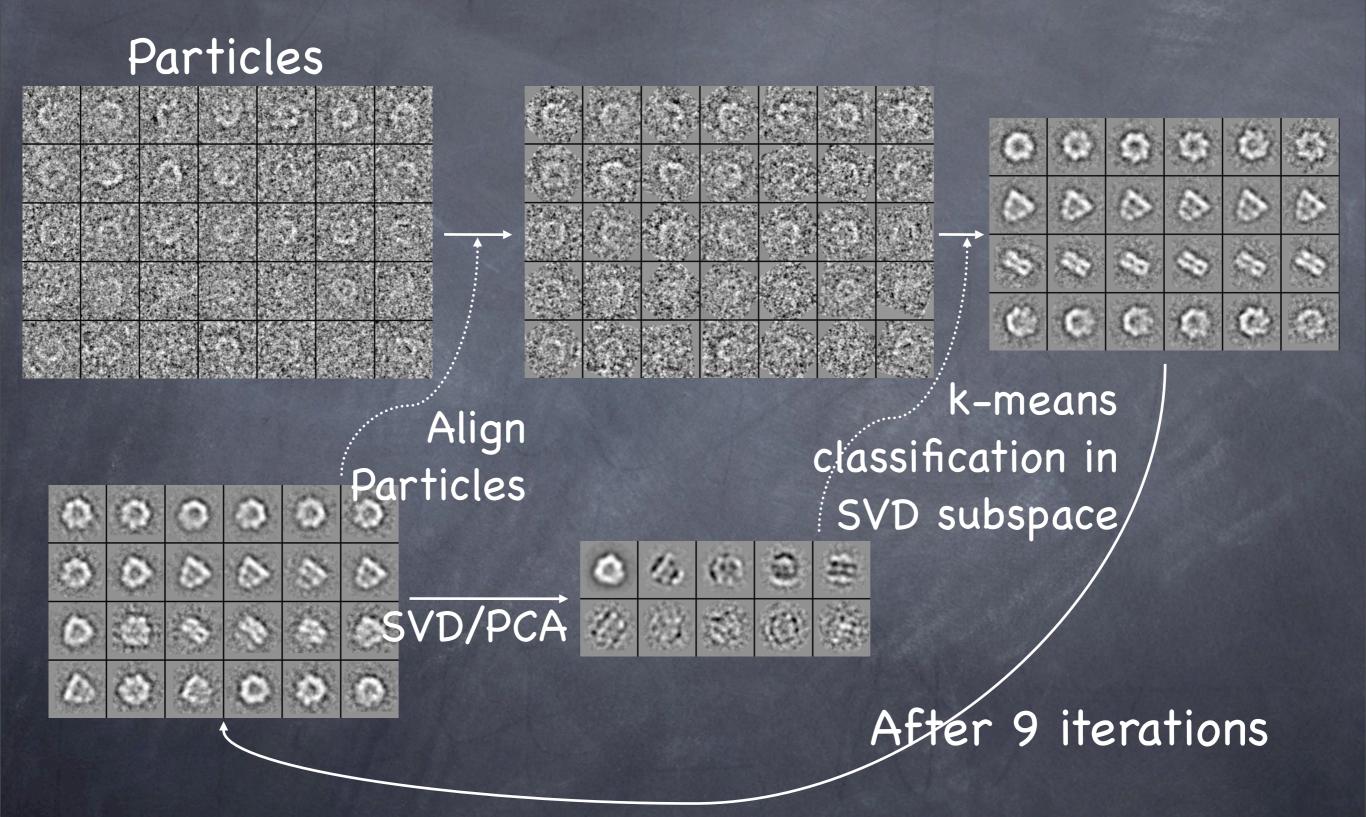


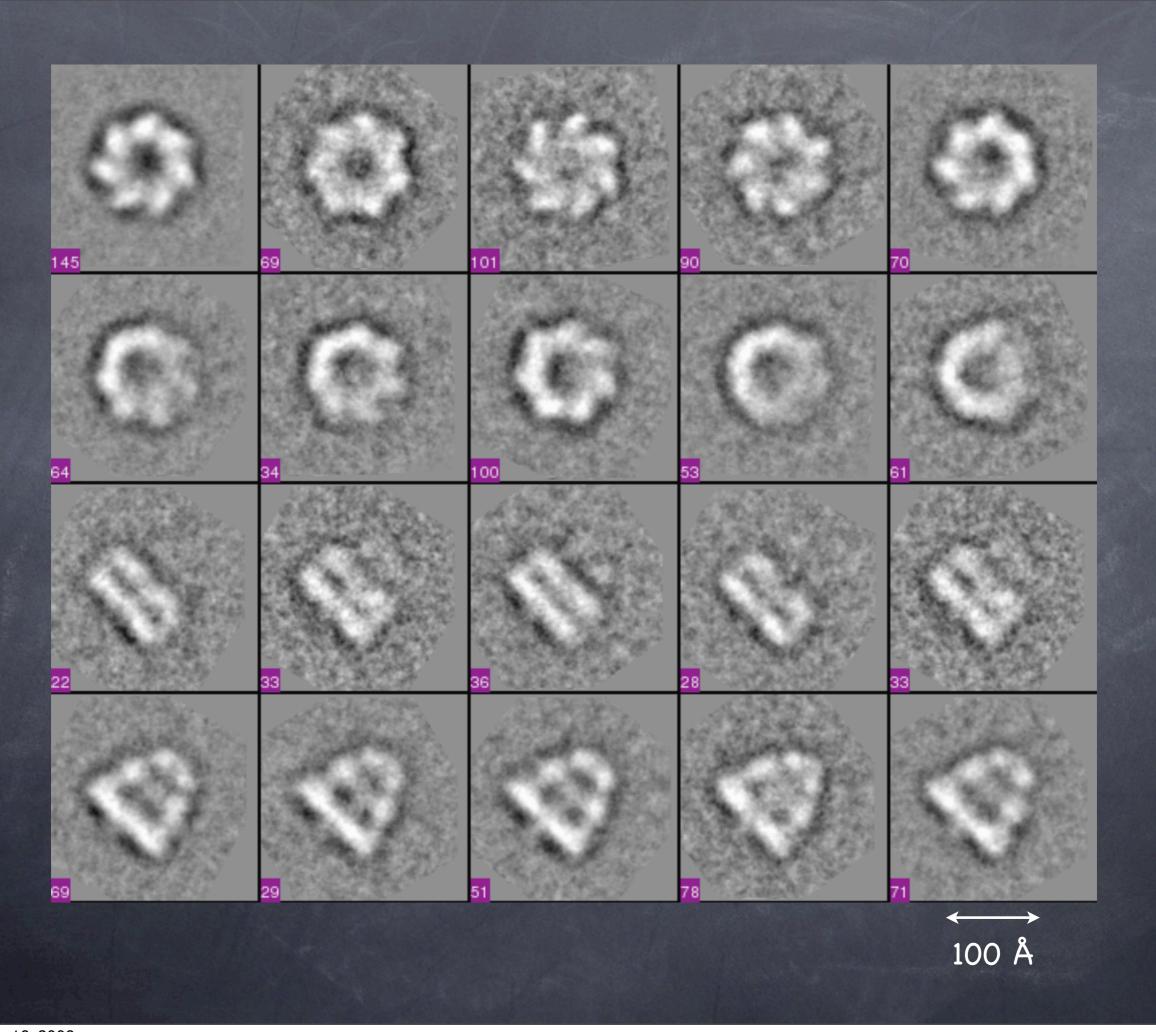




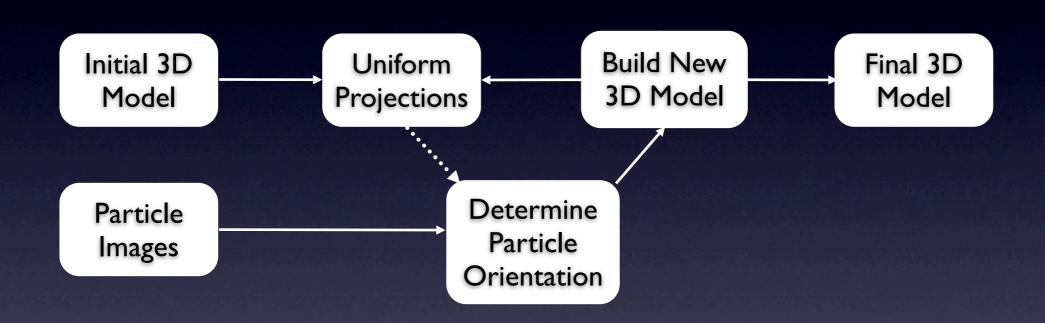






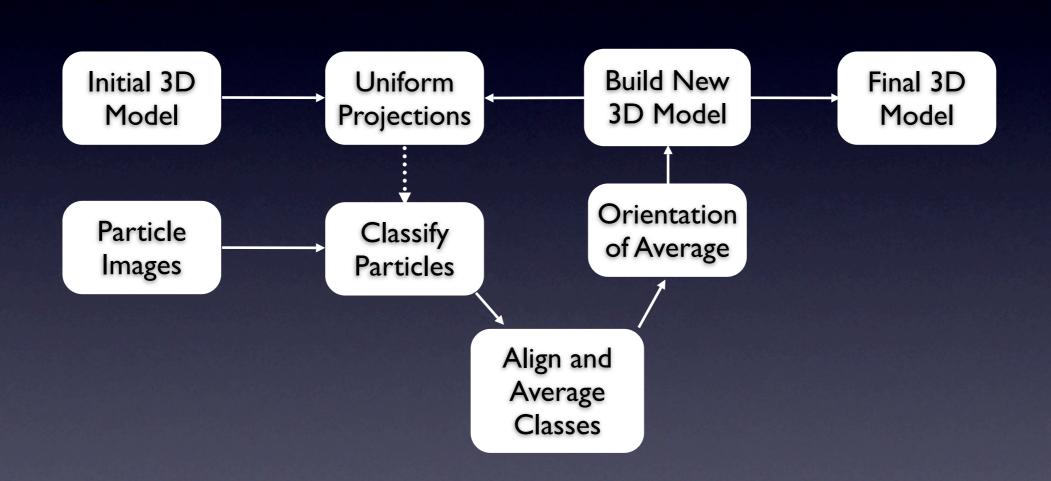


3-D Refinement (Typical) Spider Approach

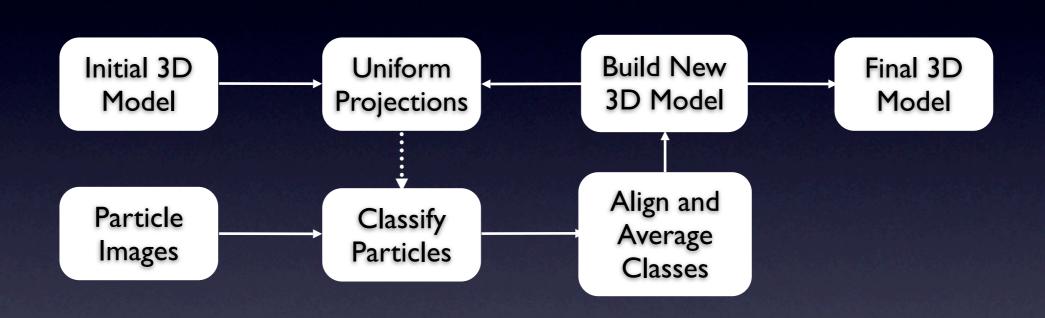


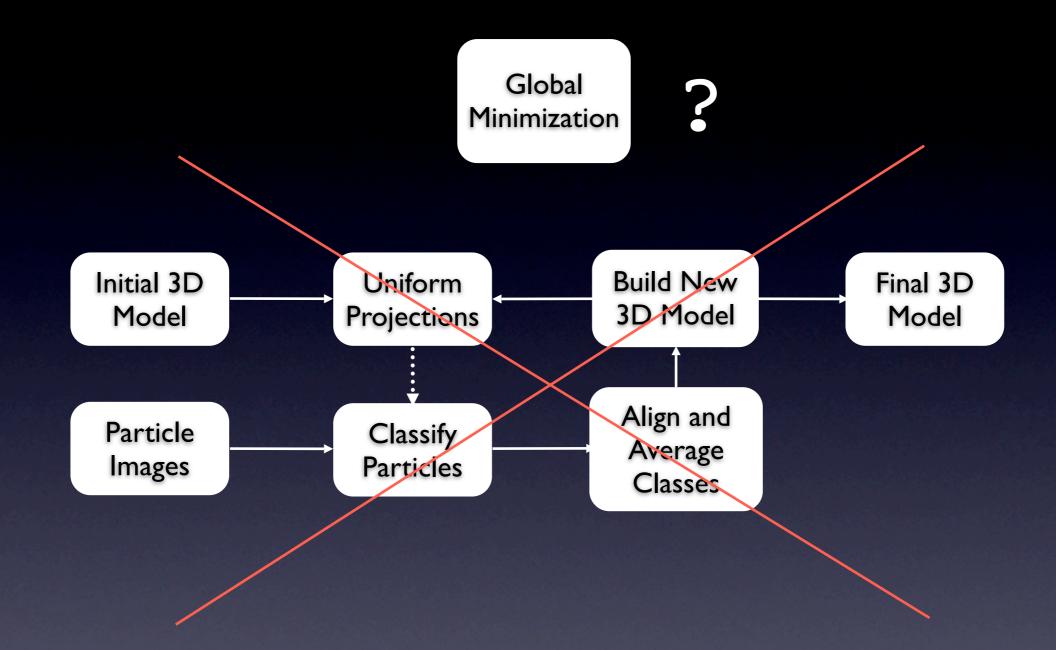


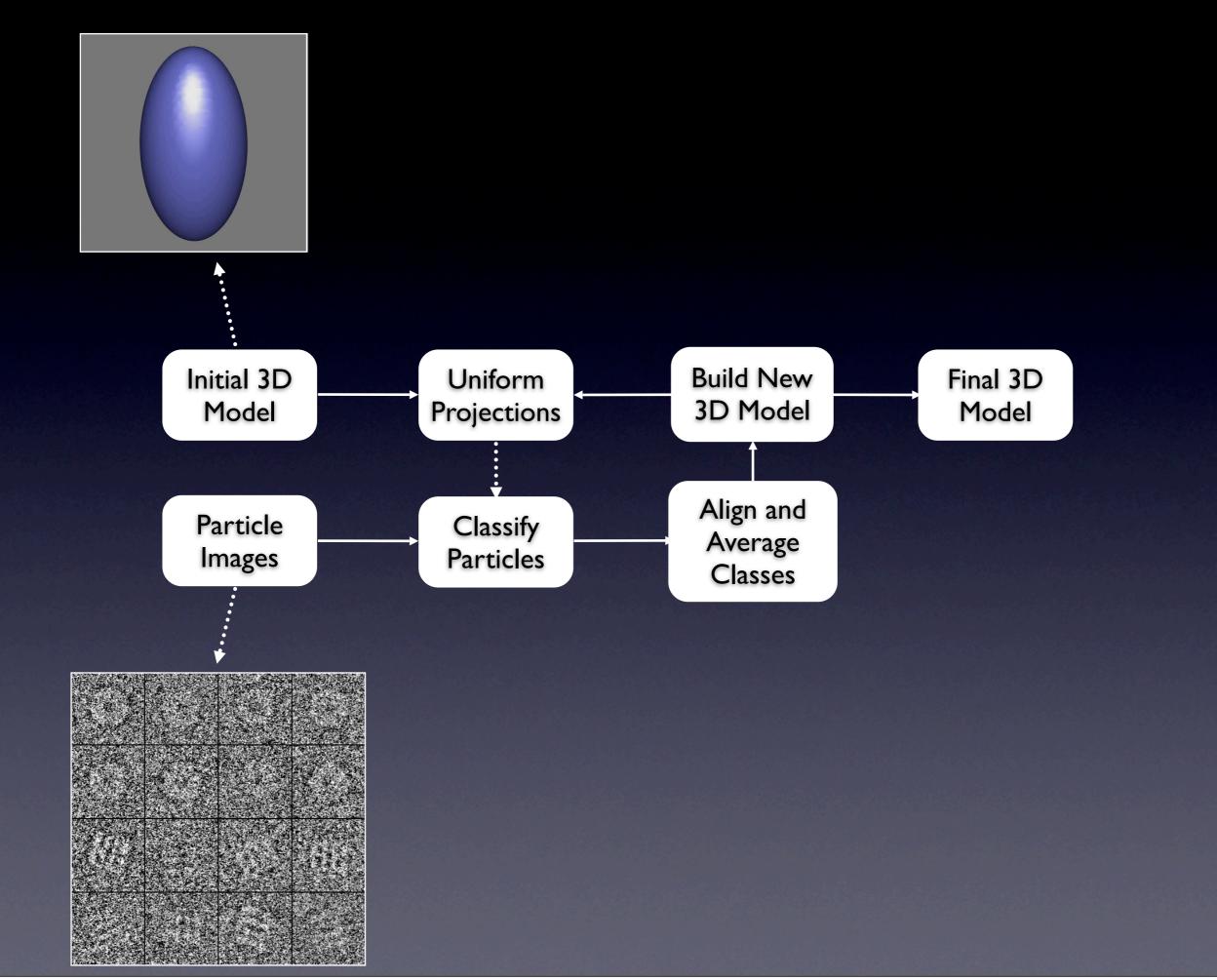
3-D Refinement (Typical) Imagic Approach

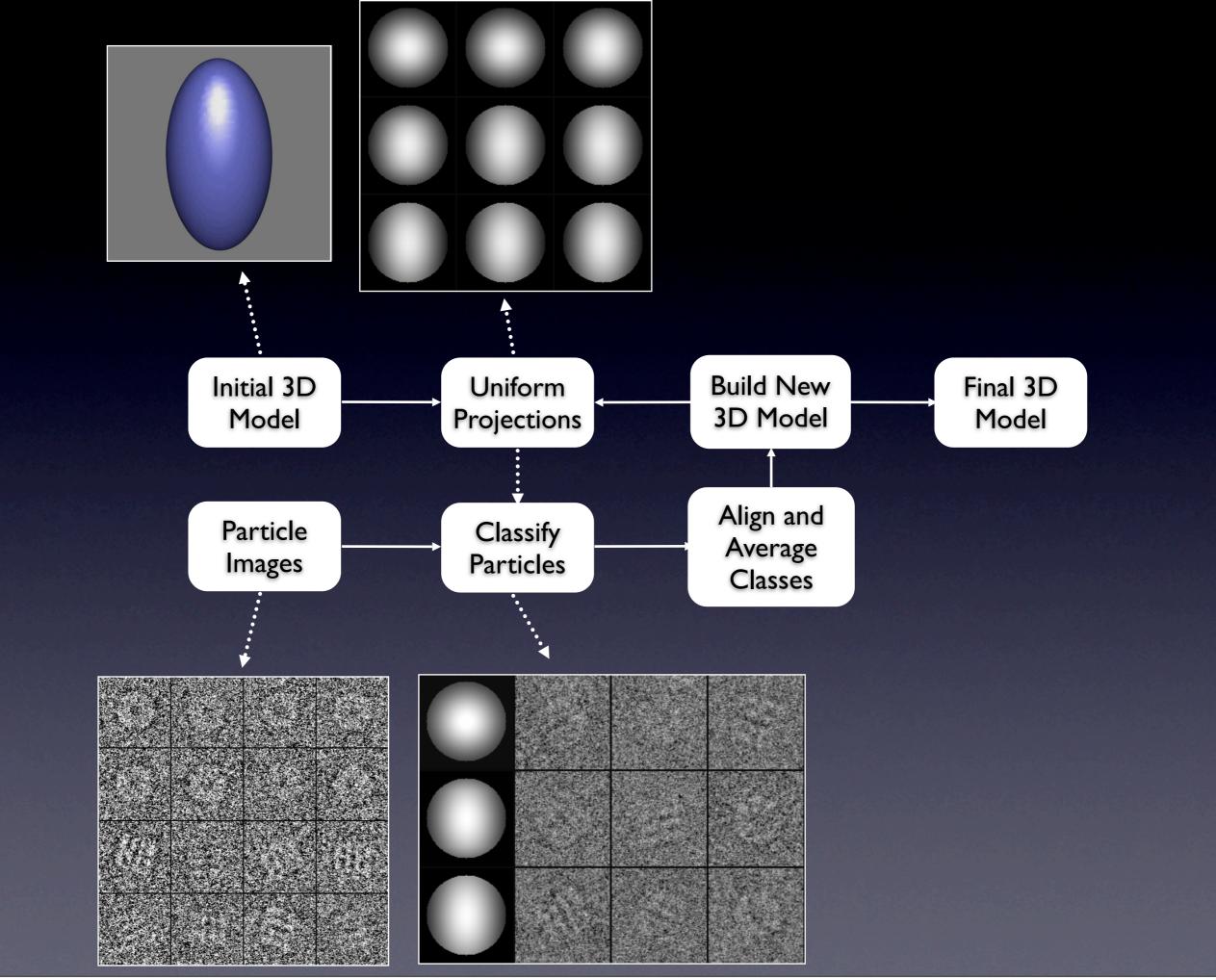


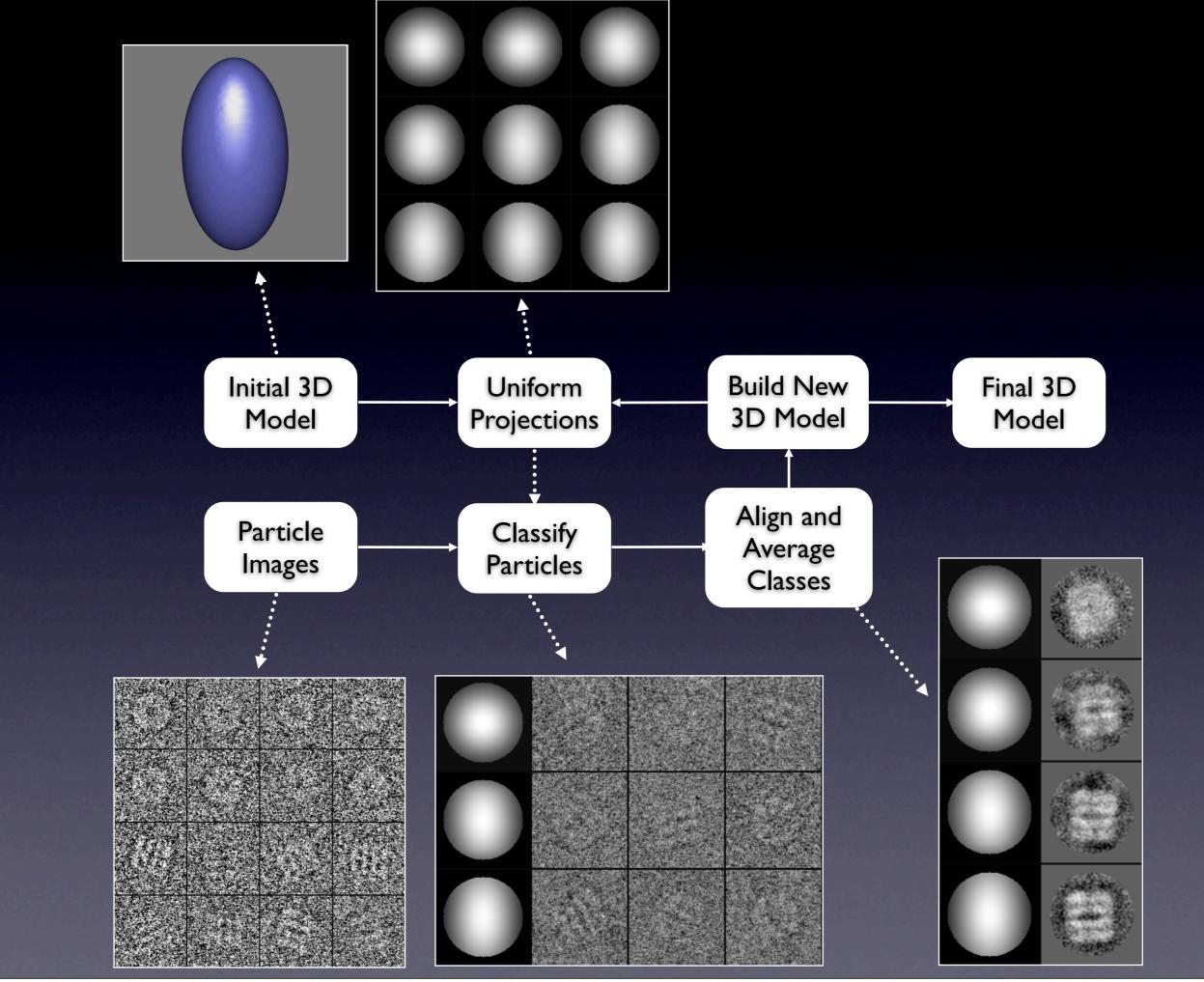
3-D Refinement EMAN Approach

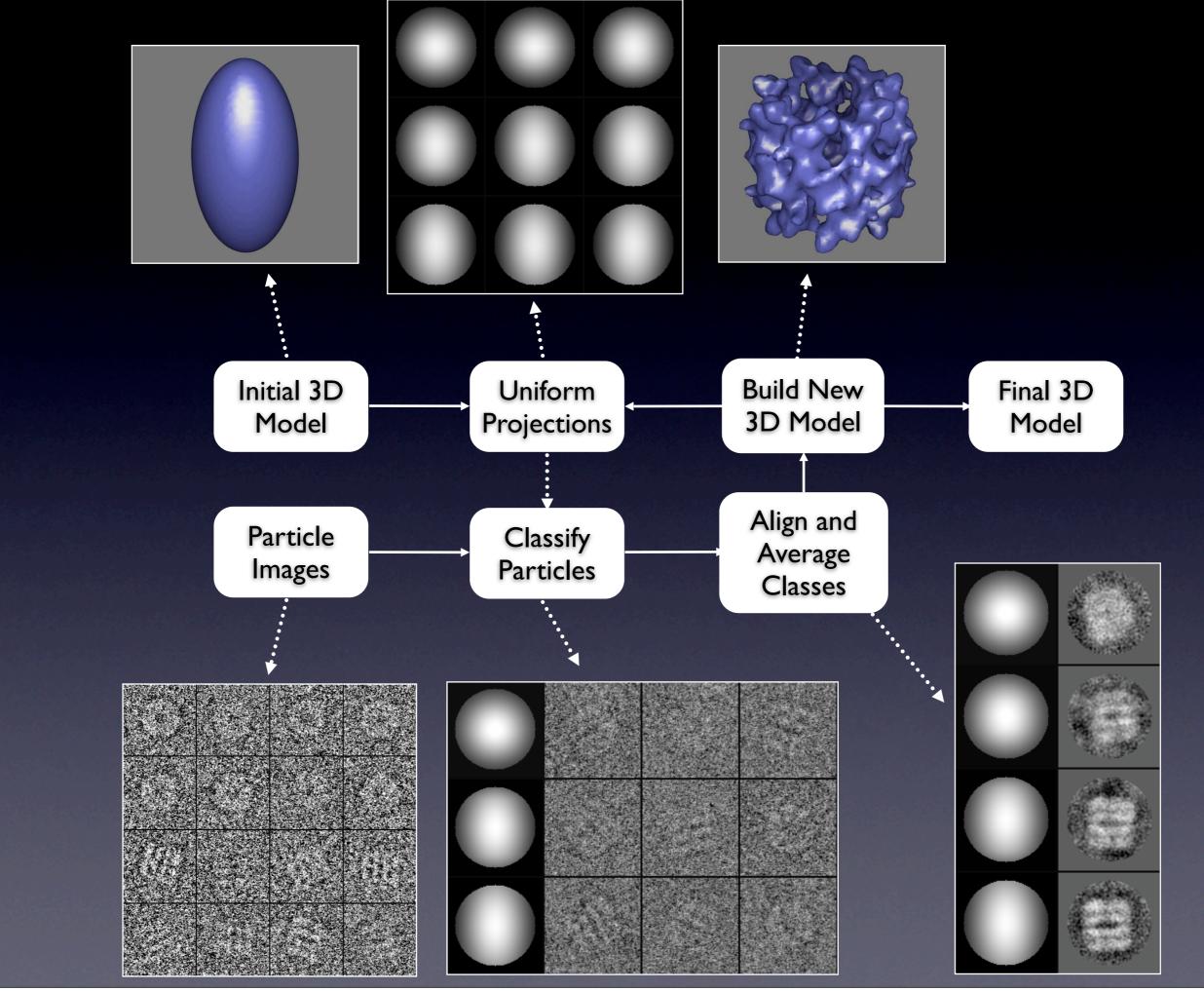


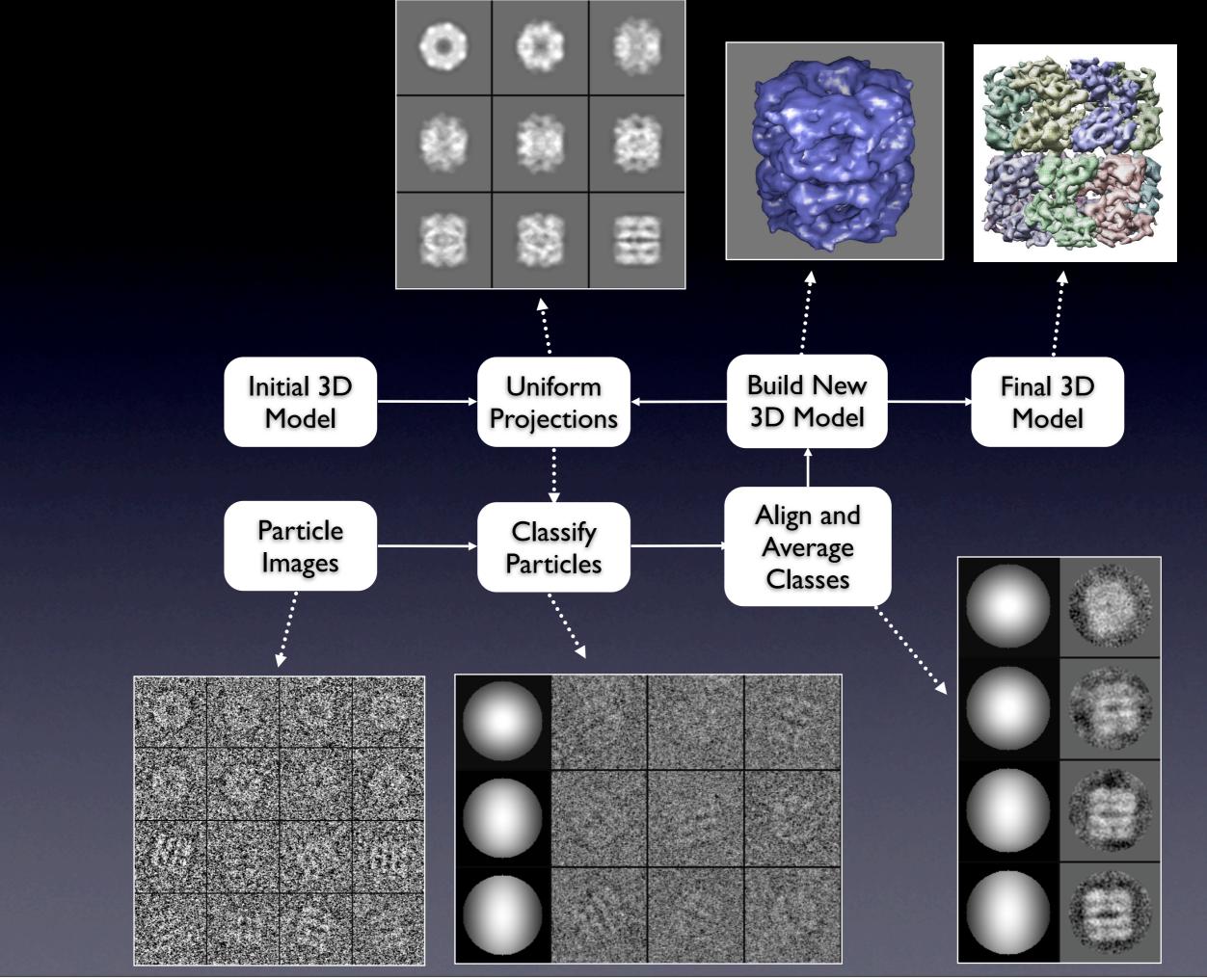




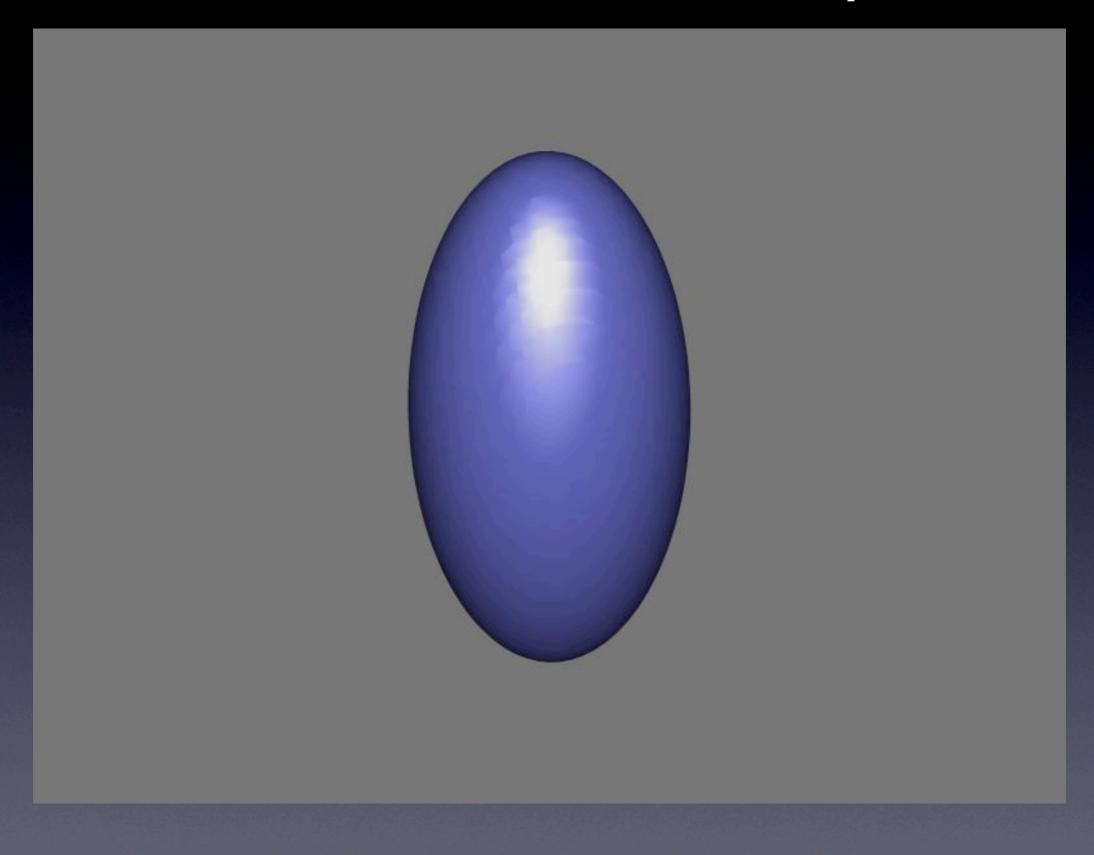




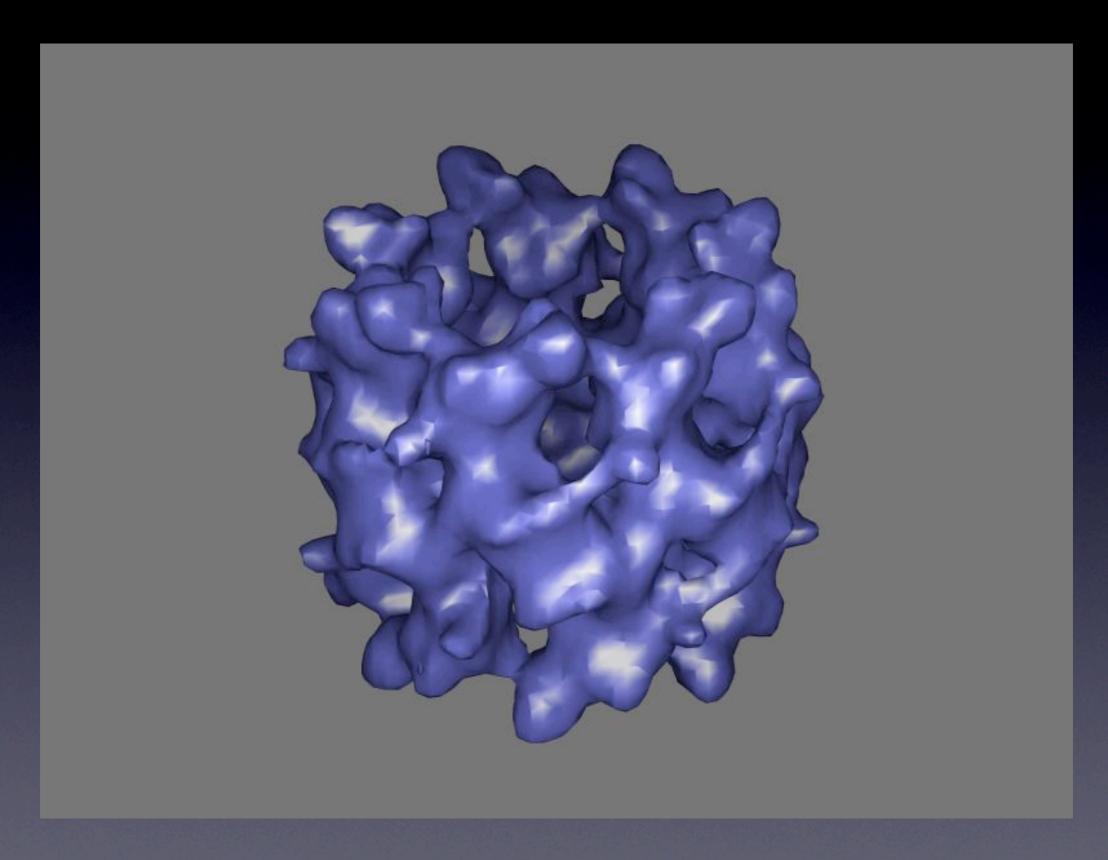


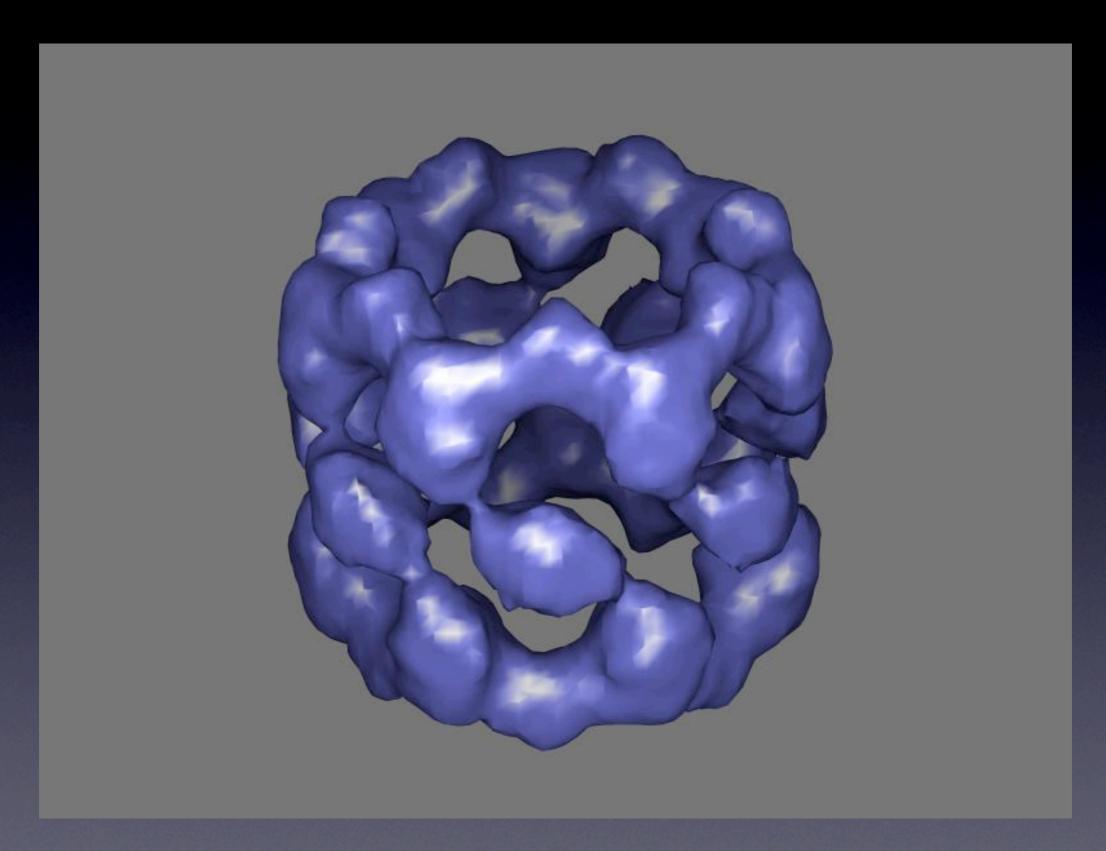


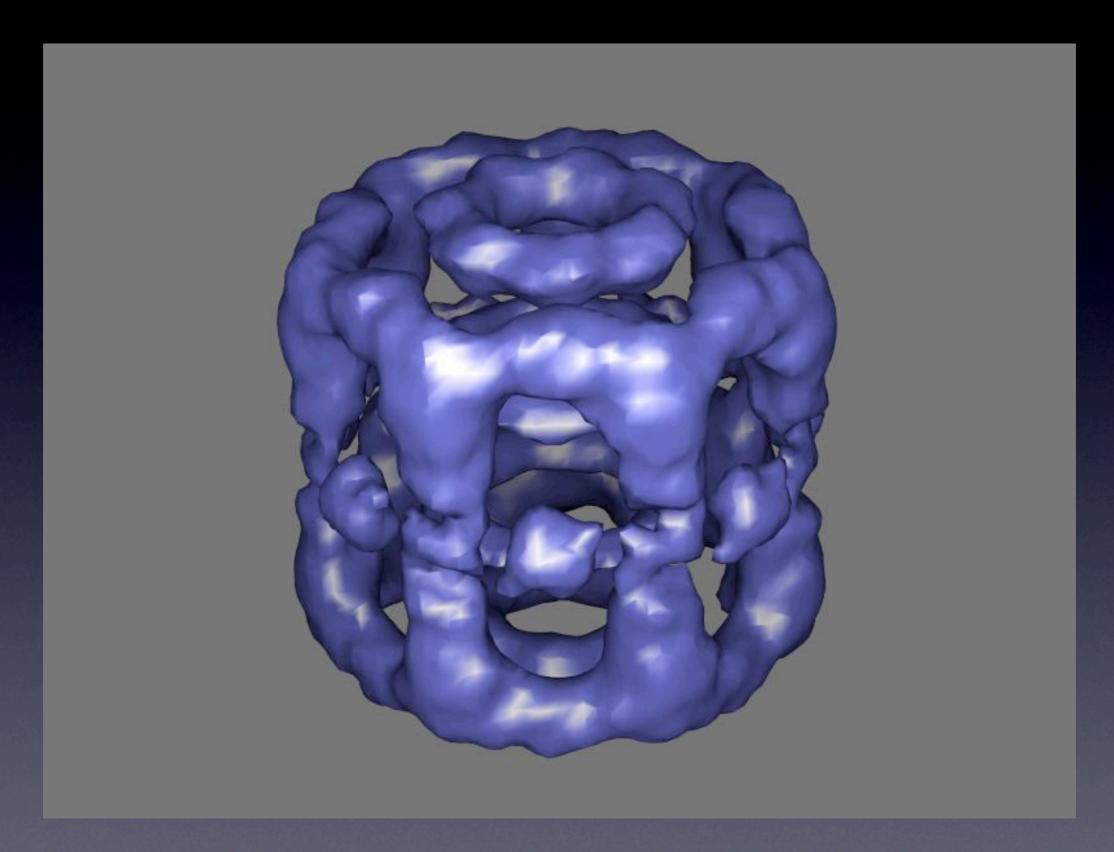
Refine from Gaussian Ellipsoid

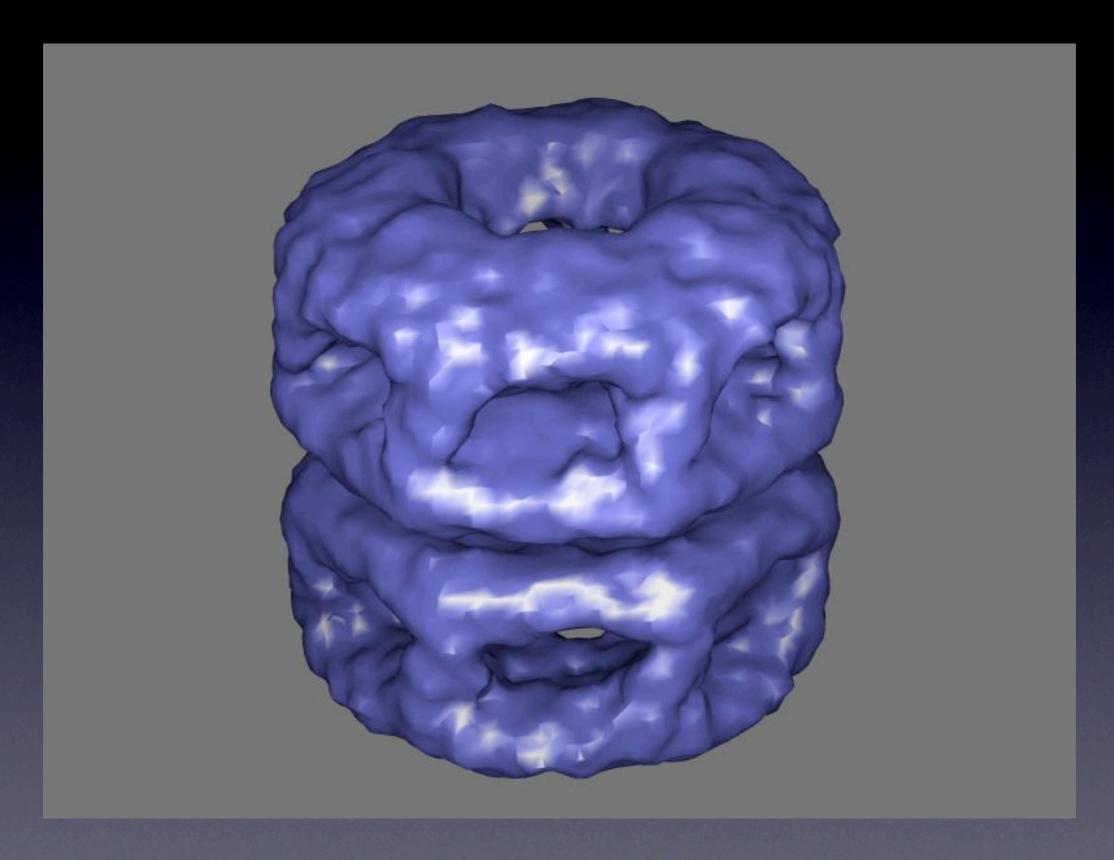


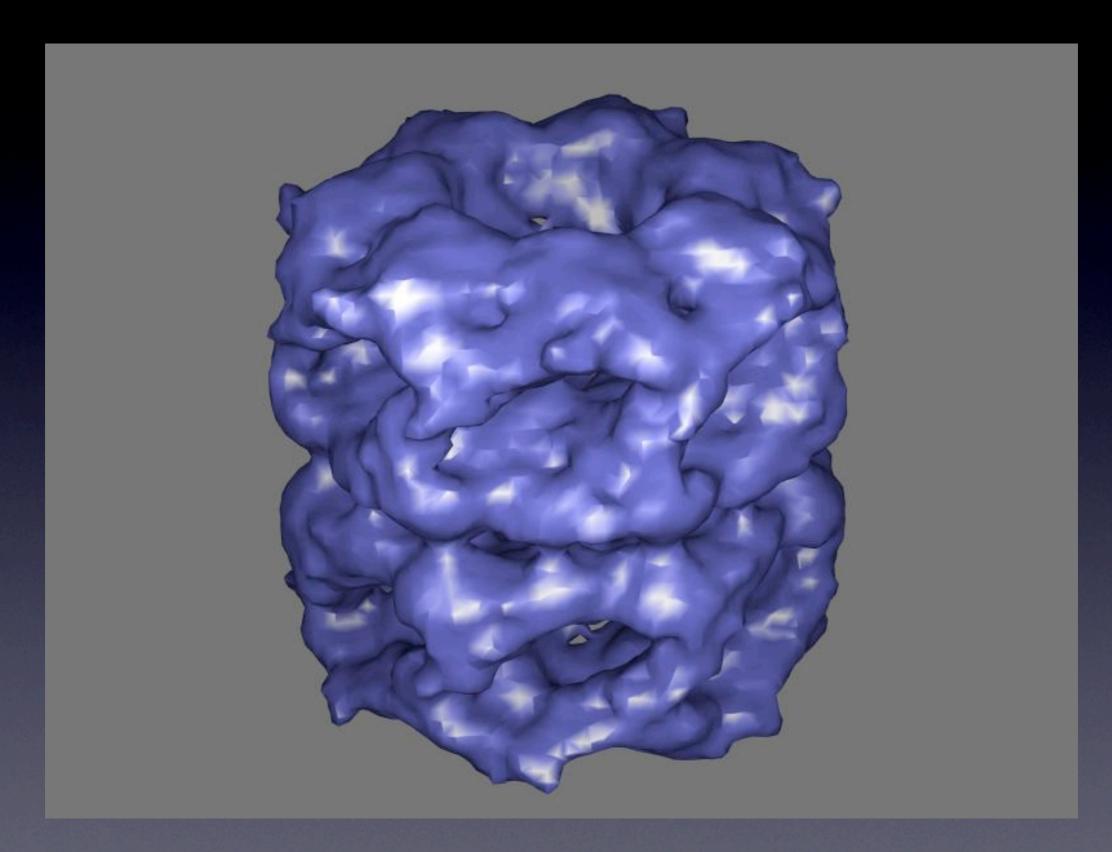
Iteration I





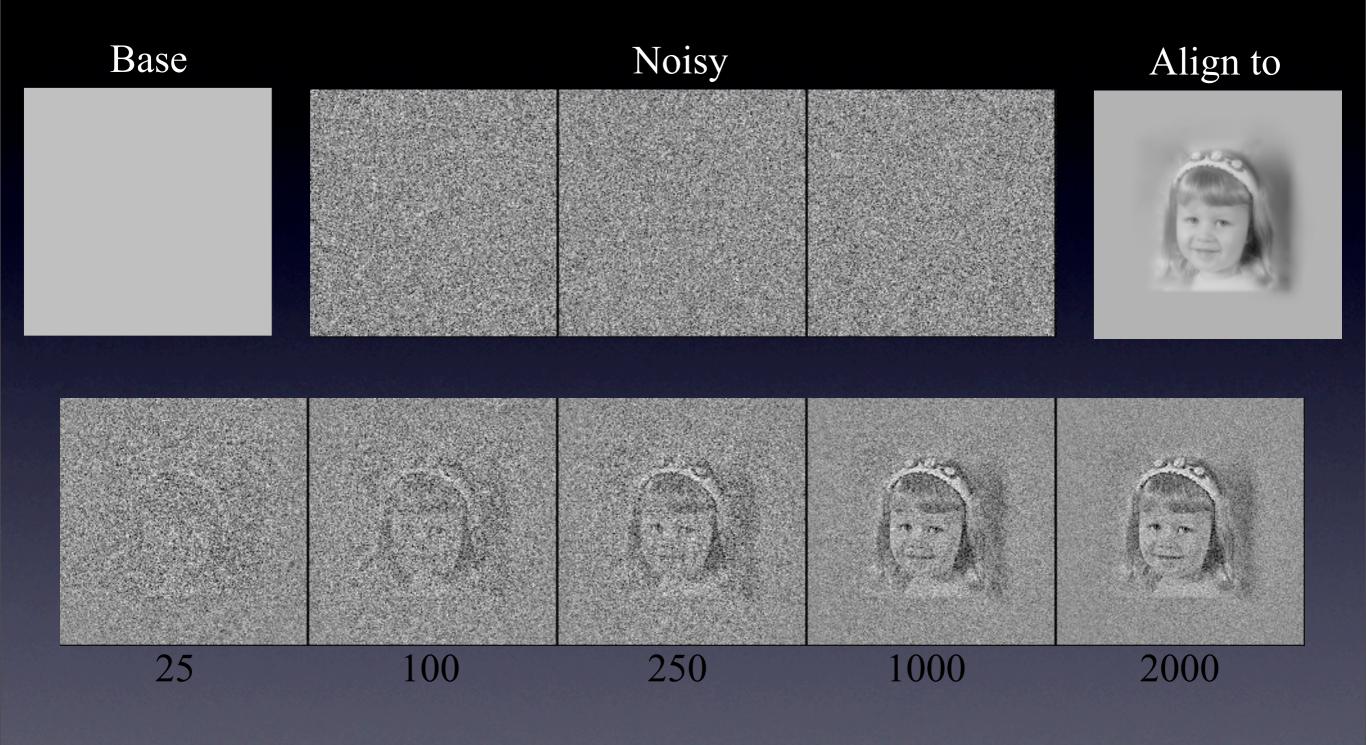




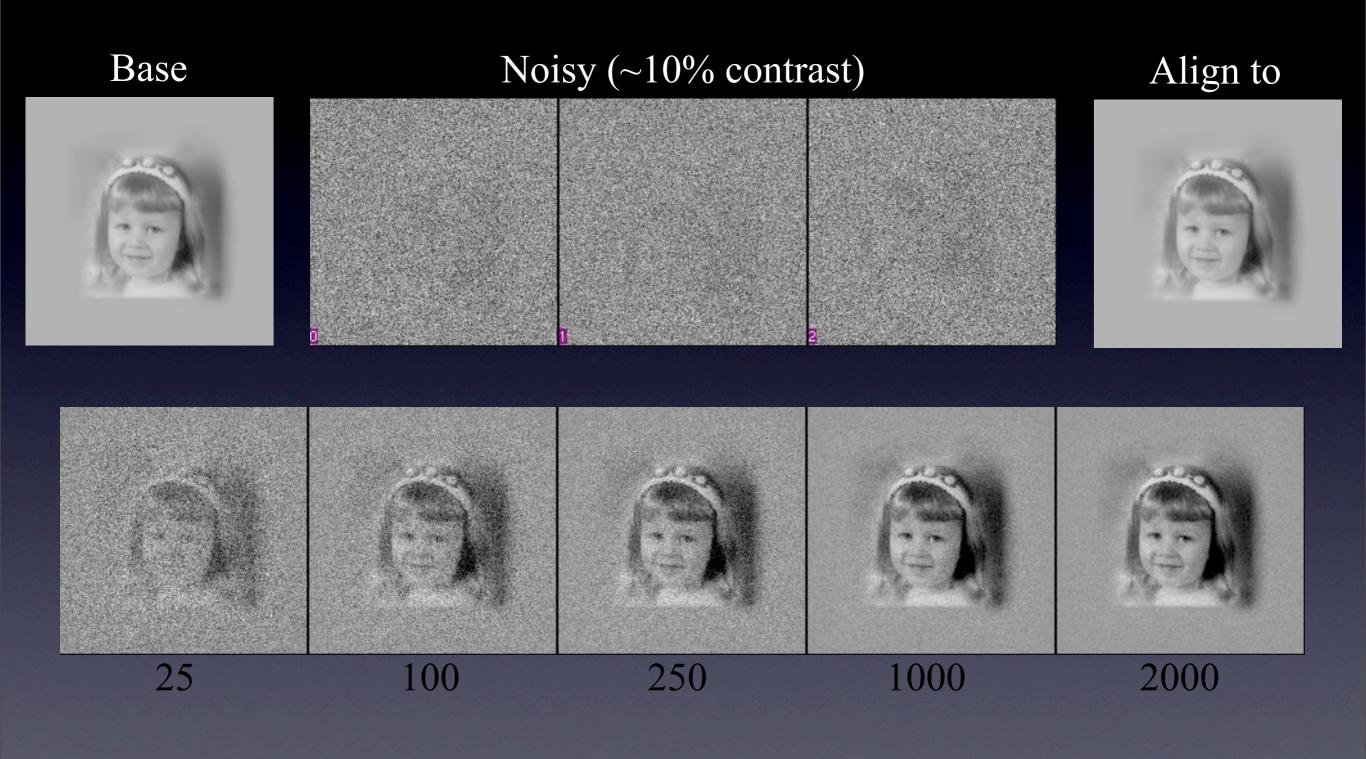


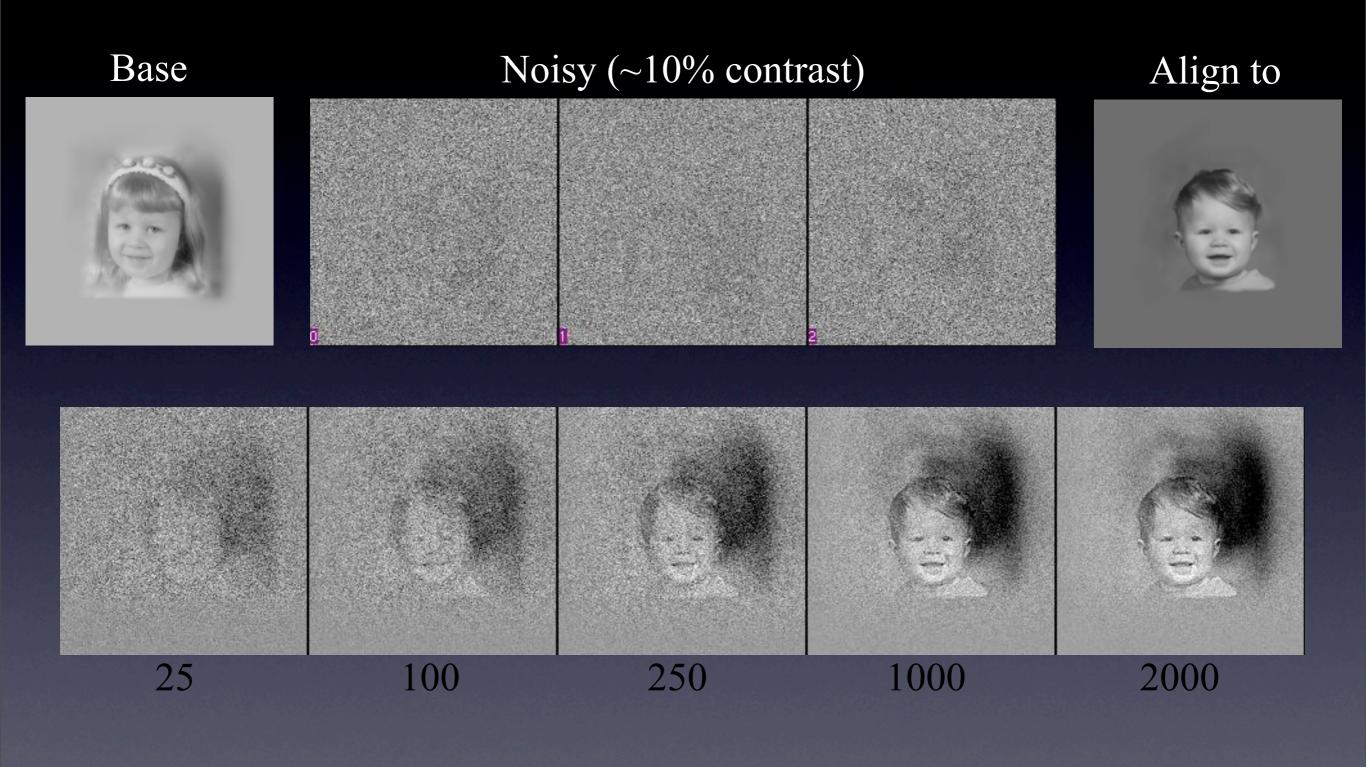
Model Bias?

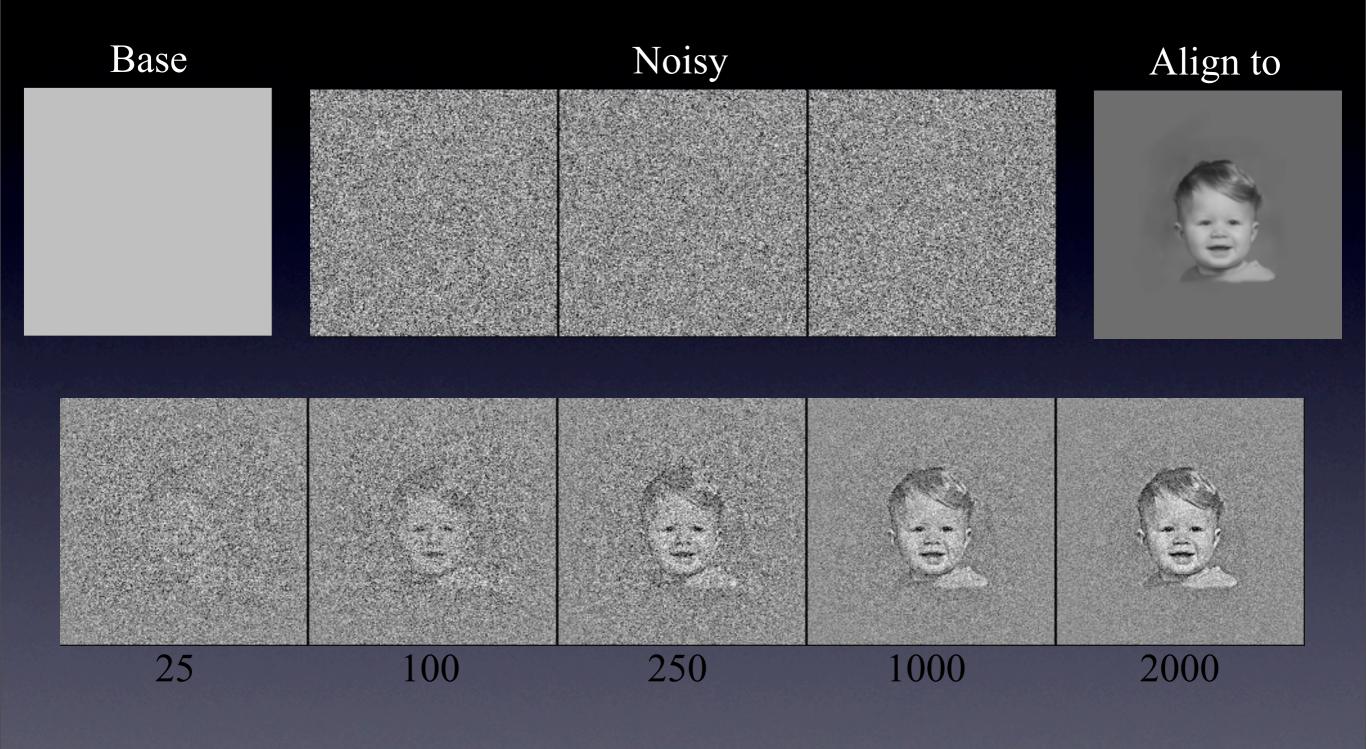
Model Bias

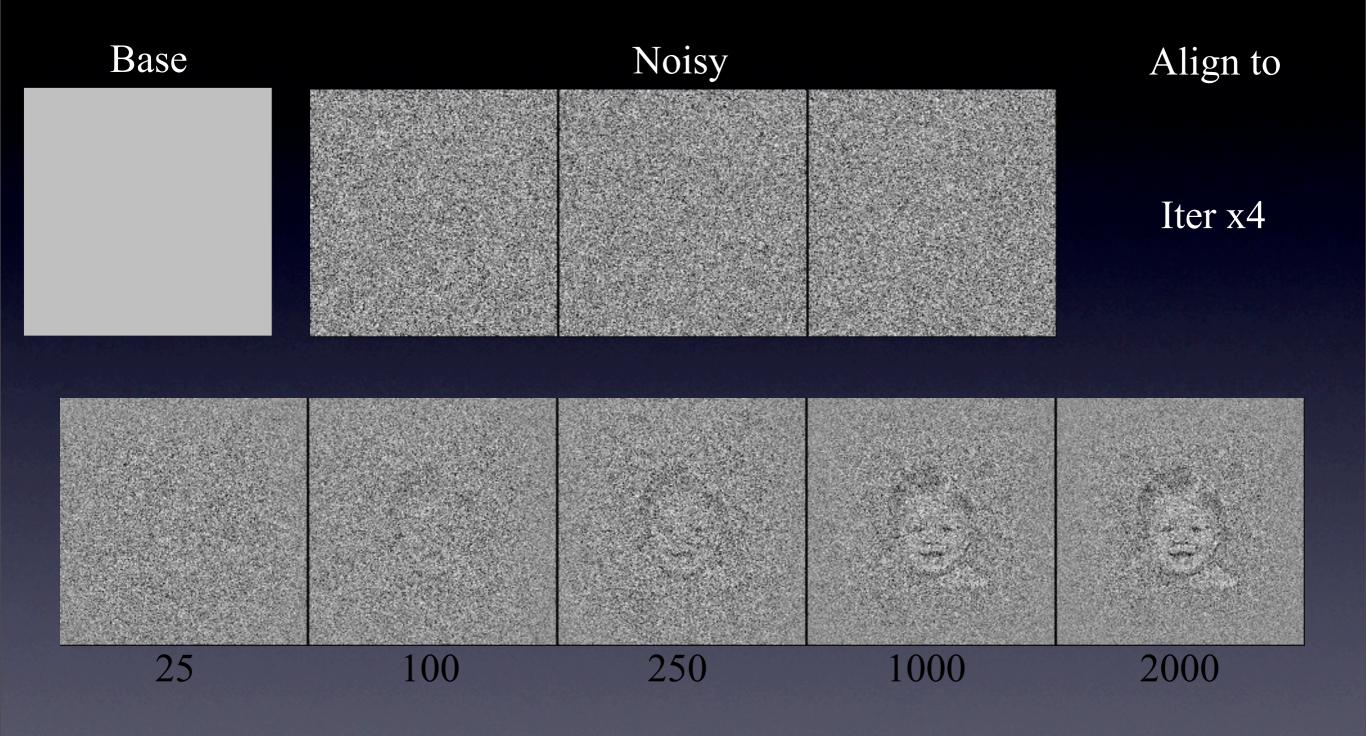


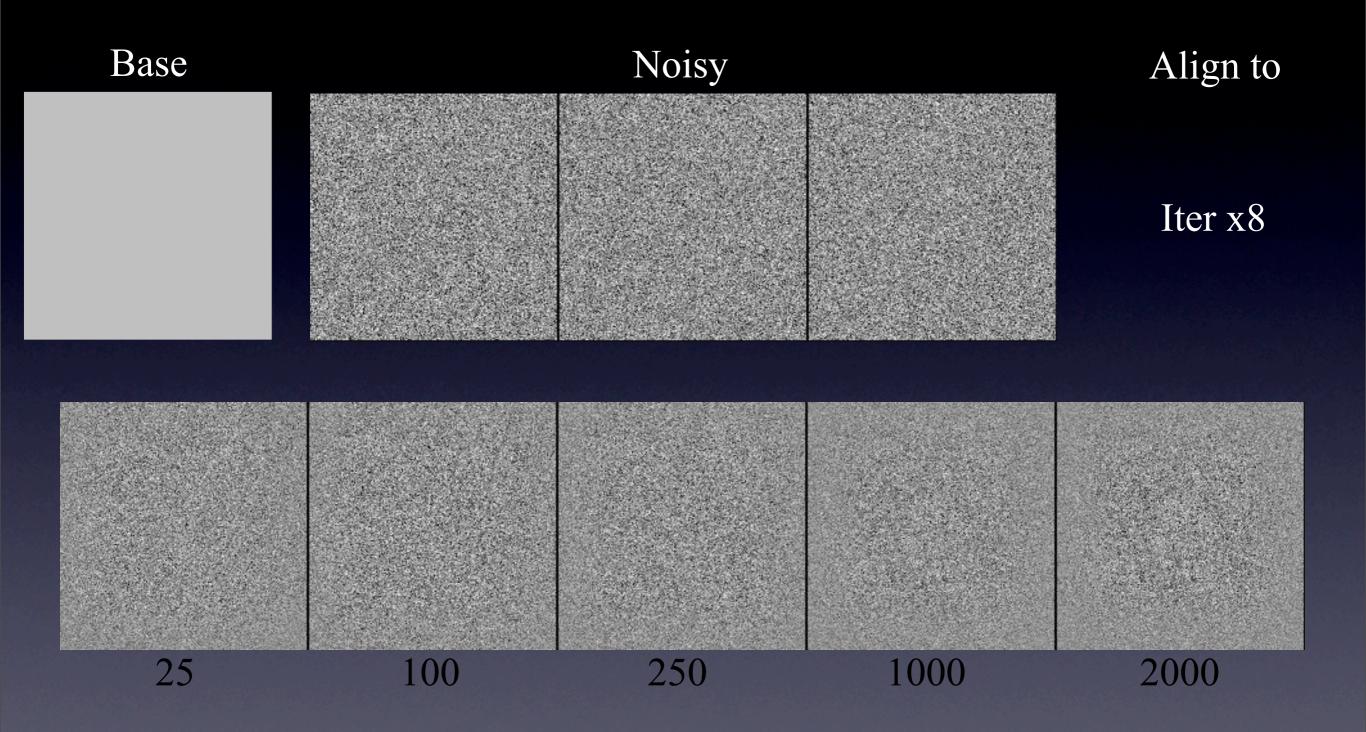
Model Bias

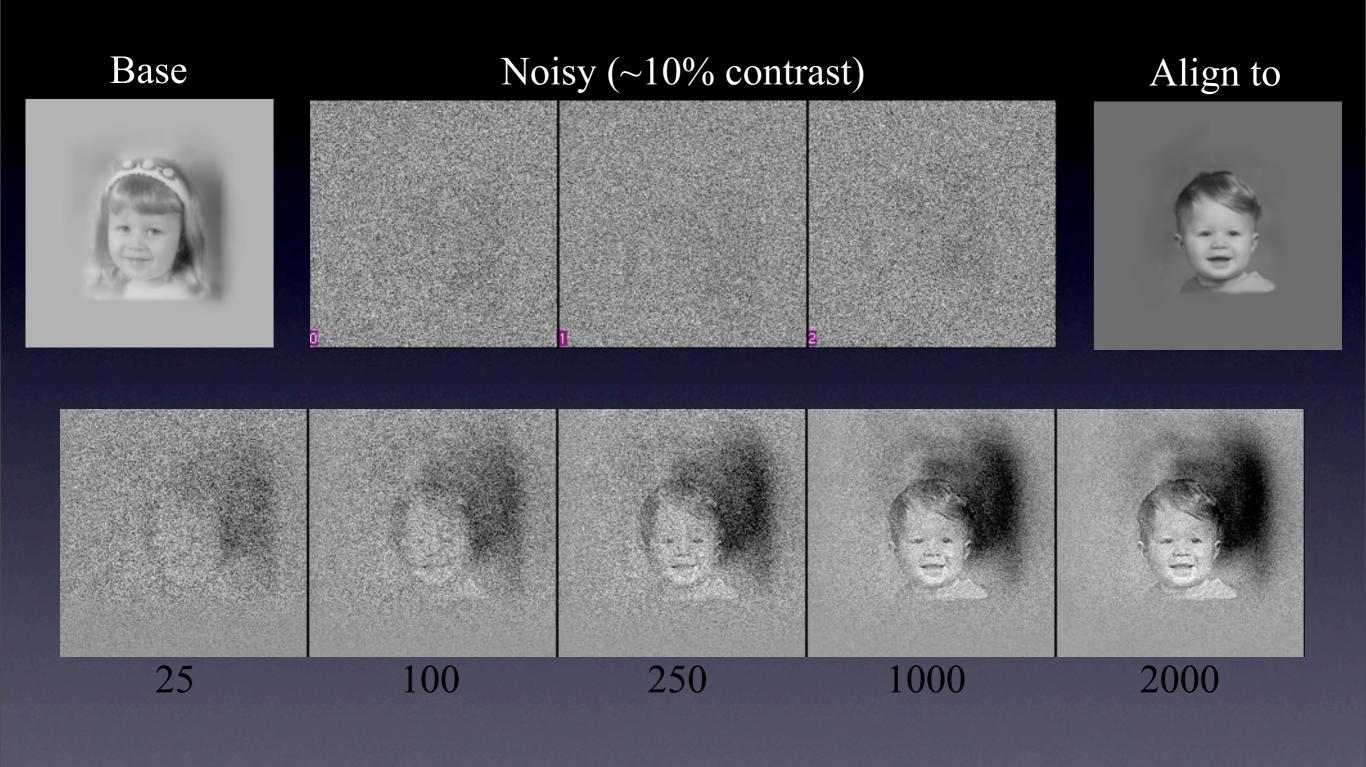


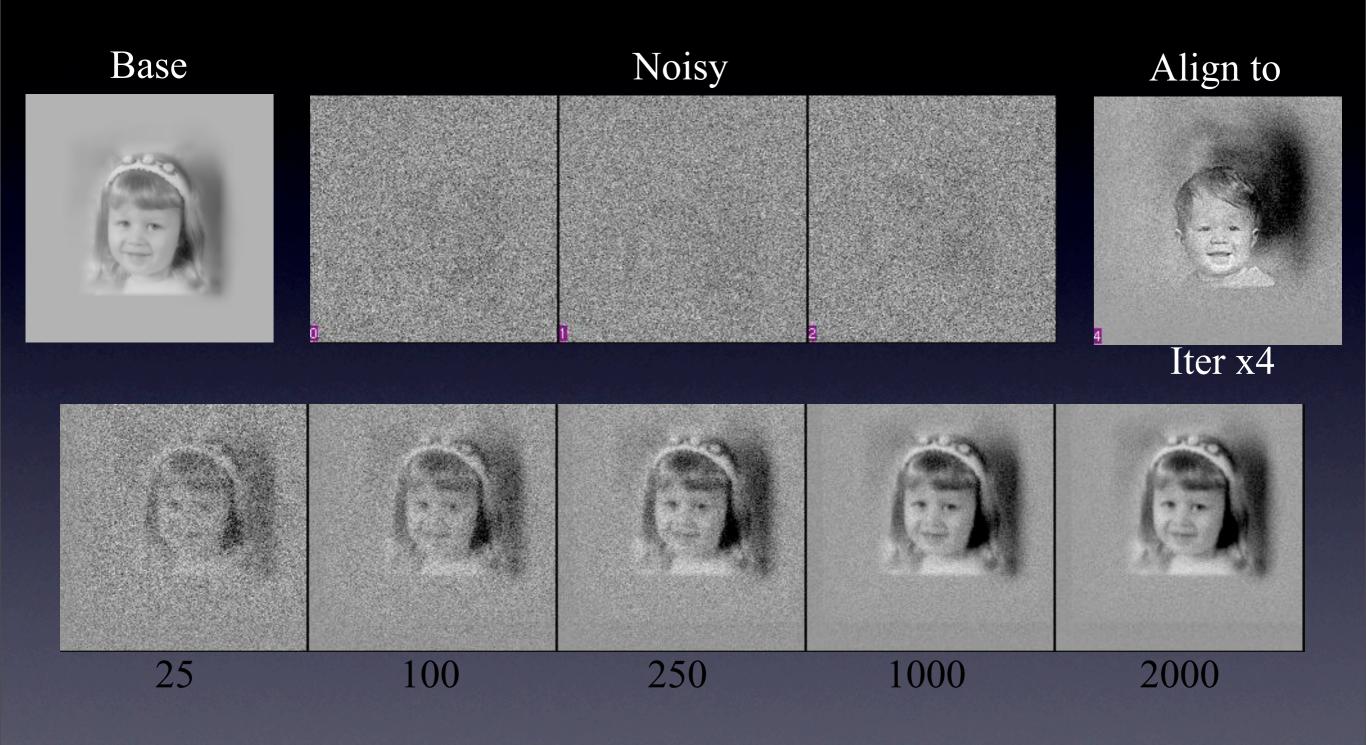






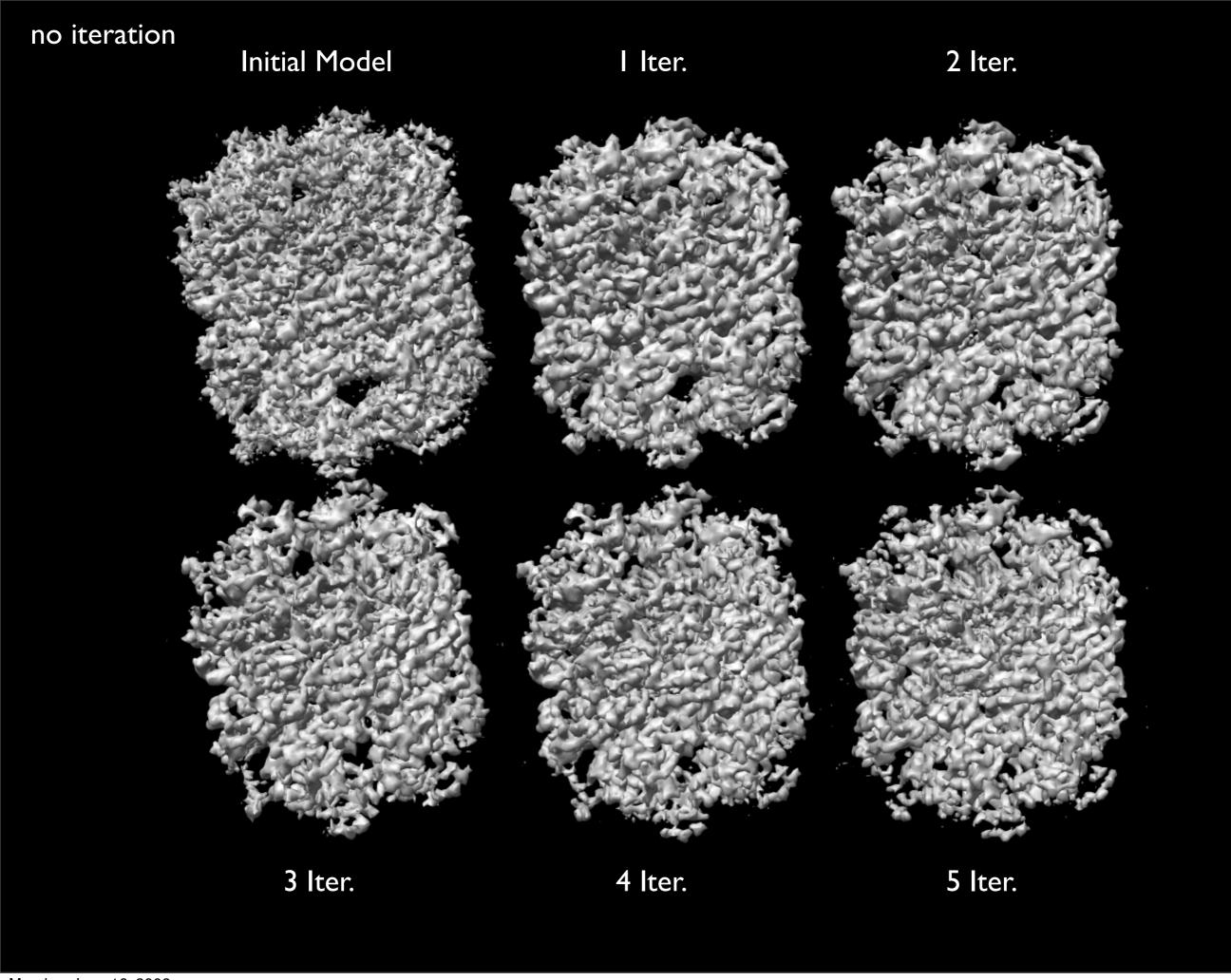


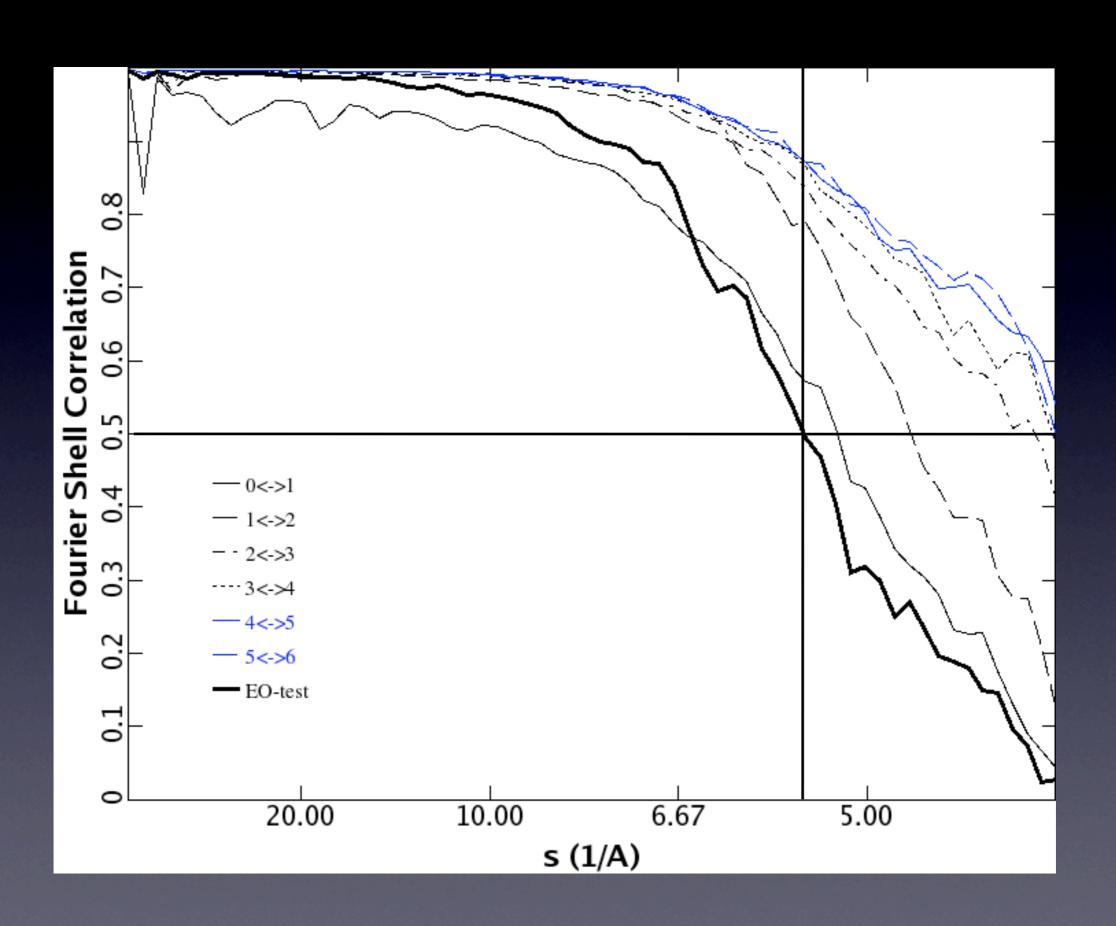


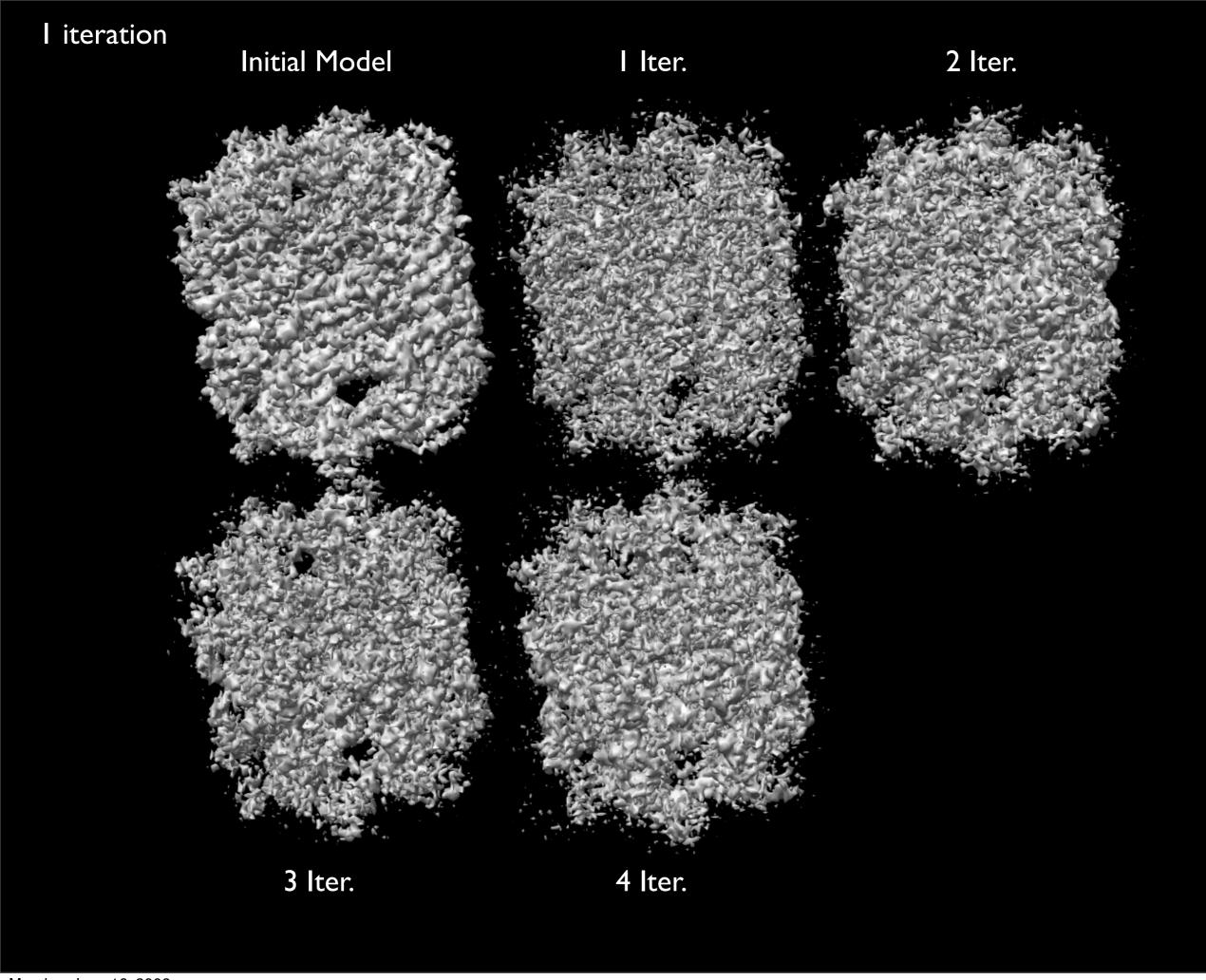


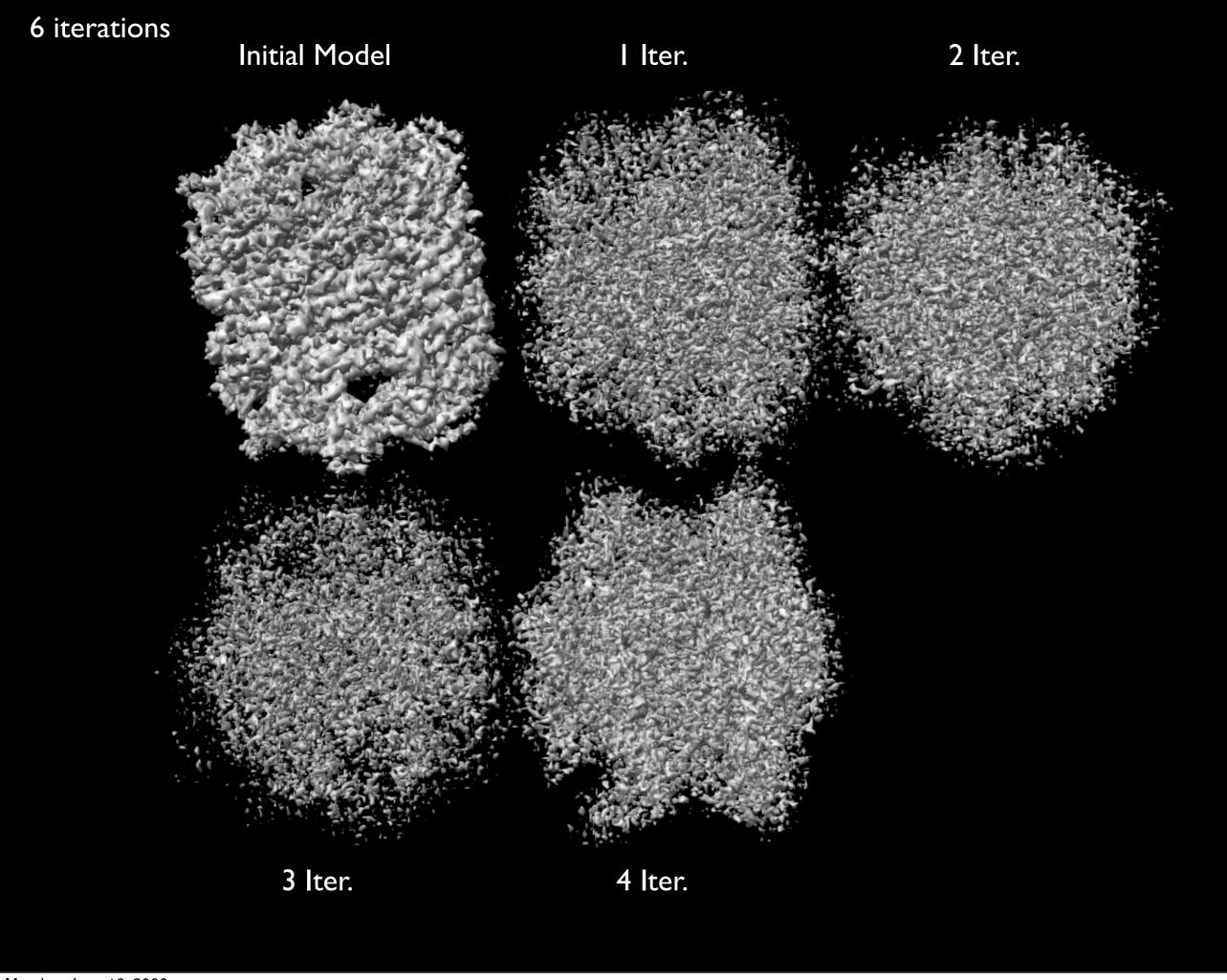
How About 3-D?

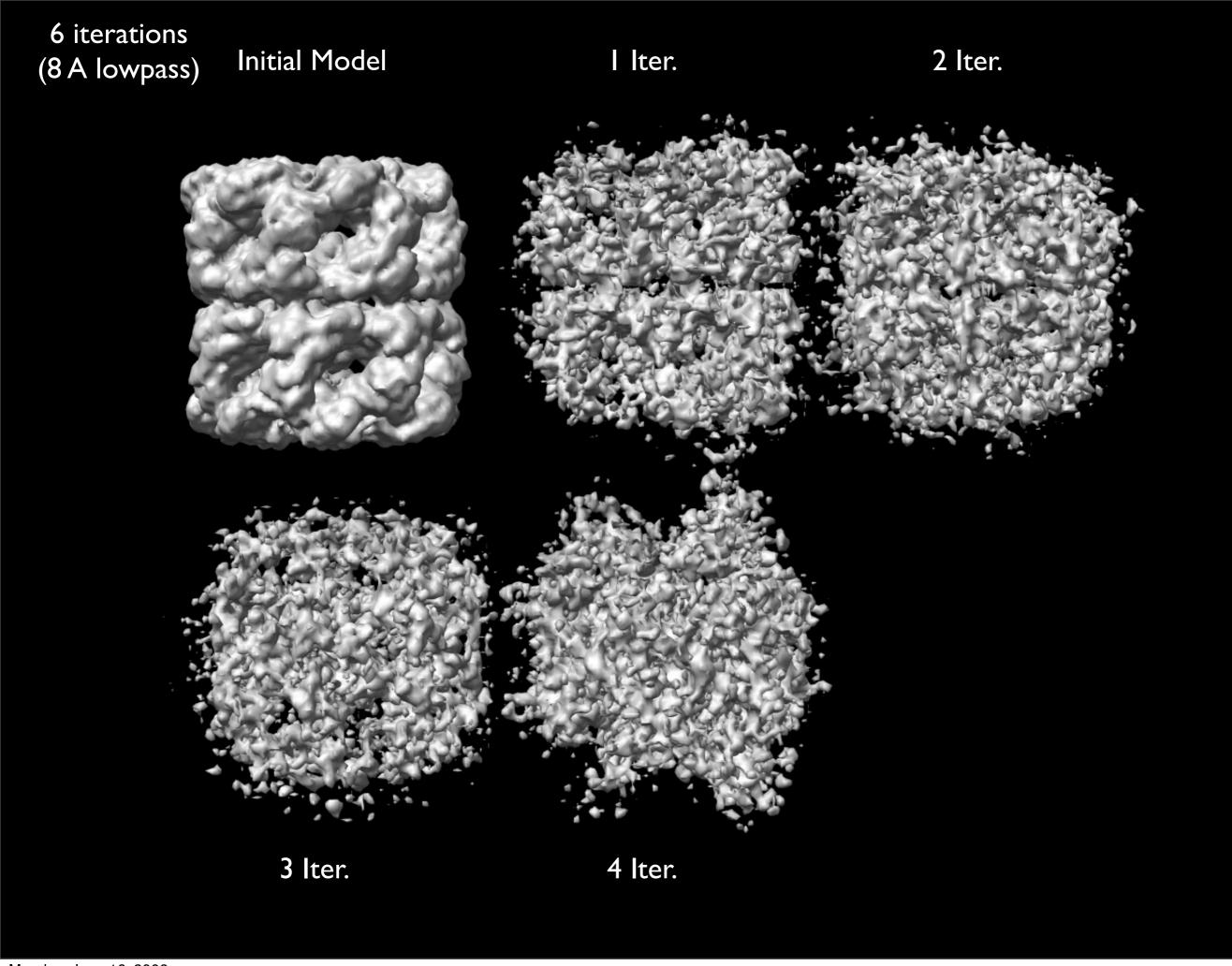
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	refine 6 ma files=2,800	sk=56 hard ,99 amask=	=90 sym=d 15,.9,16 ph	7 ang=1.60 asecls class	71 pad=160 keep=10 se	0 p=3

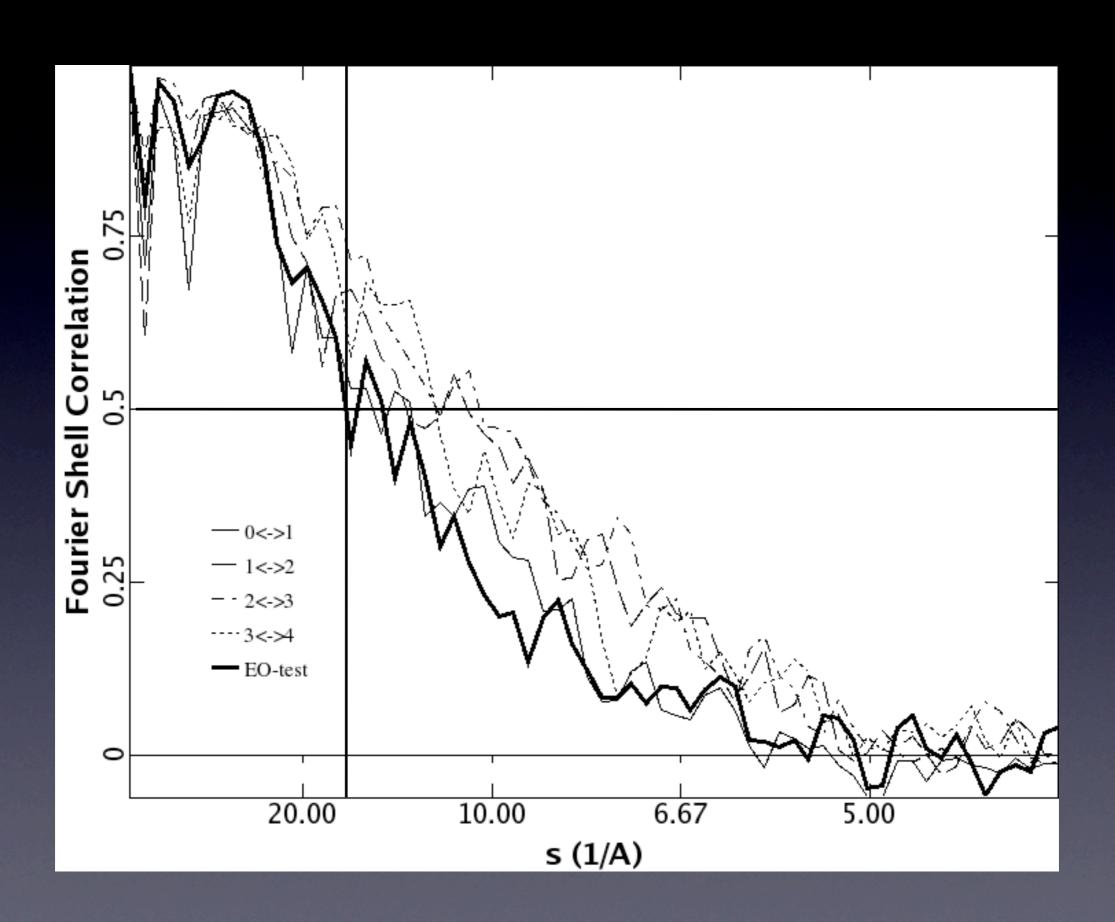


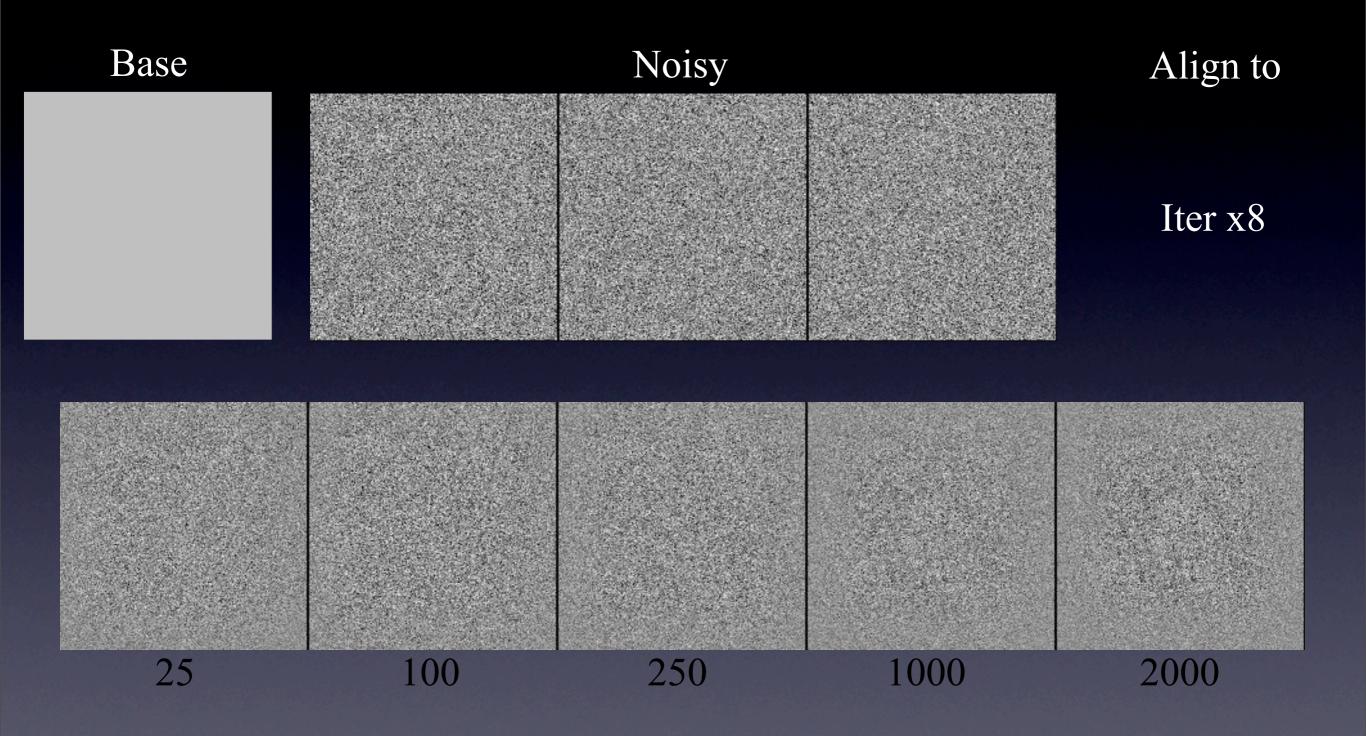


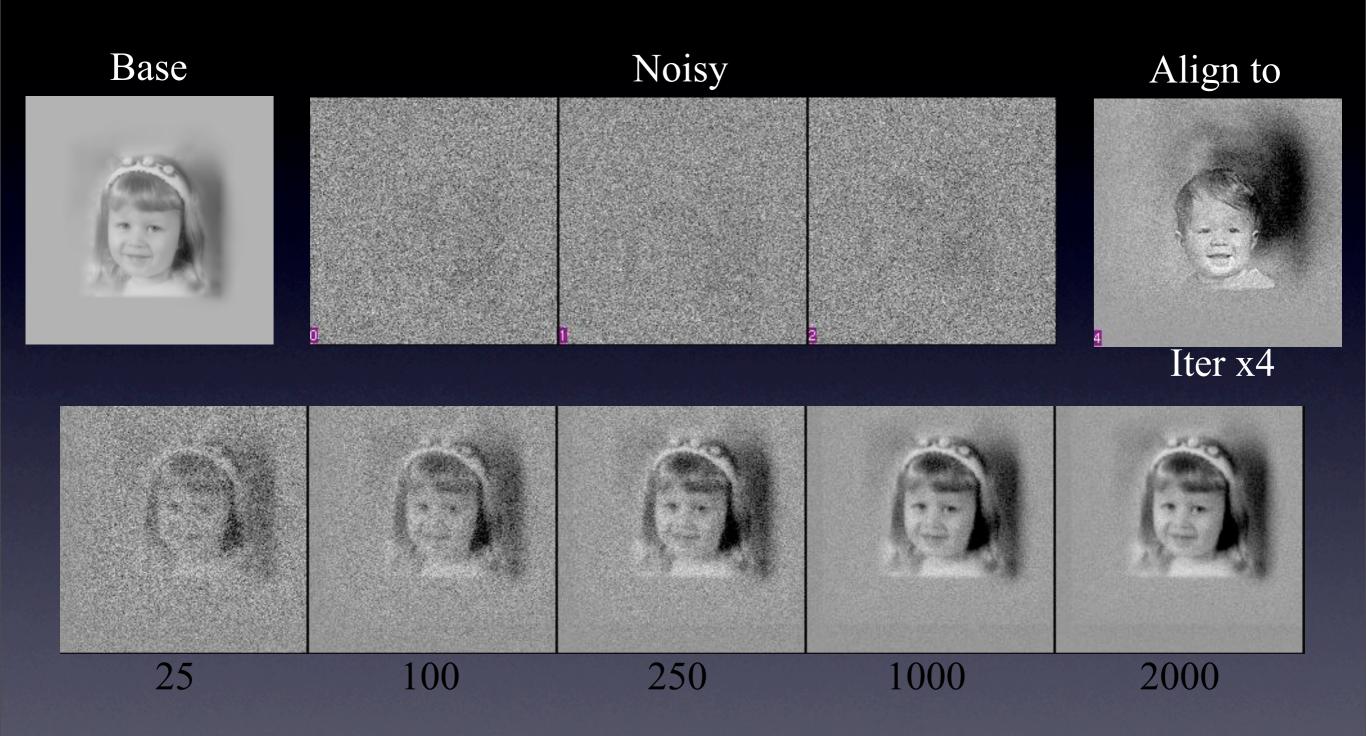






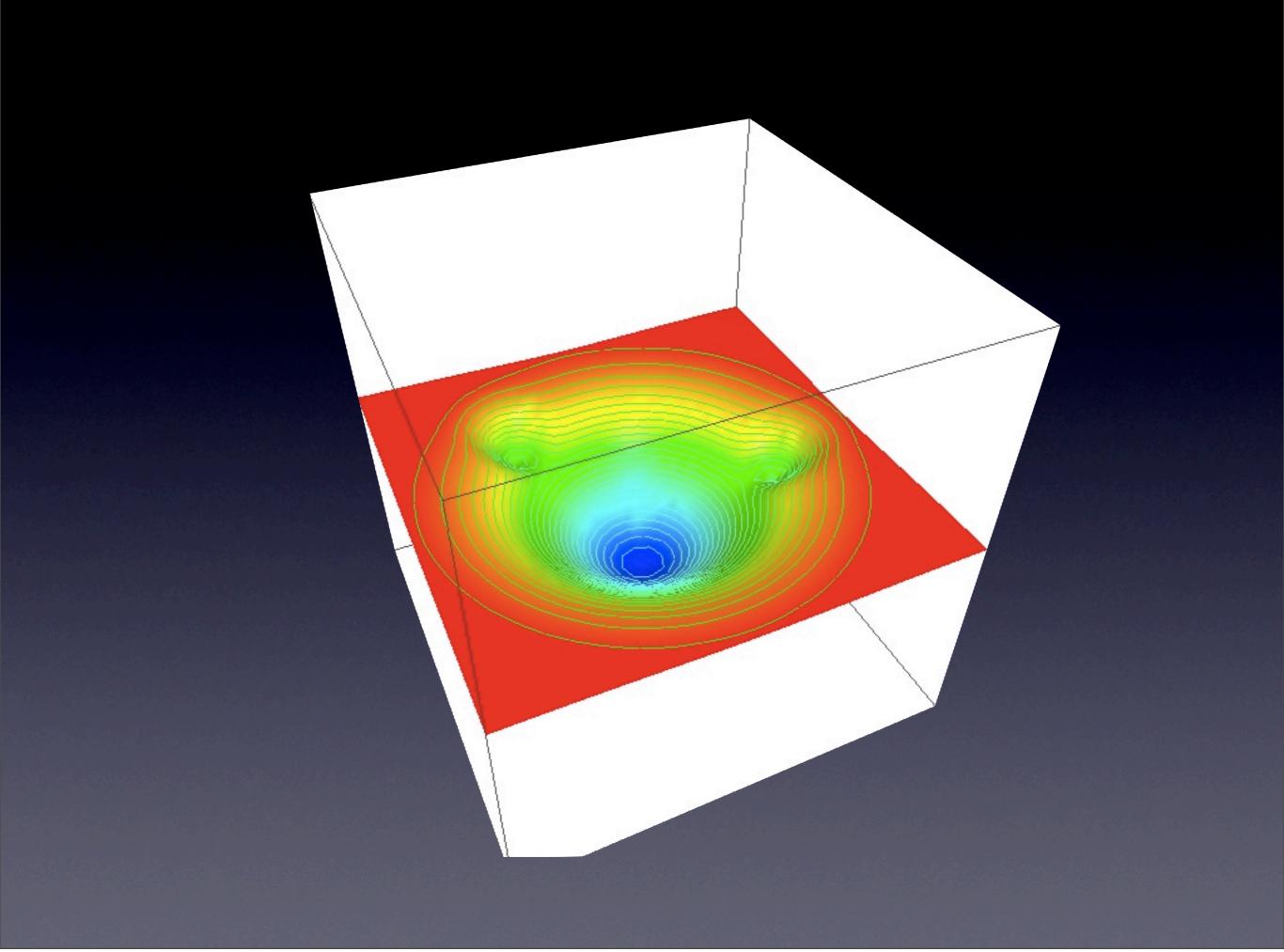




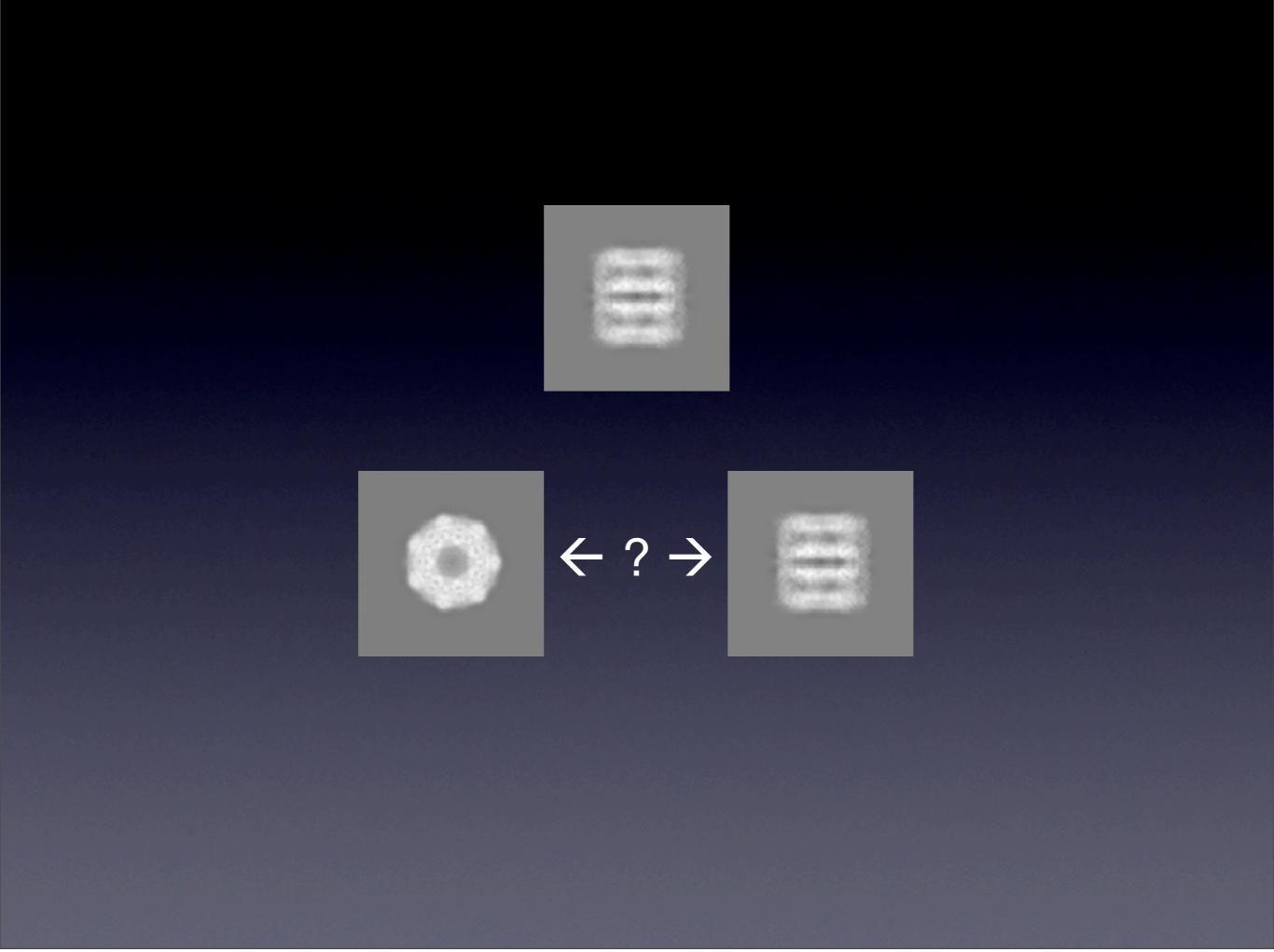


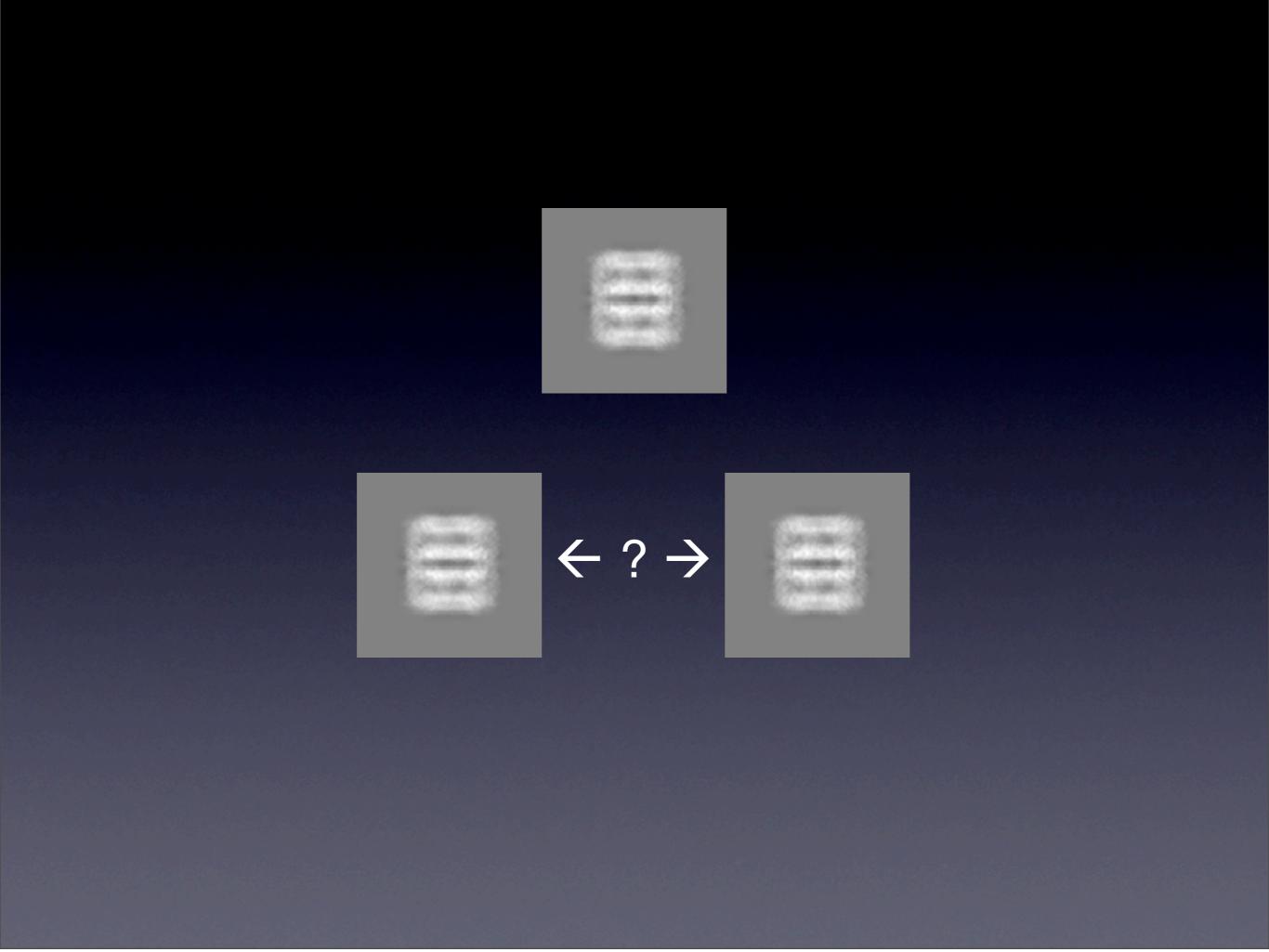
How Do we Stop This?

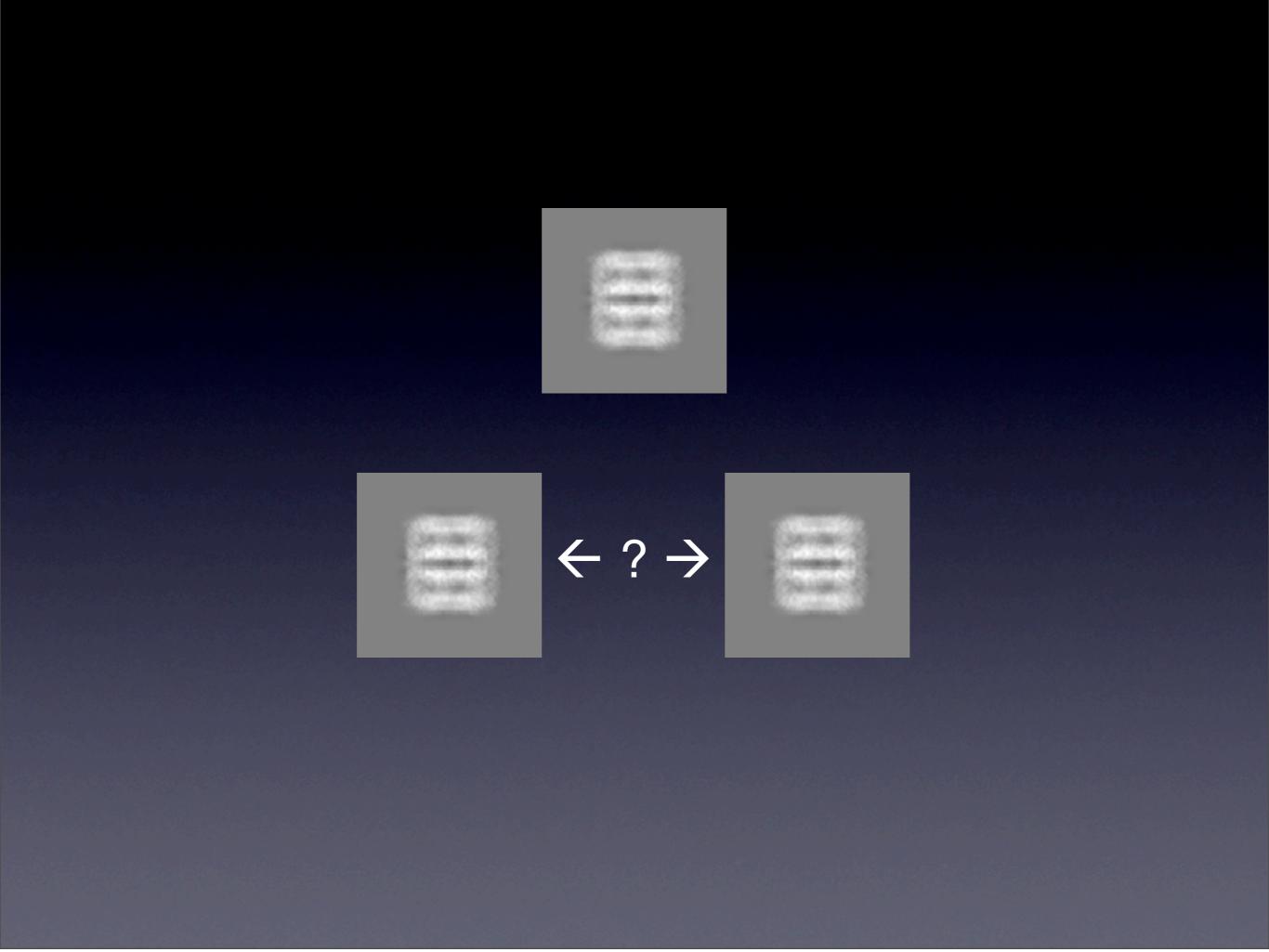
- (In EMAN) use classiter>3 for a few rounds
- Always refine from multiple starting models (note - you can shrink the data first)
- If the results are not effectively the same, try to establish which one is correct by looking at self consistency of projections/class-averages
- Compare with results of 2D analysis



Measures of Similarity

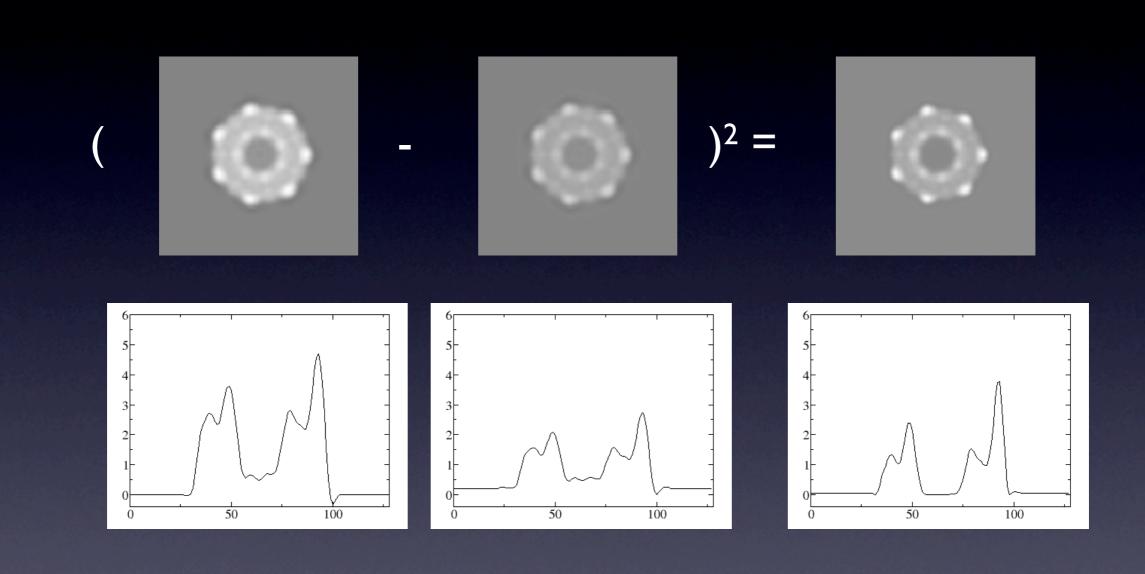


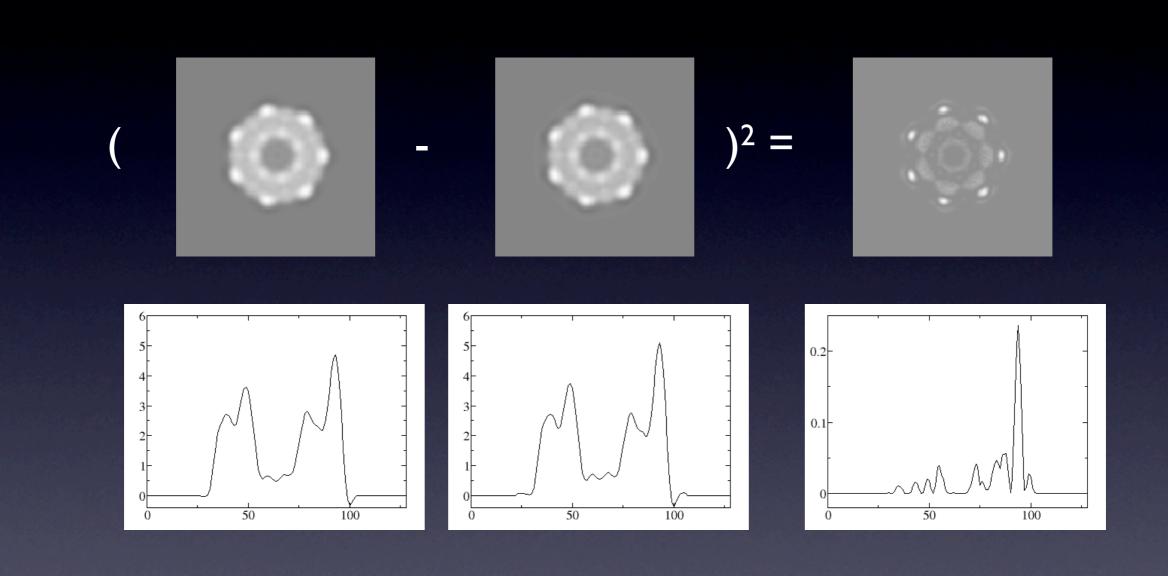


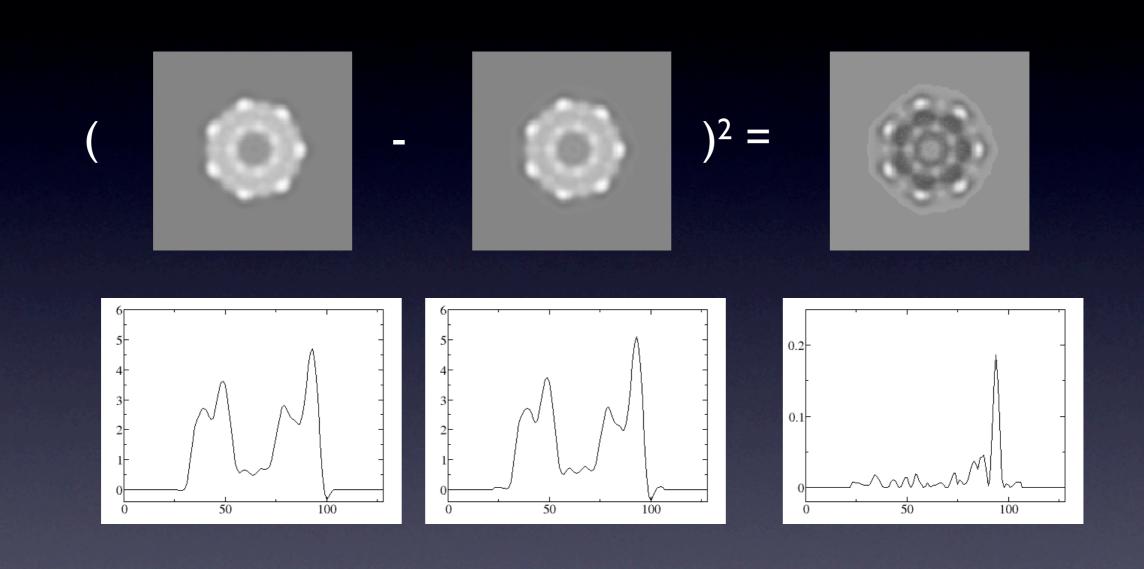


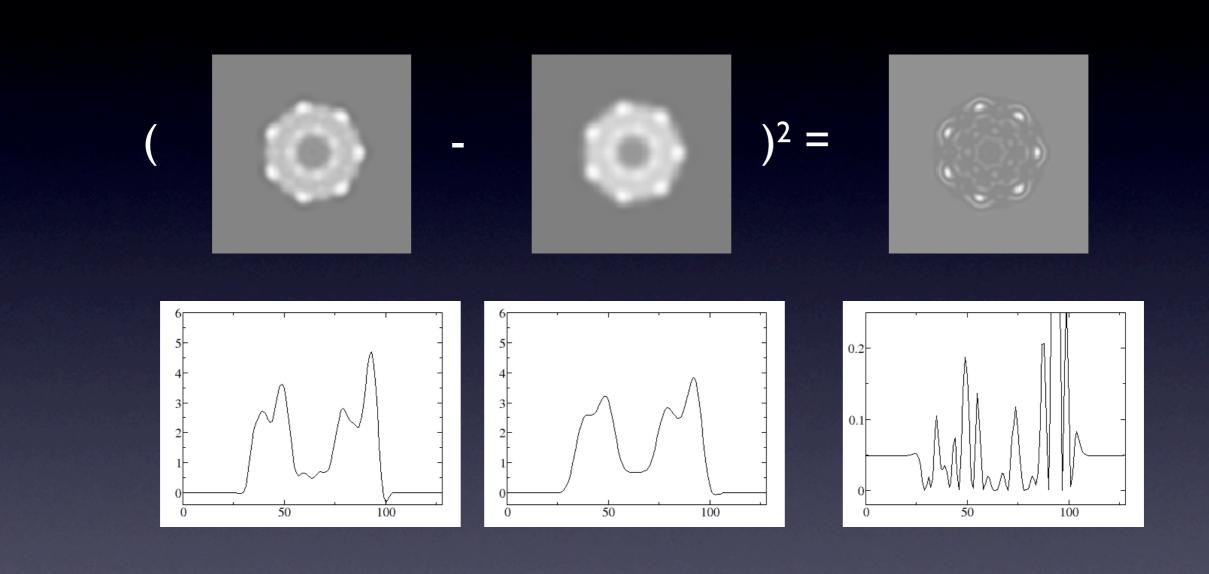
Measures of Similarity

- Correlation coefficient
- Variance (equivalent)
- Phase Residual
- FSC
- Mutual Information
- etc...









One Answer ...

- Wiener filter particle
- Filter reference to match
- Normalize reference density to particle
- Calculate variance

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