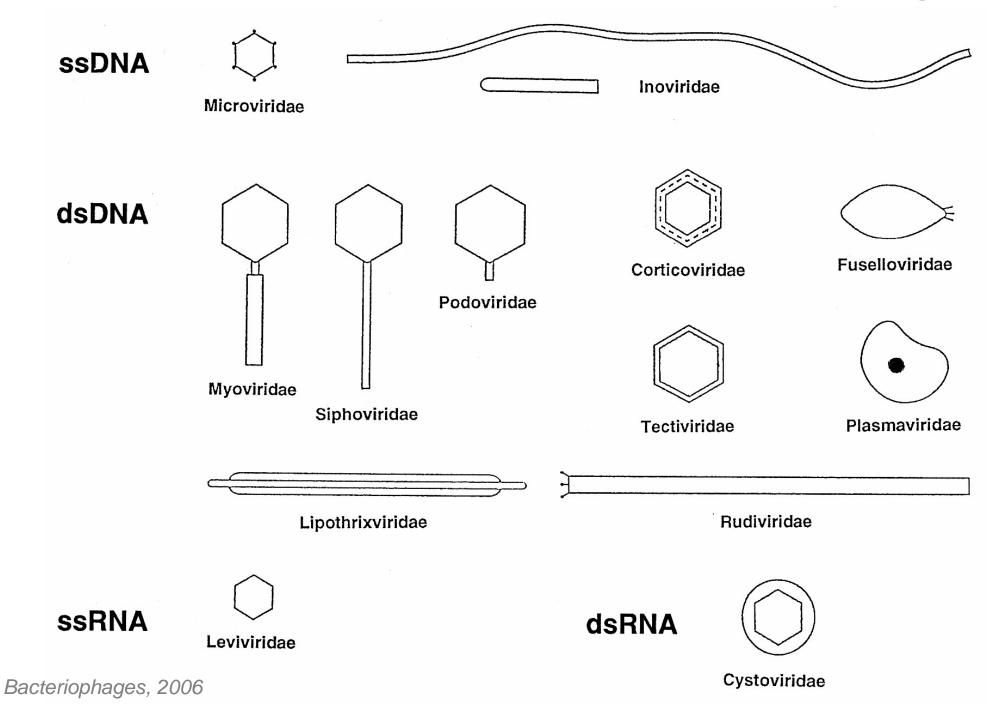
Icosahedral Reconstruction

Wen Jiang



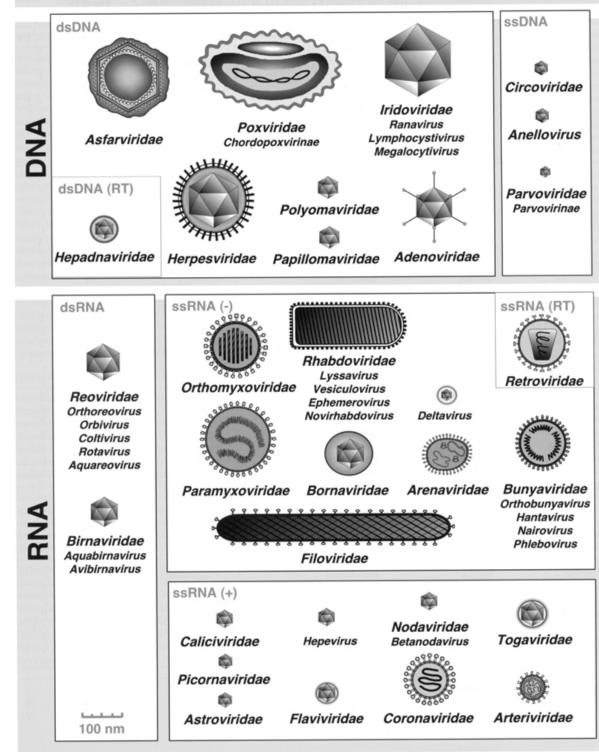


Icosahedral Viruses: Bacteriophages



I cosahedral Vertebrate Viruses

Families and Genera of Viruses Infecting Vertebrates

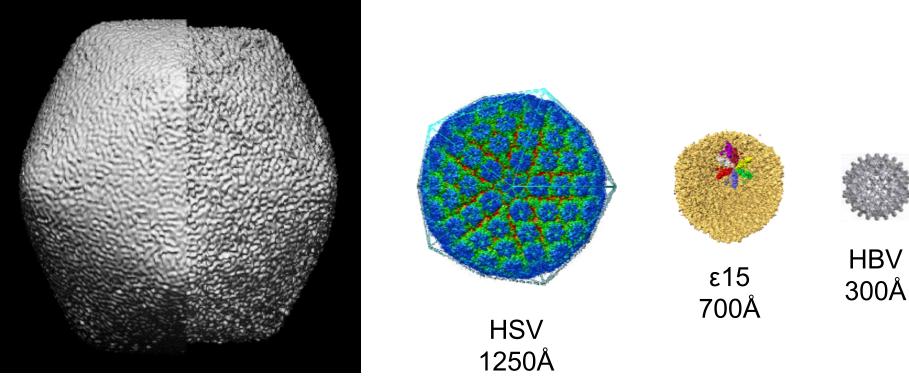


Fields Virology, 2006

I cosahedral Particles

PDC

200Å



Mimivirus 5000Å

Icosahedral Symmetry

- 5, 3, 2 fold axes
 - 6 five fold axes
 - 10 three fold axes
 - 15 two fold axes
- 60 fold symmetry in total
- Asymmetric unit: 1/3 of the triangular face

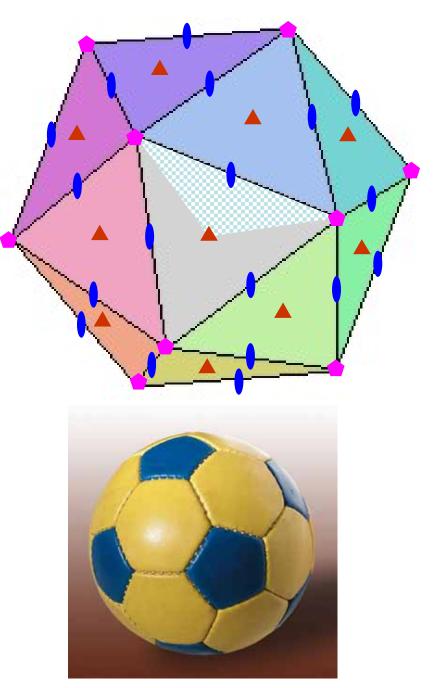


Image Processing

 In EMAN, icosahedral reconstruction is essentially treated the same as other symmetries

 However, one should pay special attention to the "large" problems

Specialized methods exist for more efficient processing

Image Processing

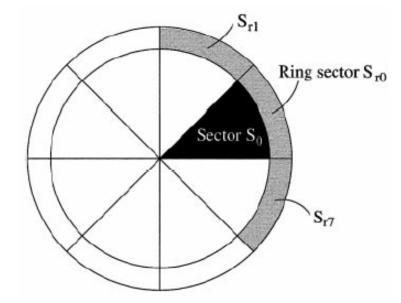
- Preprocessing
 - Particle selection
 - CTF fitting

Build initial model

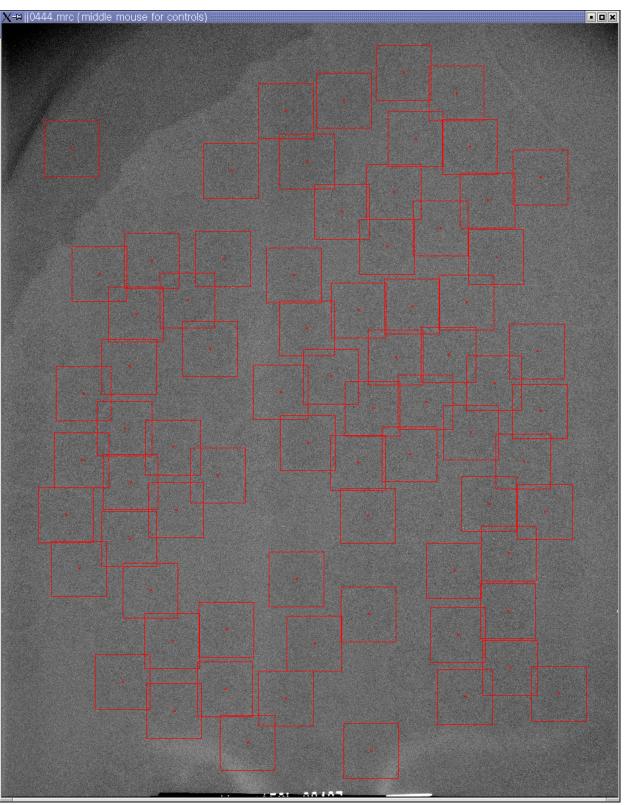
- Image refinement
 - Orientation determination
 - 3-D reconstruction

Particle Selection

- Manual selection
 - boxer
- Automated selection
 - batchboxer
 - ethan (for spherical particles)



- By Kivioja and Bamford et al.
- "Ring Filter"
- Only ONE parameter (*Particle Size*)
- Fast, 10-15 seconds / micrograph
- Tend to over-select



Ethan Example

Herpes 2.1 Å/pxiel 6662x8457 pixels 15 seconds in total

\$ time ethan.py jj0444-8bit.mrc 298 600 jj0444.box jj0444.img Opening file jj0444-8bit.mrc Width: 6662 Height: 8457 Averaging 121 pixels Filtering jj0444-8bit.mrc: ******** Total number of squares is 567 Number of peaks after sector test is 163 Number of peaks after first distance check is 81 Number of peaks after discarding too small ones is 80 Defining centers

Refining centers

74 particles found from jj0444-8bit.mrc

10.31s user 2.08s system 84% cpu 14.578 total

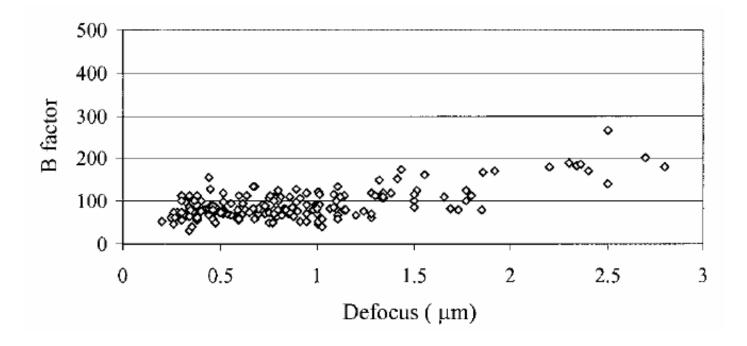
Particle Selection

Suggested practice:

- 1. Automated selection using ethan
- 2. Manual screening using boxer

CTF Fitting

To reach high resolution, small defocuses (0.5-1.5 $\mu m)$ are often used for imaging large icosahedral particles



CTF Fitting

- Manual fitting
 - Ctfit
- Automated fitting
 - fitctf
 - fitctf.py

Algorithm:

constrained nonlinear optimization using a sequential quadratic programming (SQP) method)

$$\min \left| I_{image}(s) - I_{s}(s)CTF^{2}(s)e^{-2Bs^{2}} - N(s) \right|^{2}$$

subject to:

$$I_{image}(s) = I_s(s)CTF^2(s)e^{-2Bs^2} + N(s)$$

$$ctf(s) = A(\sqrt{1-Q^2}\sin(\gamma(s)) + Q\cos(\gamma(s))))$$

$$\gamma(s) = -2\pi(C_s\lambda^3s^4 + Z\lambda s^2/2)$$

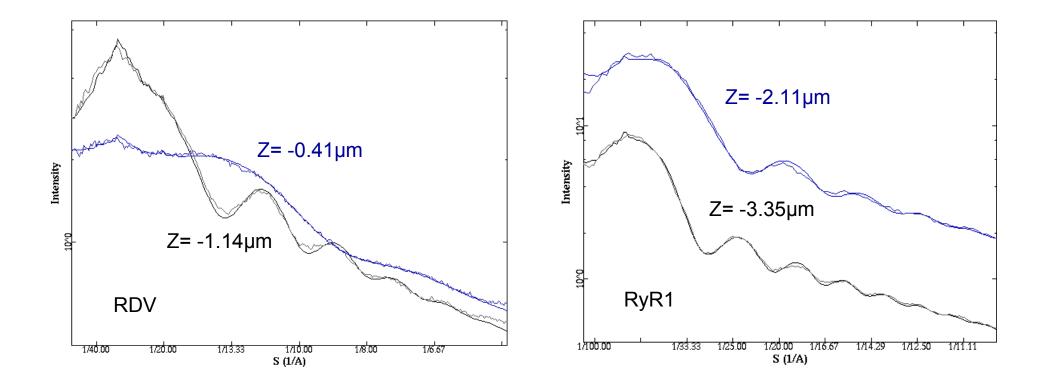
$$N(s) = n_3 e^{-n_1\sqrt{s} - n_2 s - (\pi n_4 s)^2/4}$$

8 unknown parameters: *Z*, *B*, *A*, *Q*, *n1*, *n2*, *n3*, *n4*

 $I_{image}(s) > N(s)$ A > 0 $B \ge 0$ $1 \ge Q \ge 0$ $\Delta Z < 0 \text{ (under focus)}$

> Yang C. et al: http://ncmi.bcm.edu/software/fitctf

fitctf.py Examples

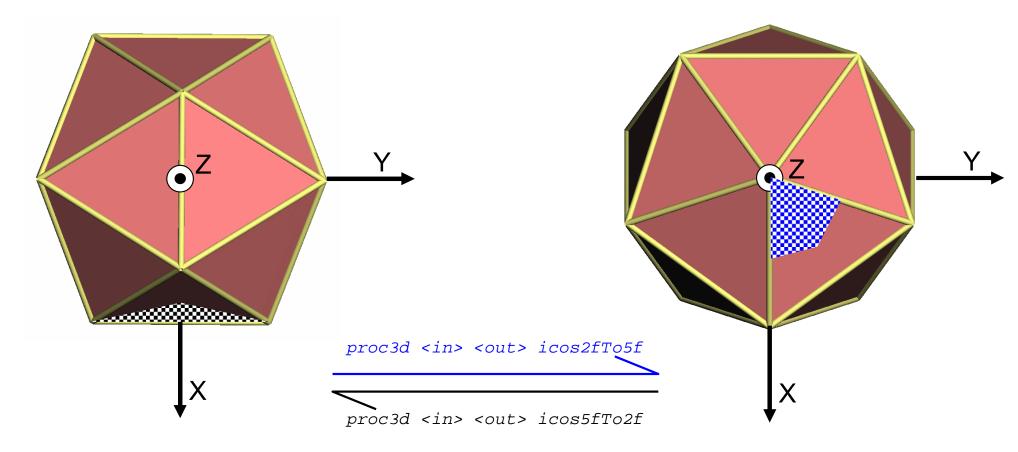


CTF Fitting

Suggested practice:

- 1. Automated fitting using fitctf.py
- 2. Manual screening using ctfit

Conventions: Orientation Origin



MRC

- X, Y, Z axes along 2 fold sym axes for orientation (0,0,0)
- Euler: $Z \rightarrow Y' \rightarrow Z''$

EMAN

- Z along 5 fold sym axis
- Y along 2 fold sym axis
- X near 3 fold sym axes for orientation (0,0,0)
- Euler: $Z \rightarrow X' \rightarrow Z''$

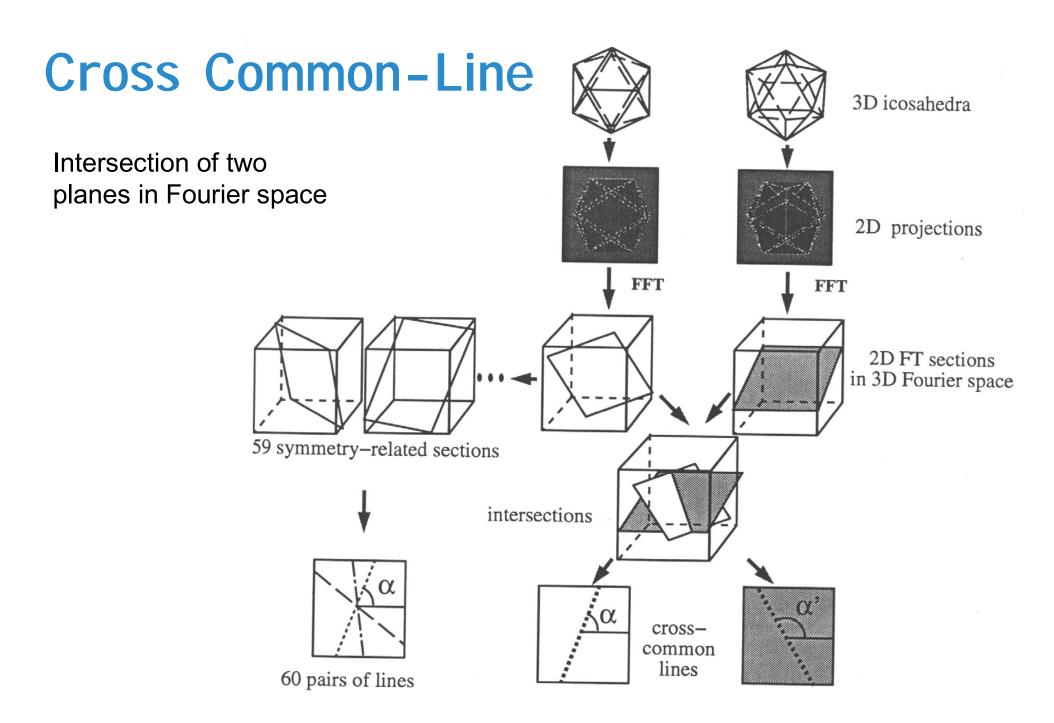
Build Initial Model

- Classic method: self common-line
 - Small number of particle with large defocus
 - Self common-lines cluster for views near symmetry axes
- Standard EMAN method: starticos
 - Find best 5-, 3-, 2-fold view particles
 - Spherical particles cause problems
- New method: random model
 - Build 3-D model from particles with randomly assigned orientations
 - Relying on the wide convergence range to reach a correct structure

2-D Alignment Methods

- Common-line method:
 - Classic implementation: self common-line (global search to get coarse initial orientation) and cross common-line (local refinement) in tandem
 - EMAN implementation: Cross common-line method for both global search and local refinement (EMAN crossCommonLineSearch.py command)

Projection matching method (EMAN refine command)



Orientation → Common Line Locations

0

0

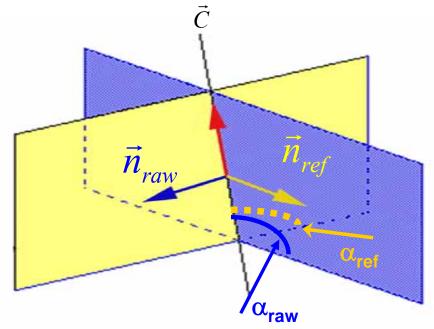
Fourier plane normal in 3D:

$$\vec{n}_{ref} = \vec{R}_{ref} \cdot \begin{bmatrix} 0\\0\\1 \end{bmatrix} \qquad \qquad \vec{n}_{raw} = \vec{R}_{raw} \cdot \begin{bmatrix} 0\\0\\1 \end{bmatrix}$$

common line in 3D:
$$\vec{C} = \vec{n}_{raw} \times \vec{n}_{ref}$$

common line in 2D:

$$\vec{C}_{ref} = \vec{R}_{ref}^{-1} \cdot \vec{C} \qquad \vec{C}_{raw} = \vec{R}_{raw}^{-1} \cdot \vec{C}$$
$$\alpha_{ref} = \cos^{-1}(\vec{C}_{ref} \cdot \begin{bmatrix} 1\\0\\0 \end{bmatrix}) \qquad \alpha_{raw} = \cos^{-1}(\vec{C}_{raw} \cdot \begin{bmatrix} 1\\0\\0 \end{bmatrix})$$



Common Line Search: Scoring Functions

search for the **orientation** and **center** parameters that minimize the mean phase differences among all the pairs of common lines

$$R_{i}(\phi, \theta, \omega, x, y) = \frac{\sum_{j=1}^{N} \sum_{k=1}^{k_{\max}(j)} \sum_{s=s_{\min}}^{s_{\max}} f(\psi_{i}(s, x_{i}, y_{i}, \alpha_{i,j,k}), \psi_{j}(s, x_{j}, y_{j}, \alpha_{j,i,k})) \times w(s, \alpha_{i,j,k}, \alpha_{j,i,k})}{(s_{\max} - s_{\min}) \sum_{j=1}^{N} k_{\max}(j)}$$

i: particle image

s: spatial frequency

k: common - lines

j: reference projections

f(): scoring function

w(): weighting function

Search Strategy

- Classic implementation
 - **1. center** the particle by cross-correlation
 - self common-line to determine initial orientation by exhaustive searching orientation at 1° step
 - Cross common-line to locally refine the orientation and center by Gradient or Simplex.

Issues:

- 1. Self common-line is not very robust
- 2. Error propagation

Search Strategy

- Exhaustive cross common line search
 - enumerate all centers and orientations in an asymmetric unit (5-level loops !)
 - simple but really slow
 - for 1 degree, 1 pixel step: 3X10⁷ trials/particle

Search Strategy

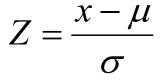
- Multi-path Simulated Annealing
 - Multiple randomly seeded SA processes
 - Cross-communication among SA processes
 - Global search for both orientation and center
 - Accurate and fast
 - $\sim 4x10^3$ trials/particle.
 - >10⁴ times faster than exhaustive search

Is The Best Solution Correct?

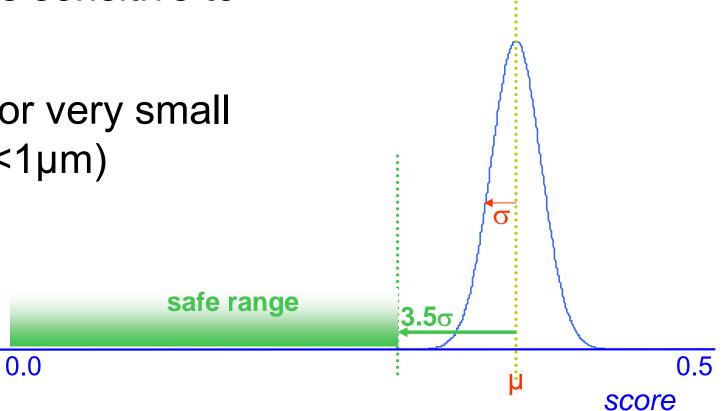
- Absolute score (residual) cutoff
 - popular criterion
 - needs different cutoff values for images at different defocuses
 - how to pick a single number that suits all imaging conditions?

Is The Best Solution Correct?

• Z score cutoff



- better, less sensitive to defocus
- unstable for very small defocus (<1µm)



Is The Best Solution Correct?

- Consistency criterion
 - agreement among different methods (projection matching vs. common line)
 - agreement among multiple runs of the global common line search
 - more reliable than absolute value and Zscore cutoff
 - bias toward "safer side"

3-D Reconstruction Methods

- Fourier-Bessel Synthesis:
 - Classic method for icosahedral particles
 - Very efficient in computation

- Direct Fourier Inversion
 - EMAN make3d command
 - Needs lot of memory

Fourier Bessel 3-D Reconstruction

 $F(R,\Phi,Z) = \sum G_n(R,Z)i^n e^{in\Phi}$ Sz FFT of $n = -\infty$ 2D images $g_n(r,Z) = \int_0^\infty G_n(R,Z) J_n(2\pi Rr) 2\pi R dR$ ••••S_y $\rho(r,\varphi,z) = \sum_{-\infty}^{\infty} \int_{-\infty}^{\infty} g_n(r,Z) e^{in\varphi} e^{2\pi i z Z} dZ$ 3D map $n = -\infty$

- Efficient but incomplete use of data
 - Anisotropic artifacts often seen

Icosahedral Reconstruction Using EMAN

Two approaches

• Standard way using projection matching:

refine sym=icos <other options>

• Cross common-line method:

crossCommonLineSearch.py <options>

Special Considerations

- Load projections to memory in batches instead all at once: add "projbatches=<n>" with n>1 to refine
- Use half maps instead of full map to start refine: use "proc3d <in> <out> tophalf" to generate top half map
- Use fewer CPUs for projection and class averaging step to avoid IO timeout errors. Use "proc=16,64" instead of "proc=64" option for refine

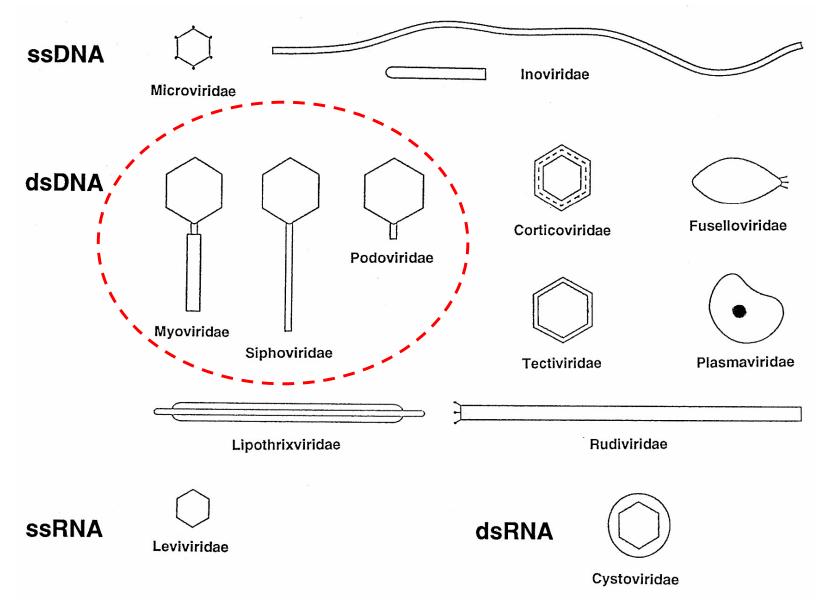
Special Considerations

 Use parallel reconstruction instead of single CPU reconstruction. make3d is now parallelized using mpi.

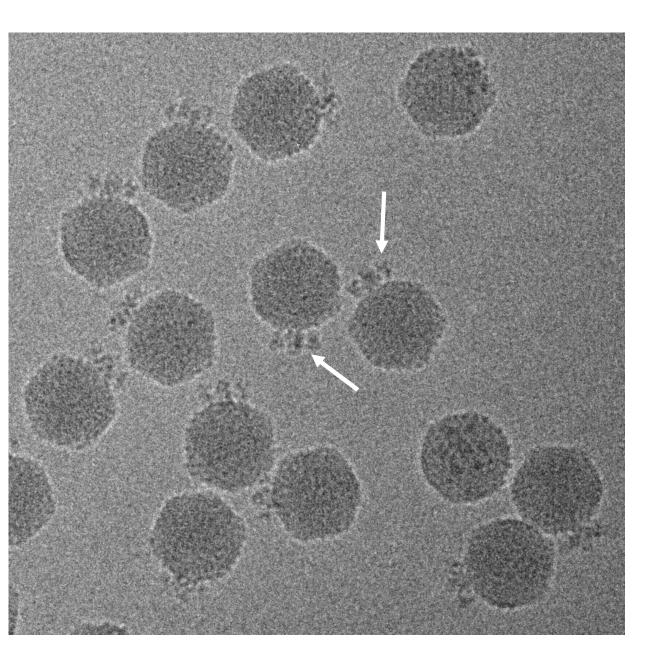
mpiexec -n <# cpu> make3d ...

- Map size limits: 512³ for 4GB, 768³ for 8GB, 900³ for 12GB
- Support mixed platform processing: one 64bit node with 12GB memory + many 32bit nodes with 4GB memory

I cosahedral Reconstruction → Non-I cosahedral Reconstruction



Bacteriophage Epsilon15



icosahedral reconstruction (shell only)

Asymmetric Reconstruction

WHAT'S IN A NAME? 'Planet' 2003 UB313 weighs in

2 February 2006 | www.naturejpn.com

MALARIA IN AFRICA Weather forecasts Lack epidemic risk

DNA REPLICATION A new look at old problems

SPHERICAL VIRUS STRUCTURE

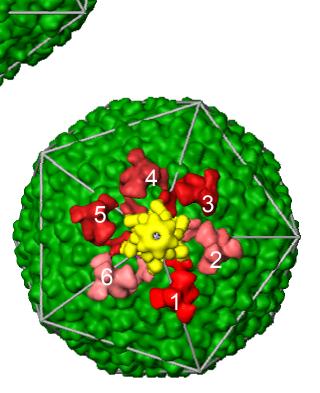
DNA packaging and injection in a Salmonella phage

NATUREJOBS Mental matters

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

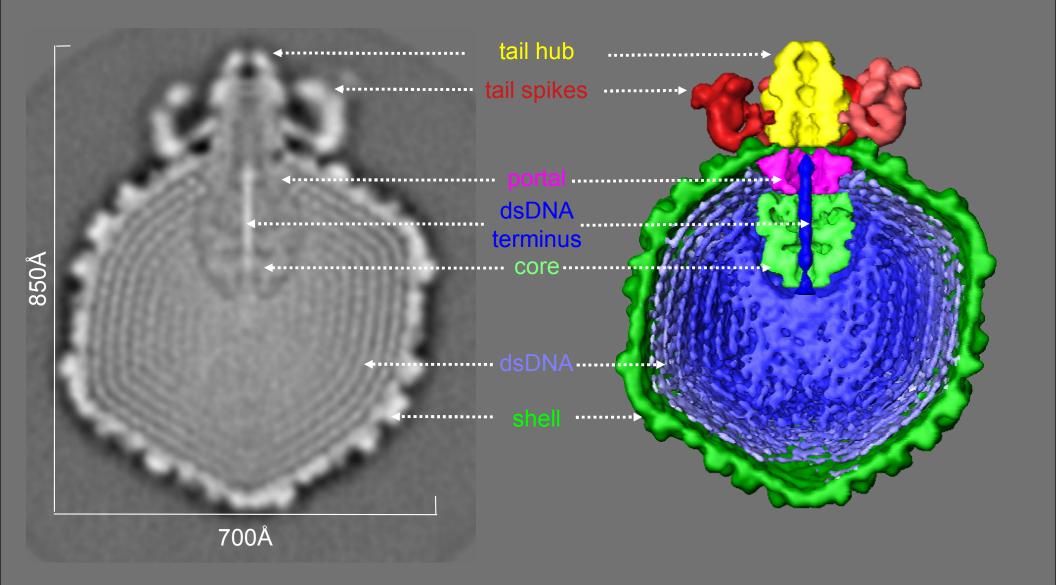
ure

top view



side view

"Virus Anatomy"



I cosahedral Reconstruction → Non-I cosahedral Reconstruction

refine

asymerfine.py

