

# Lecture Determination E. Orlova of the image orientation

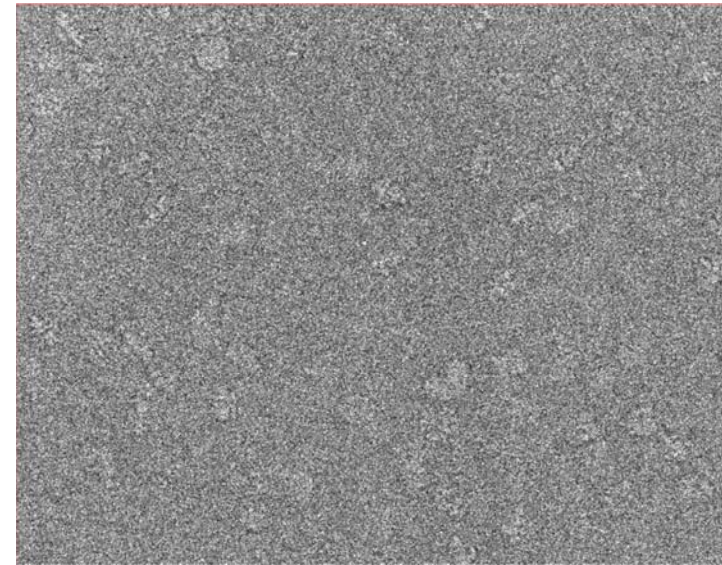
Images: shadow, projection  
Euler angles  
Methods of orientation determination:  
Common lines in Fourier space  
Common lines in real space  
Free-align  
Tomography  
Projection matching



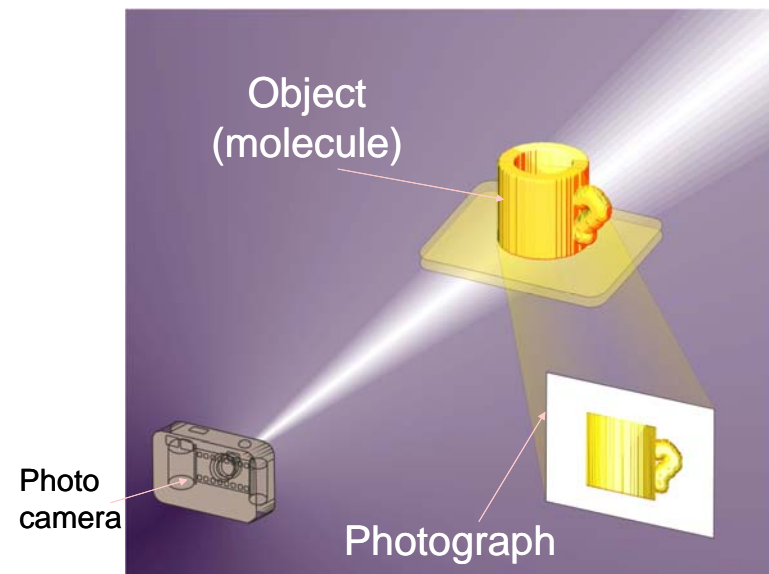
Practical Course

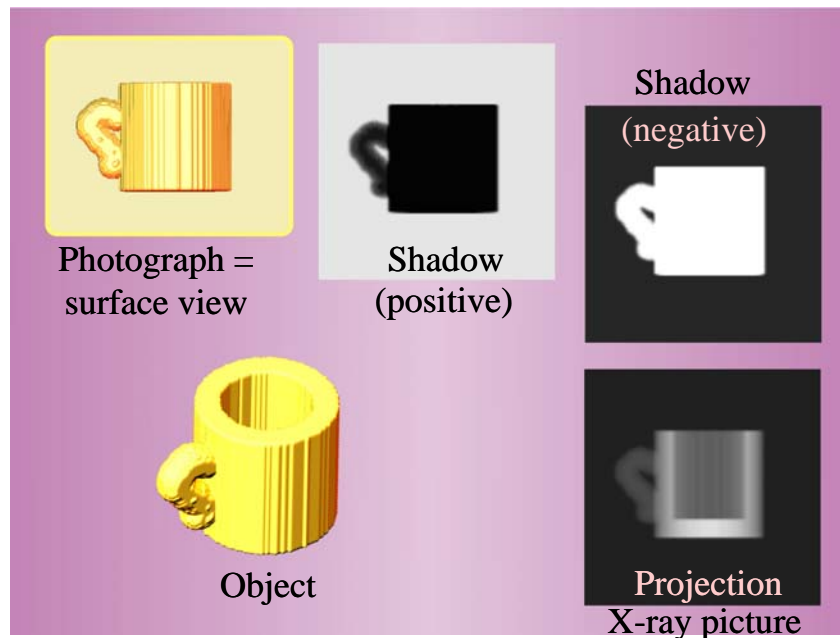
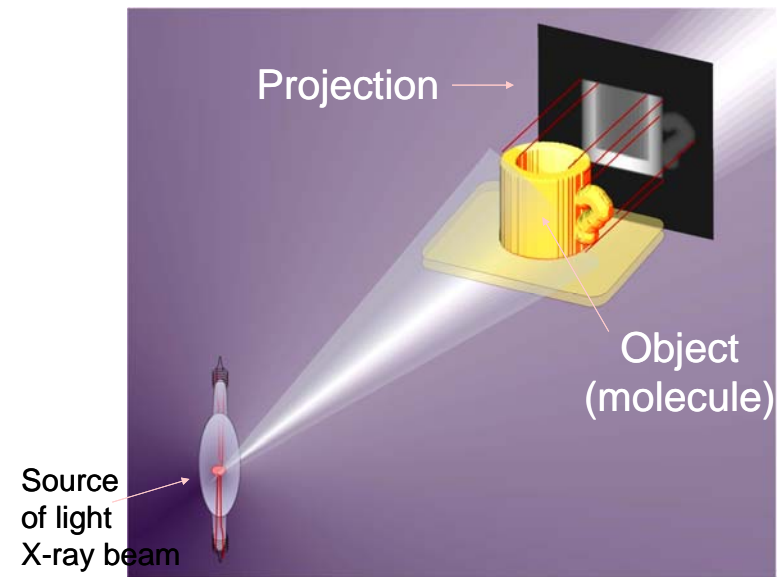
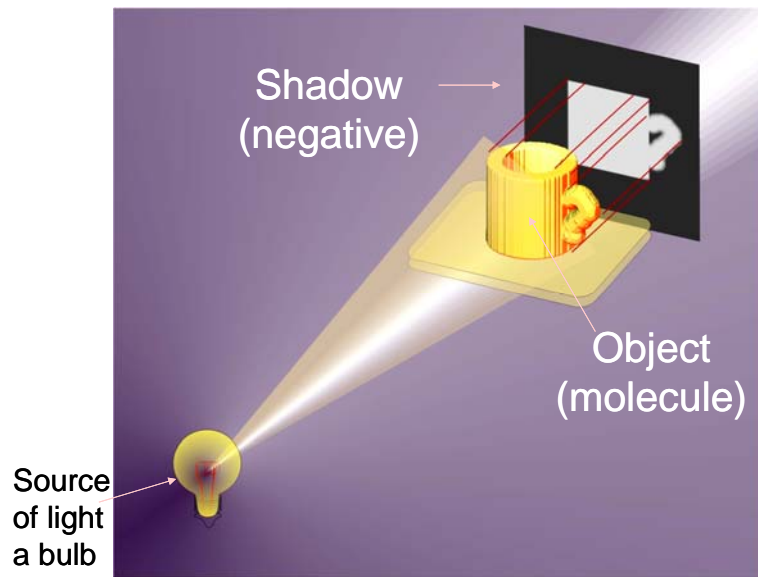
Birkbeck College  
London

## Images of molecules in vitreous ice



**Images —??— Object**  
surface view,  
shadow,  
projection





*3D object*  $\rightarrow \rho(x,y,z)$

Projection: 2D, 1D, Sinogram = ? =  $\rho(x,y,z)$

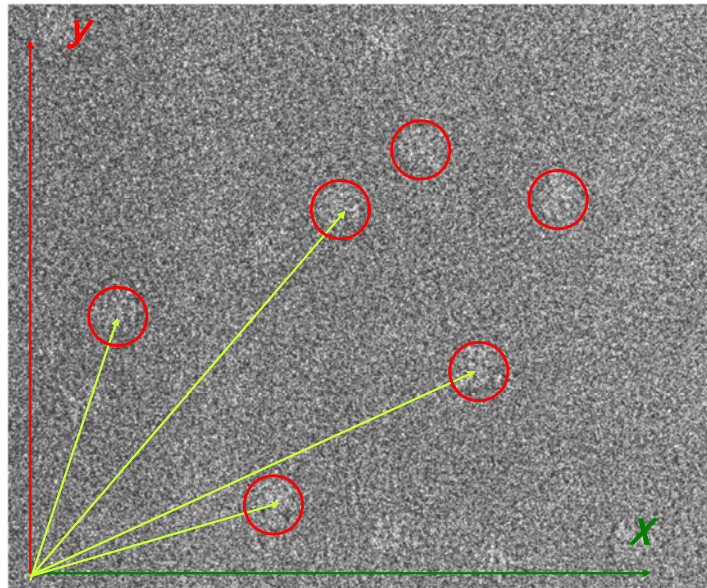
$$p(y, z) = \int \rho(x, y, z) dx$$

$p(y,z)$  – 2D projection

$$l(y) = \int p(x, y) dx$$

$l(y)$  – 1D projection

## Ribosomes in vitreous ice – translational freedom

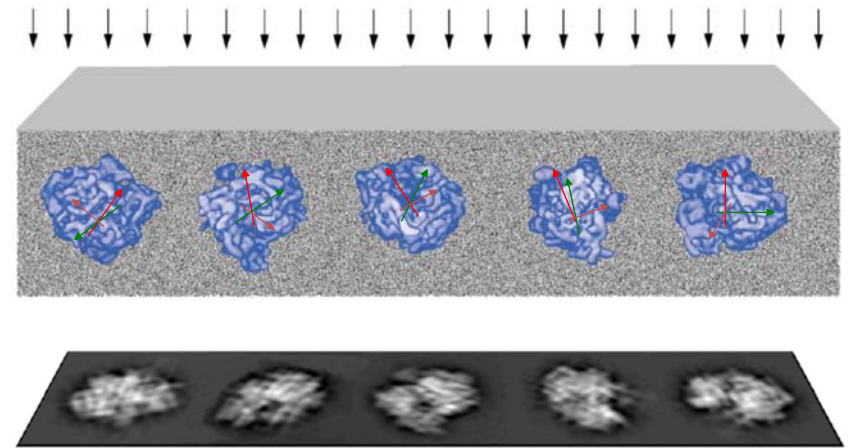


X and Y

2

## Ribosomes in vitreous ice – rotational freedom

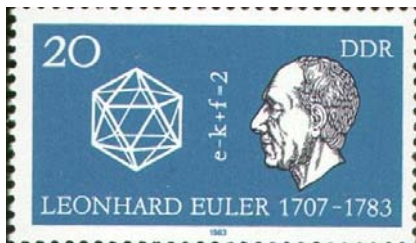
$\alpha, \beta, \text{ and } \gamma \rightarrow 3$



J.Frank, *Annu. Rev. Biophys. Biomol. Struct.* 2002. 31:303–19

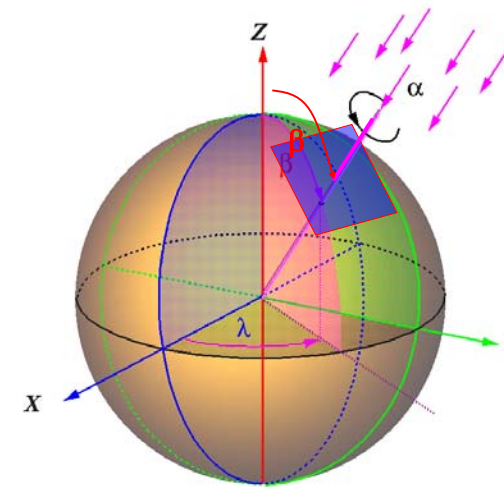
## Leonhard Euler

(15 April 1707 – 18 September 1783) was a pioneering Swiss mathematician and physicist. He made important discoveries in fields as diverse as infinitesimal calculus and graph theory. He also introduced much of the modern mathematical terminology and notation, He is also renowned for his work in mechanics, fluid dynamics, optics, and astronomy.



Euler spent most of his adult life in St. Petersburg, Russia, and in Berlin, Prussia. He is the pre-eminent mathematician of the 18th century, and one of the greatest mathematicians ever. his collected works fill 60–80 quarto volumes

[http://en.wikipedia.org/wiki/Leonhard\\_Euler](http://en.wikipedia.org/wiki/Leonhard_Euler)



*Euler Angles*

$\alpha$  - rotation in the image plane (or around new Z axis)

$\beta$  - rotation around X axis

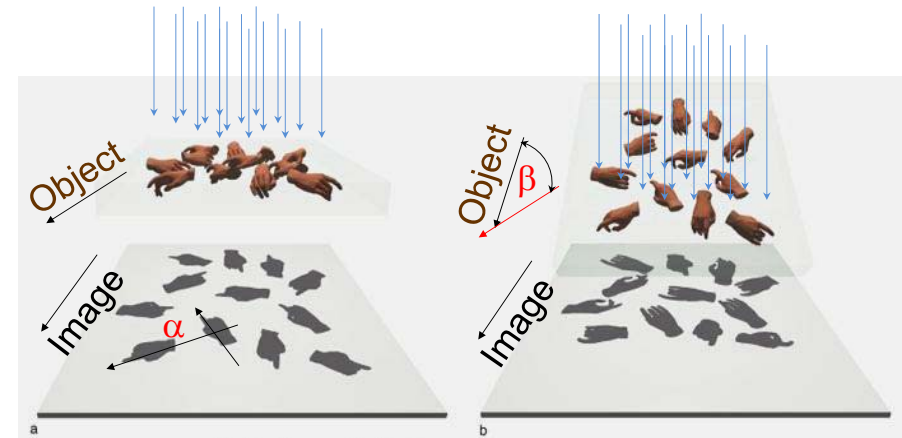
$\gamma$  - rotation around old Z axis)

(IMAGIC)

## Methods of orientation determination:

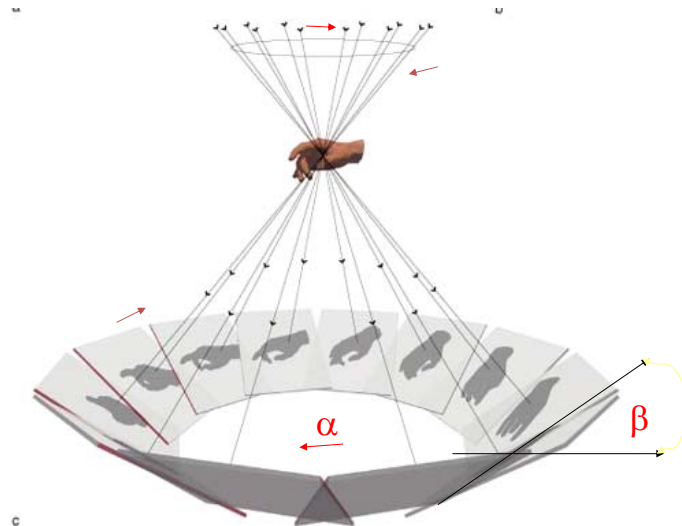
1. *Conical Tilt* – M.Radermacher, J. Frank
2. *Projection Matching* – P.Penczek, J.Frank
3. *Common Lines in Fourier Space* (viruses, phage tails) T.Crowther- MRC package + numerous modification. (S. Fuller)
4. *Common Lines in real space*  
Angular Reconstitution  
M. Van Heel
5. *Frealign* -> *projection matching in Fourier space*  
N. Grigorieff

Conical tilt , more effective for negatively stained samples

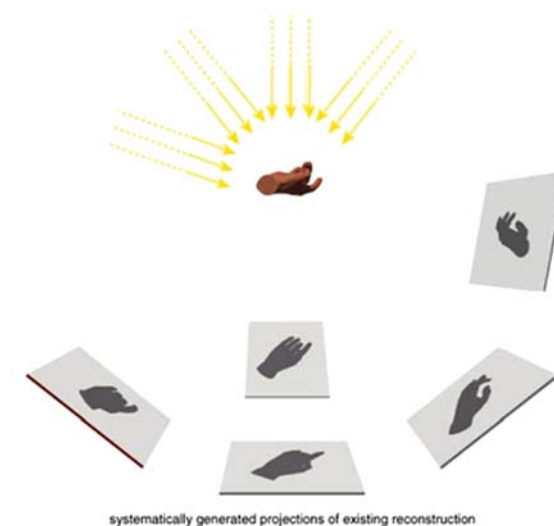


**RADERMACHER M.** Three-Dimensional Reconstruction of Single Particles From Random and Non random Tilt Series. *JOURNAL OF ELECTRON MICROSCOPY TECHNIQUE* 9:359-394 (1988)

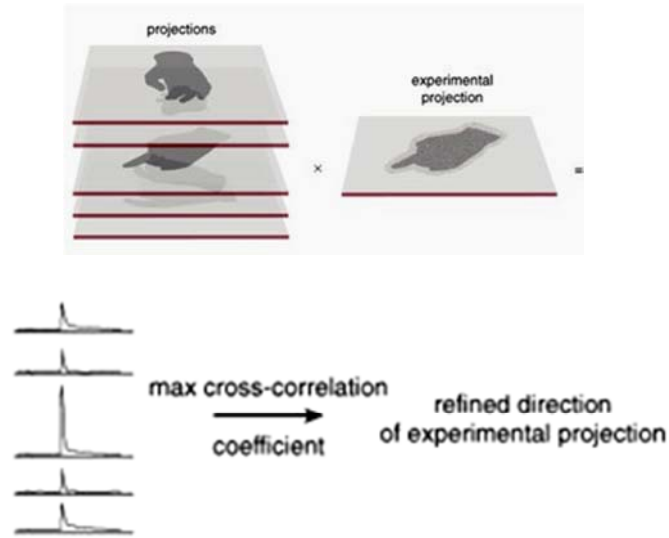
## Conical tilt



## Projection Matching



## Projection Matching



P. Penczek & J. Frank

## The section/projection theorem:

$$F \left[ \int g(x,y,z) dx \right] = G(0,Y,Z)$$

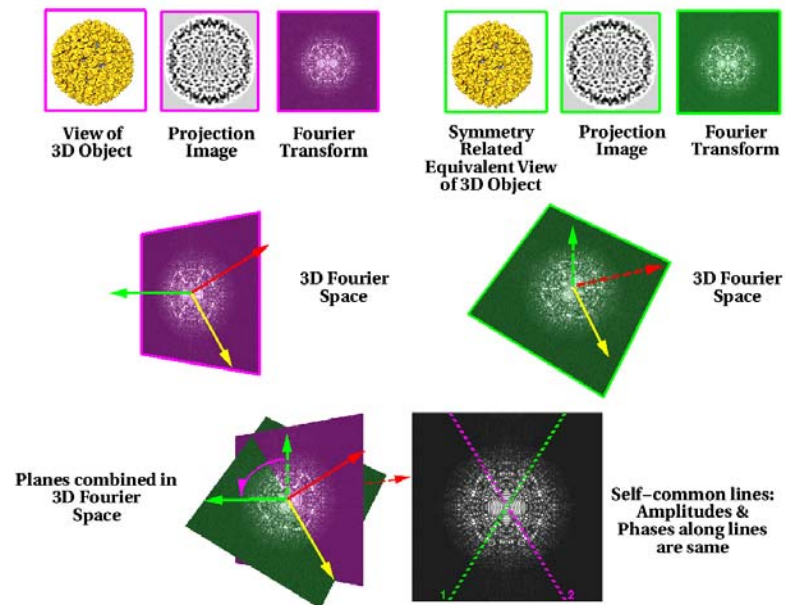
USE:

The Fourier transform of a projection of a 3D object is equal to a central section of the 3D Fourier transform of the object.

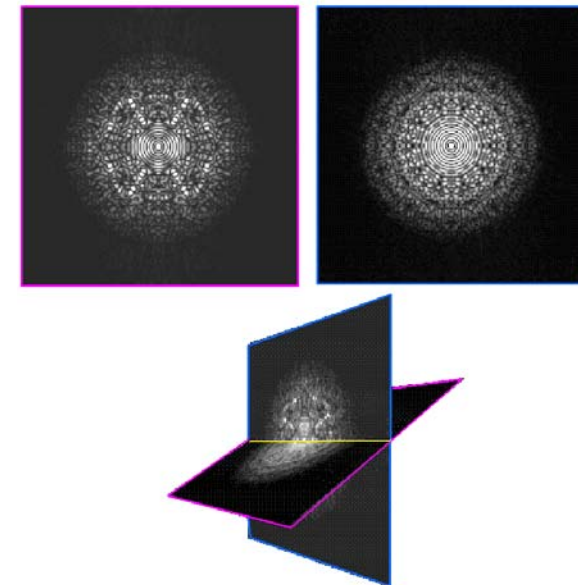
An electron micrograph is a projection of a 3D object. Its transform provides one slice of the 3D transform of the 3D object.

By combining the transforms of different views, one builds up the 3D transform section by section. One then uses the Inversed Fourier Transform to convert the 3D transform into a 3D image.

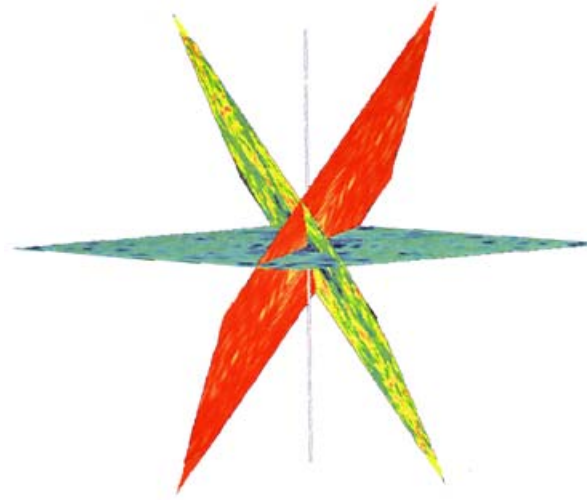
## Common lines in Fourier space



## Common lines in Fourier space

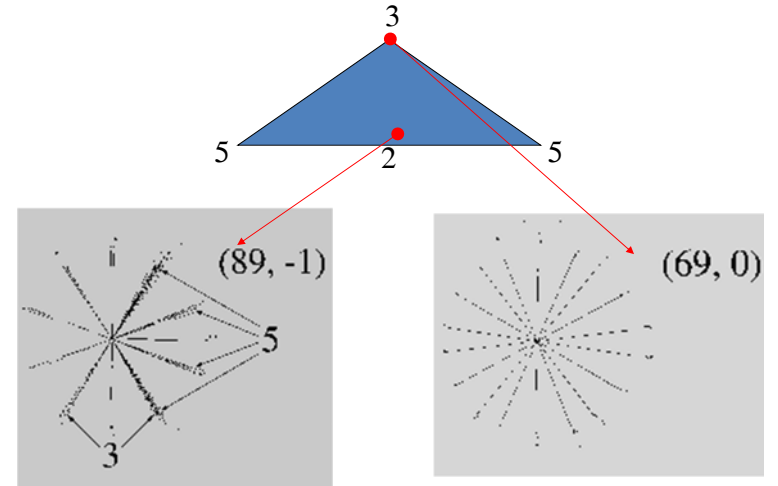


## Common lines in Fourier space



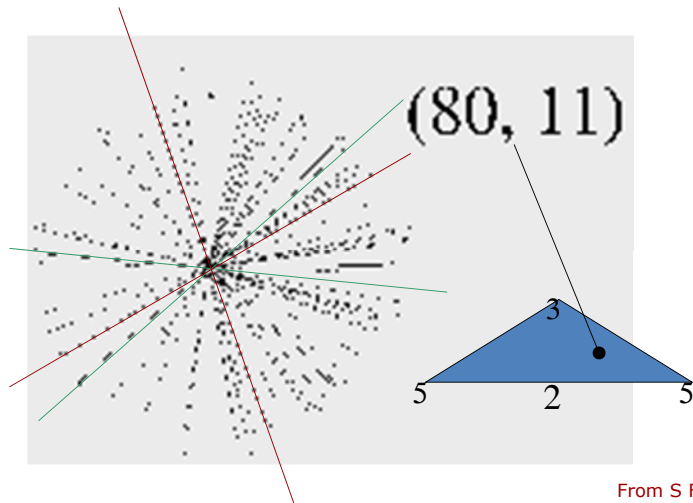
From S Fuller

## Orientations near symmetry axes



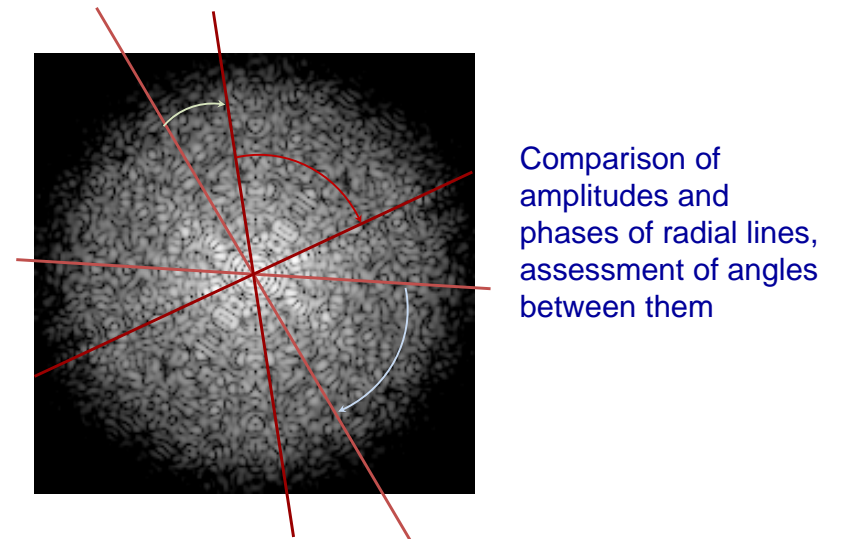
From S Fuller

## An orientation away from symmetry axes



From S Fuller

## Icosahedral symmetry, search for the common lines



Comparison of amplitudes and phases of radial lines, assessment of angles between them

## Common lines in real space

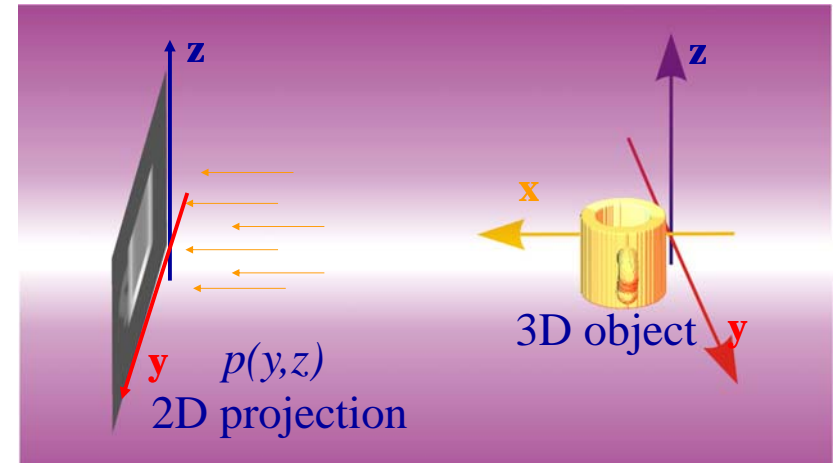
The angular reconstitution method is based on the “common-line projection” theorem:

*Any two 2D projections of a 3D object have at least ONE common 1D line projection*

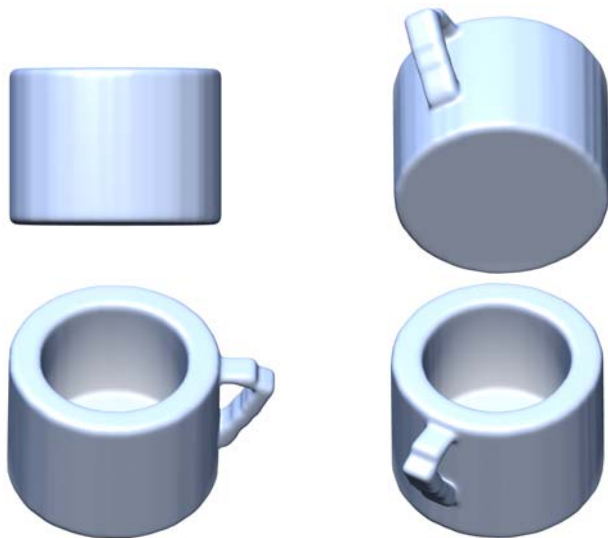
## Common lines in real space

3D  $\rightarrow$  2D  $\rightarrow$  1D projection

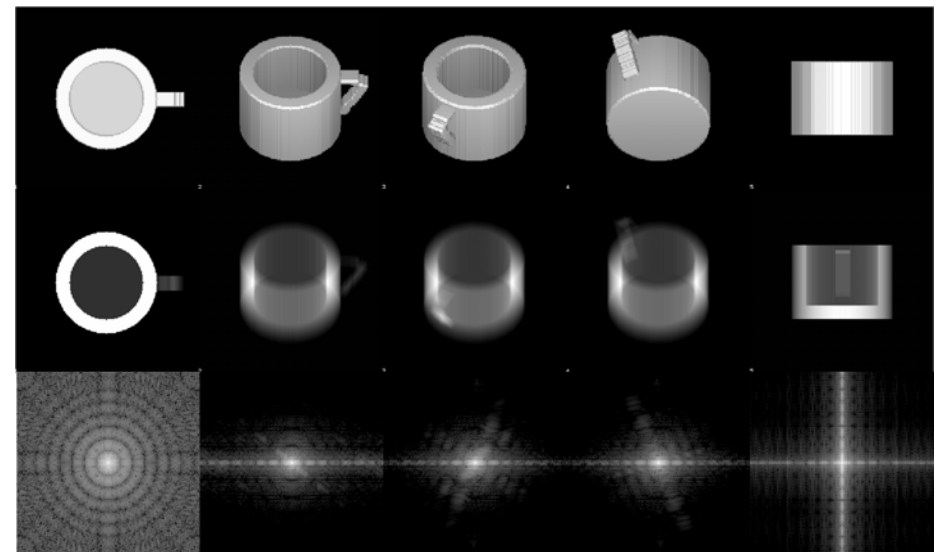
$$p(y, z) = \int \rho(x, y, z) dx$$



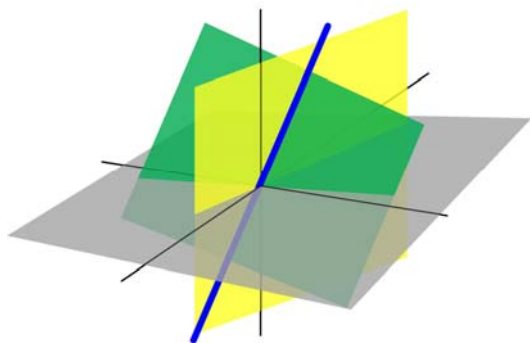
## Common lines in real space



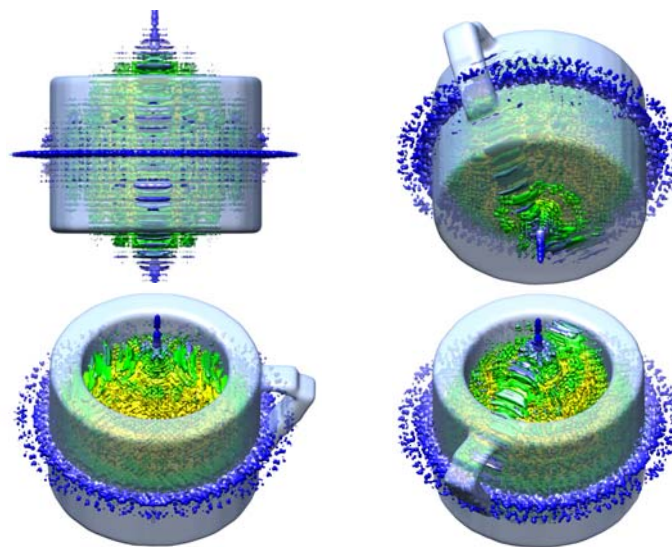
## Common lines in real space



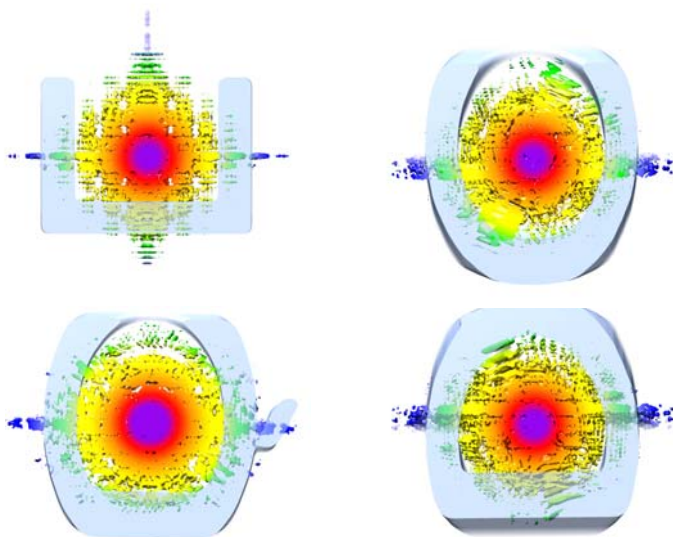
## Common lines in real space



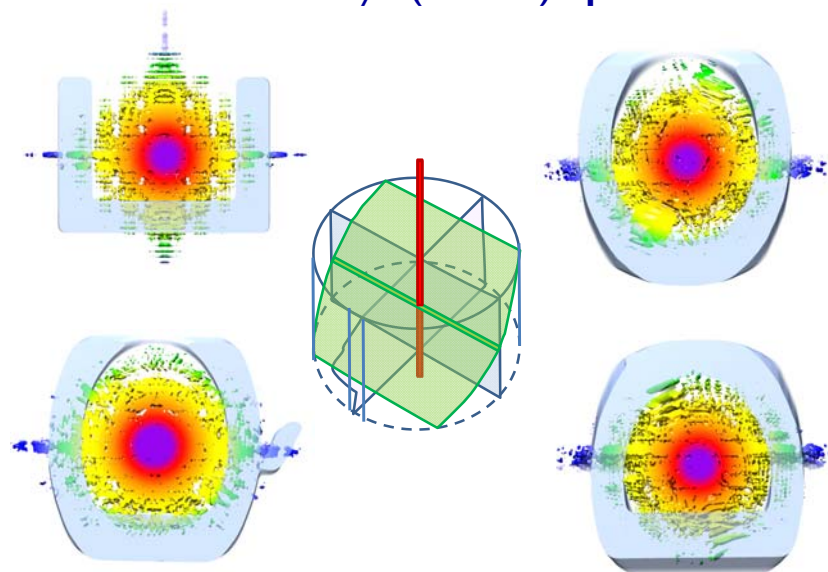
## Common lines in R/F(ourier) space



## Common lines in R/F(ourier) space

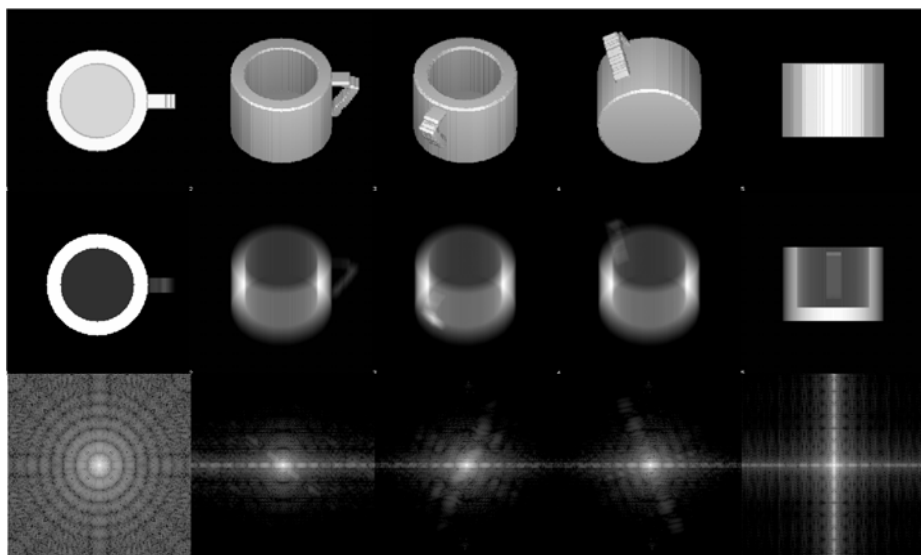


## Common lines in R/F(ourier) space

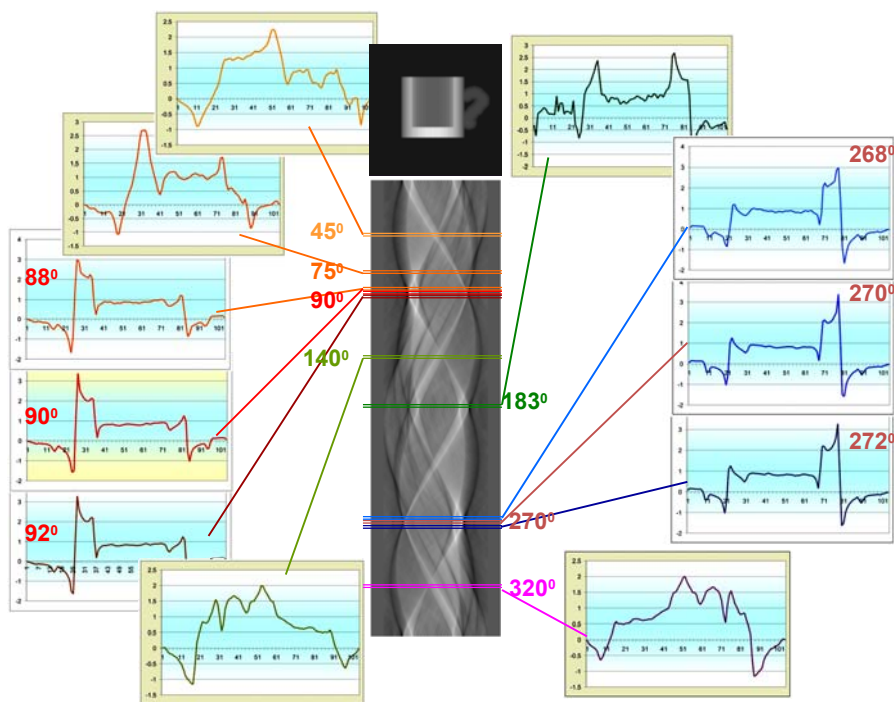
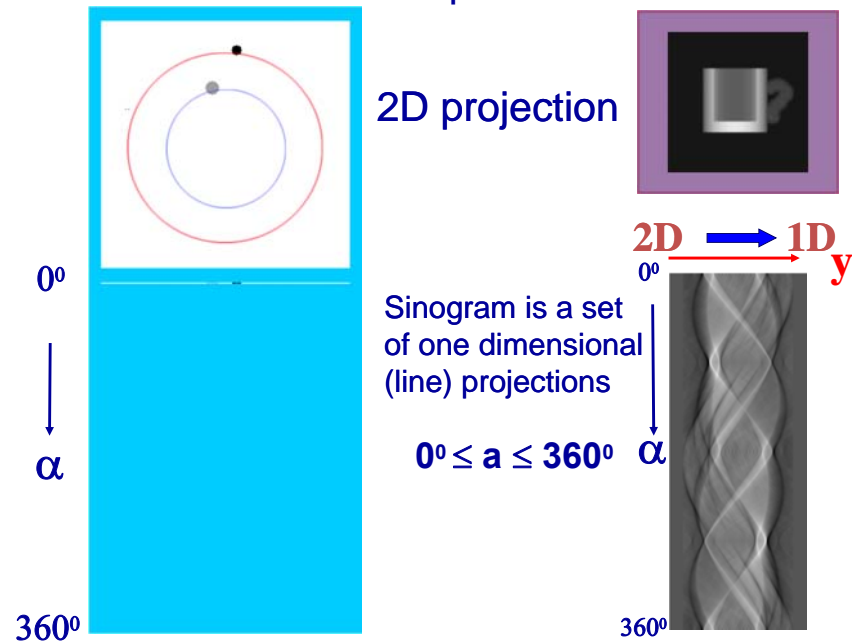




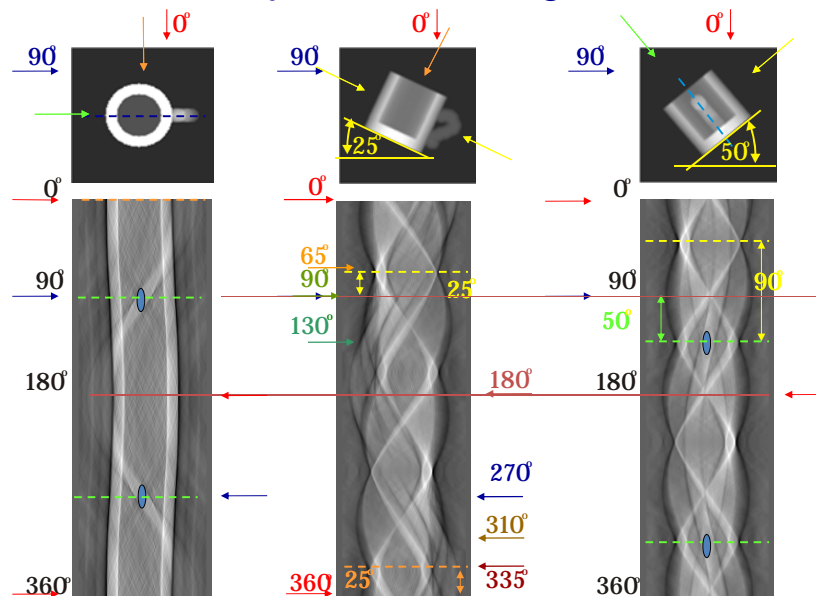
## Common lines in real space

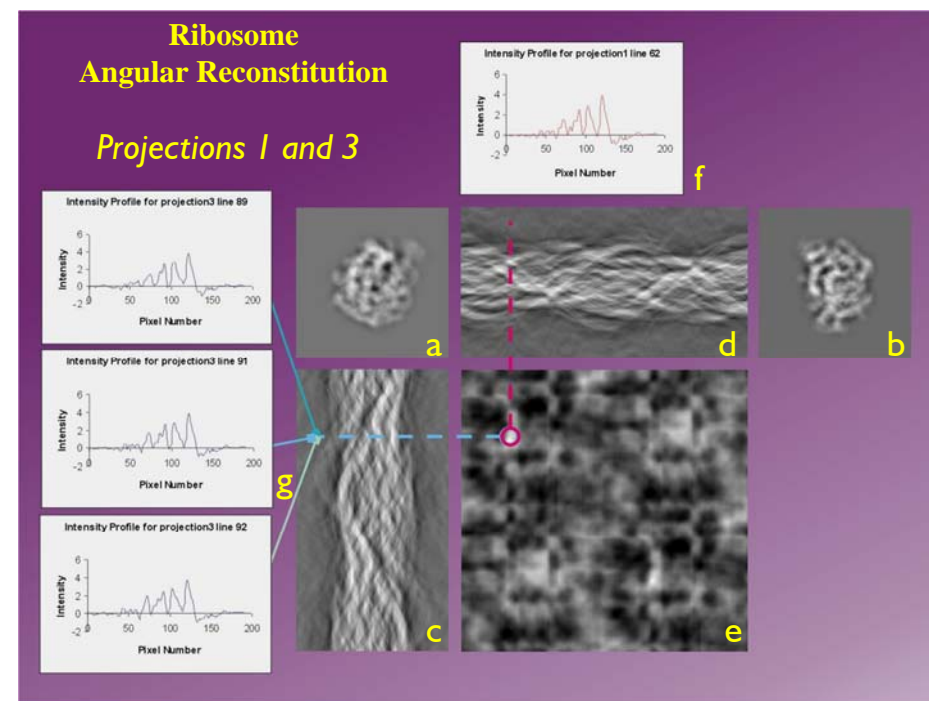
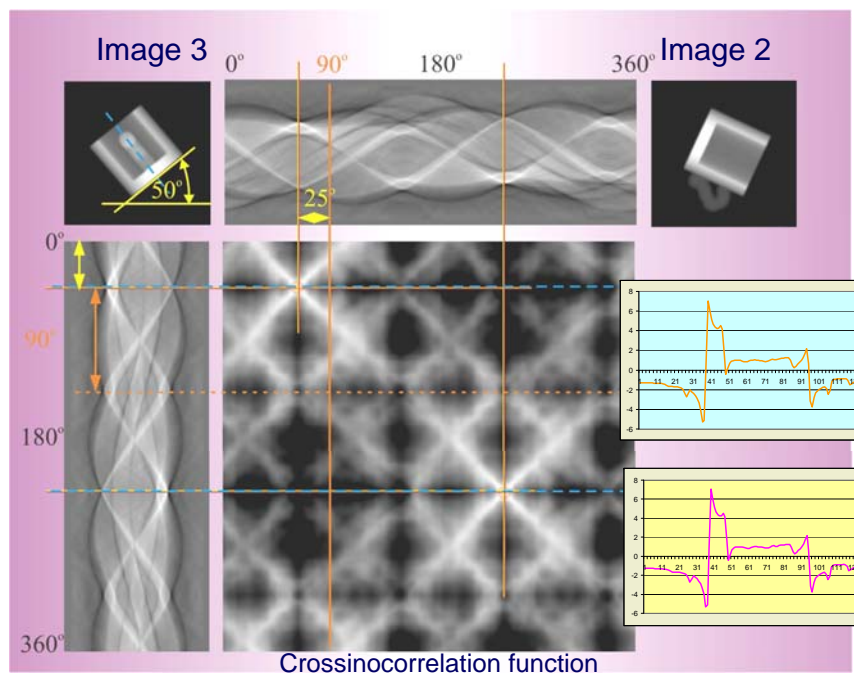
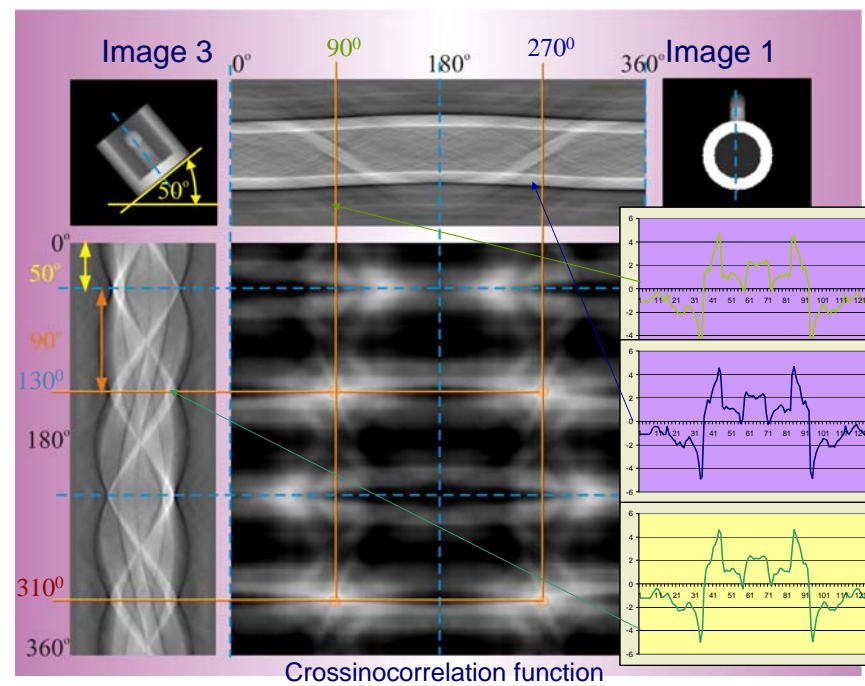
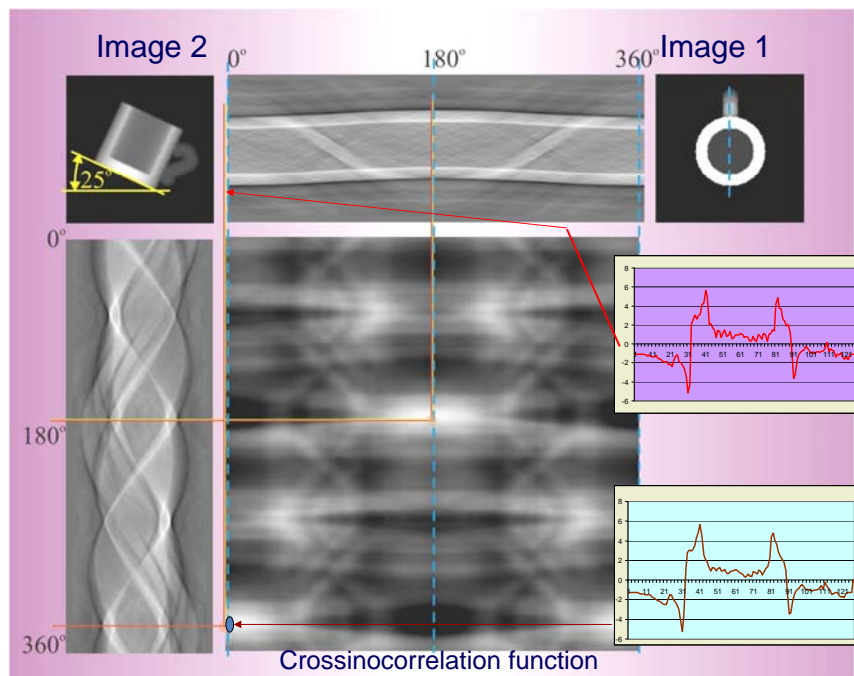


## Common lines in real space

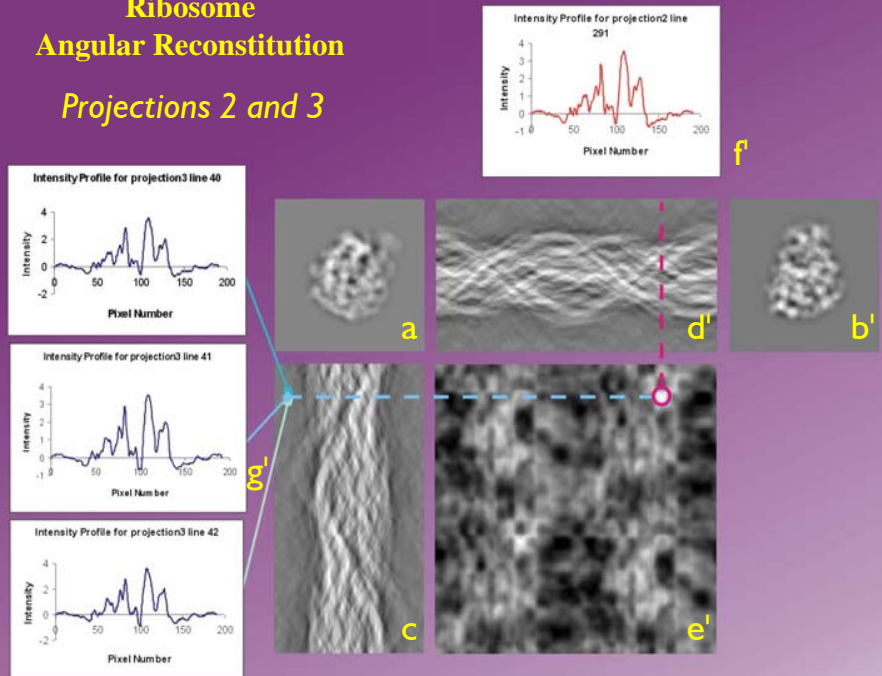


## Projections > Sinograms

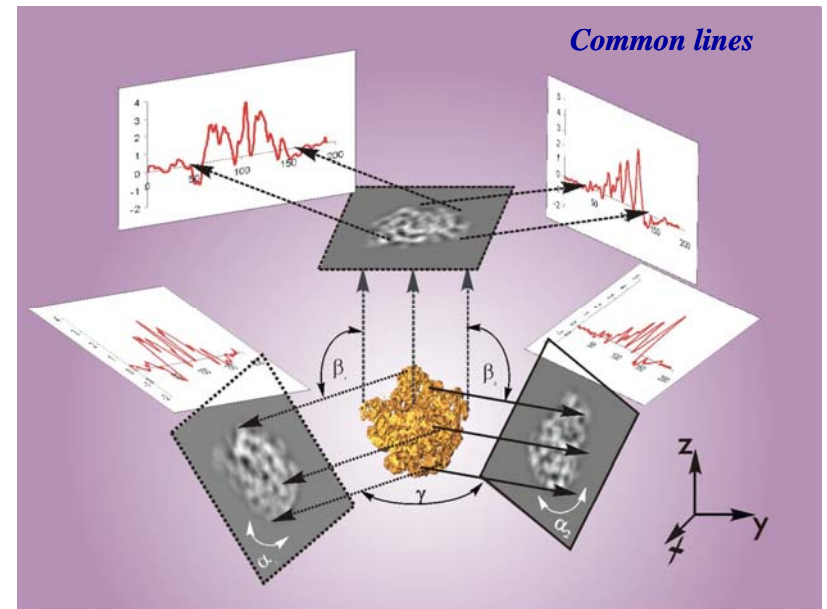




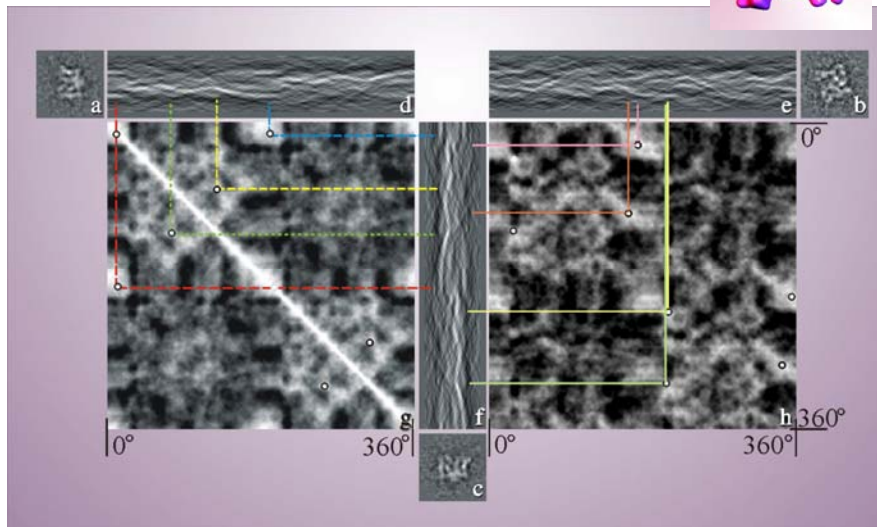
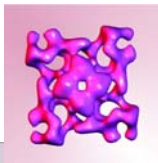
## Ribosome Angular Reconstitution Projections 2 and 3



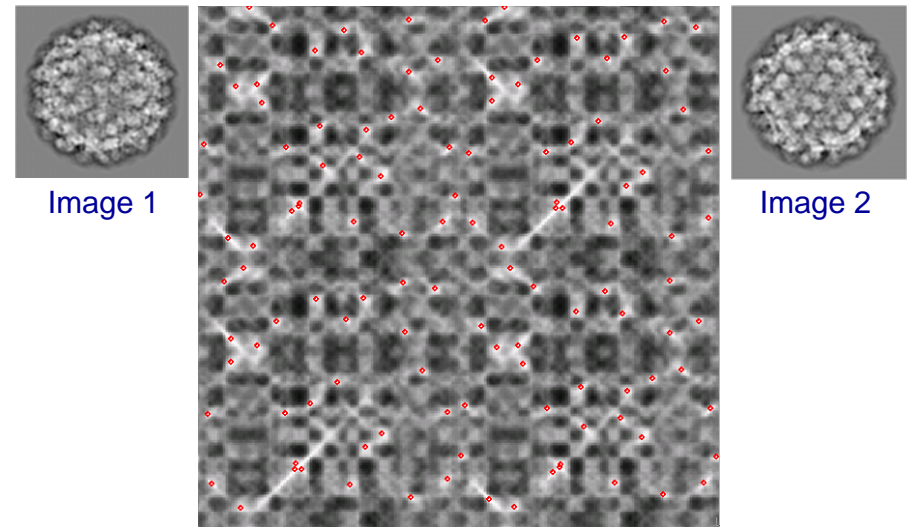
## ANGULAR RECONSTITUTION



## Calcium release channel RyR1

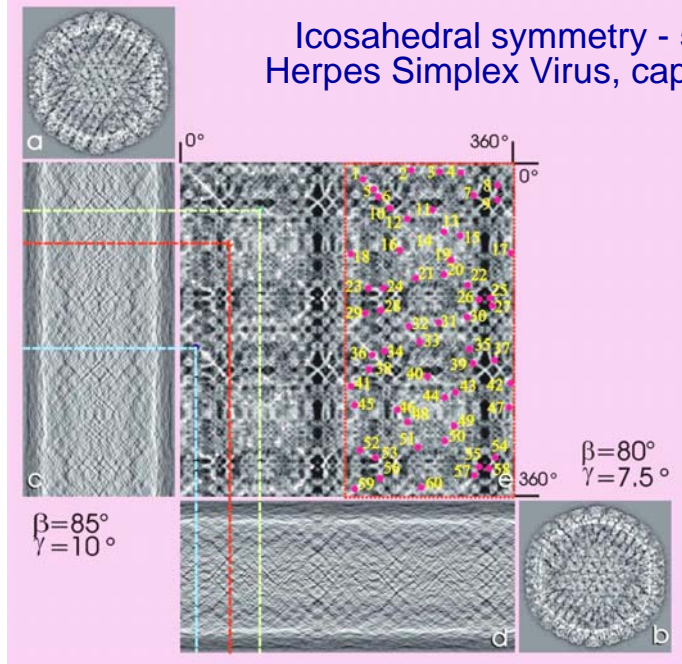


## Icosahedral symmetry

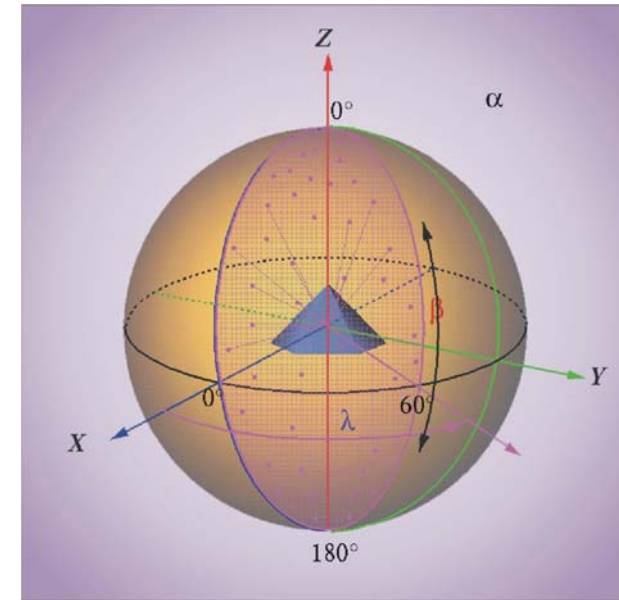


Crossinocorrelation function

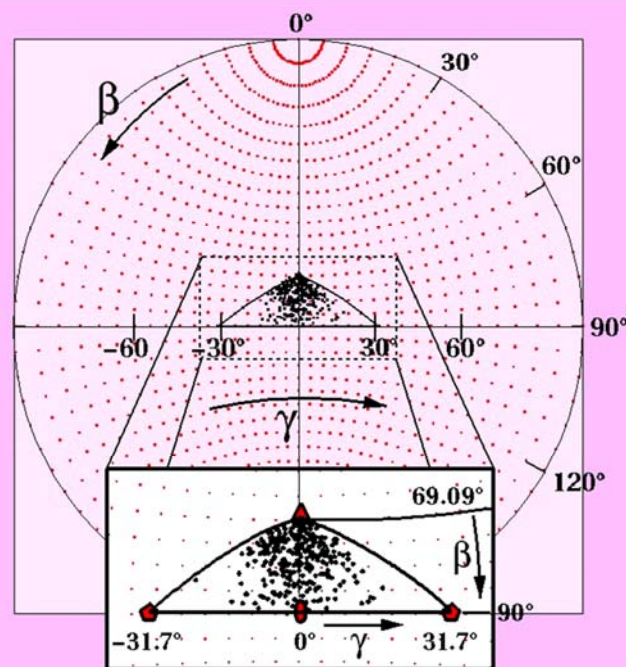
## Icosahedral symmetry - 532 Herpes Simplex Virus, capsid B



## Distribution of characteristic views - C6



## HSV-1



## Recommendations!!!

1. Don't start from a symmetrical view.
2. Try to start from the general (common) view, then the second can be symmetrical.
3. Try to use as many DIFFERENT views as possible, ideally perpendicular to each other.
4. Do not use a sequence of similar views, the program will be confused!
5. If the standard deviation of peak heights starts to increase, it means that the process is starting to diverge. You will not get a reasonable solution.
6. Keep eye on the program: the long projections should have a consistent orientation, the PRINCIPLE of the BRICK can not be violated.

## FREALIGN

### Fourier Reconstruction and ALIGNment

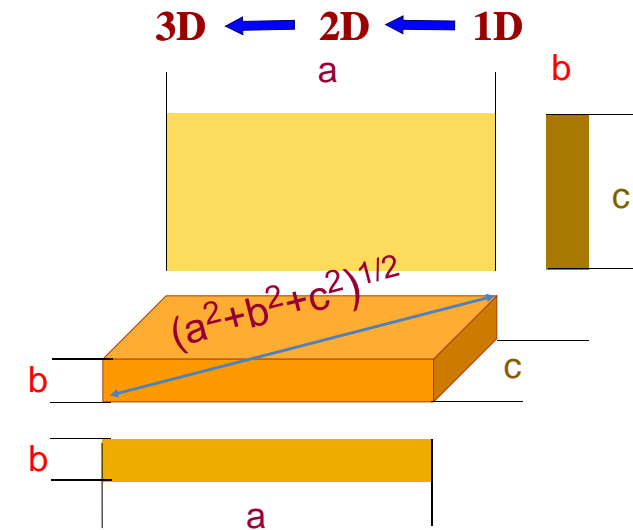
Iterations of alternating 3D reconstruction, using the improved alignment parameters, and realignment of the particles based on the updated 3D structure, are performed until the alignment parameters and 3D structure remain constant.

FREALIGN: image data (particle image stack, 3D reference reconstruction) and particle parameters (Euler angles, x, y translation, magnification, defocus and astigmatism, arc cosine of the correlation coefficient).

The algorithms in FREALIGN also introduced an efficient procedure for refining 3D structures by working entirely in Fourier space.

N. Grigorieff / Journal of Structural Biology 157 (2007) 117–125

## The principle of the BRICK



### Methods of orientation determination:

#### 1. Conical tilt. It is more efficient for negatively stained samples with a preferable orientation.

##### Missed cone

Leschziner AE, Nogales E. The orthogonal tilt reconstruction method: an approach to generating single-class volumes with no missing cone for ab initio reconstruction of asymmetric particles. *J Struct Biol.* 2006 Mar;153(3):284-99

#### 2. Angular reconstitution. It requires good signal/noise ratio, needs classification

#### 3. Common lines in Fourier space and PFT are mostly used at analysis of particles with icosahedral symmetry

#### 4. Projection matching, the most popular technique, requires an initial model.

### References:

1. Radon, J. (1917) **Über die Bestimmung von Funktionen durch ihre Integralwerte längs gewisser Mannigfaltigkeiten.** *Ber. Sachs. Akad. Wiss. Leipzig. Kl.*, 69, 1107-1114
2. Crowther, A., DeRosier, D.J., and Klug, A. (1970) **The reconstruction of a three-dimensional structure from projections and its application to electron microscopy.** *Proc. R.Soc. Lond.*, 317, 319-340
3. Van Heel, M. (1987) **Angular reconstitution: a posteriori assignment of projection directions for 3D reconstructions.** *Ultramicroscopy*, 21, 114-126
4. Serysheva, I., Orlova, E.V., Sherman, M., Chiu, W., Hamilton, S., and van Heel, M., (1995) **The skeletal muscle calcium-release channel in its closed state visualized by electron microscopy and angular reconstitution.** *Nature Struct. Biol.*, 2, 18-14
5. Radermacher, M. (1988) **The three-dimensional reconstruction of single particles from random and non-random tilt series.** *J. Electron Microsc. Tech.* 9, 359-394
6. Penczek, P., Grassucci, R.A., and Frank, J. (1994) **The ribosome at improved resolution: New techniques for merging and orientation refinement in 3D cryoelectron microscopy of biological particles.** *Ultramicroscopy*, 53, 251-270
7. Fuller SD, Butcher SJ, Cheng RH, Baker TS (1996) **Three-dimensional reconstruction of icosahedral particles--the uncommon line.** *J Struct Biol.* 116, 48-55.

## References

[Grigorieff, N.](#) 2007. [FREALIGN: high-resolution refinement of single particle structures](#). J Struct Biol. 157:117–125.

[Sindelar, CV, Grigorieff N.](#) 2012. [Optimal noise reduction in 3D reconstructions of single particles using a volume-normalized filter](#). J Struct Biol. 180:26-38.

[Lyumkis, D, Brilot AF, Theobald DL, Grigorieff N.](#) 2013. [Likelihood-based classification of cryo-EM images using FREALIGN](#). J Struct Biol. 183:377-388.