

Cryo-electron tomography



Saskia Bakker Leicester cryo-EM workshop 16 March 2021

3D cryo-EM structure





that all the molecules are in the same orientation

These "aligned" molecules are then added together, and this summed image provides a more detailed view of the molecule in this orientation



de coursesy Gabriel Lander



We perform this same process for the different orientations of the molecule

Shide coursesy Gabriel Lander

Then we gather all these views and combine them computationally



This provides us with a 3D reconstruction of our molecule





Electron tomography

- Allows 3D images of complex samples to be obtained
- No need for averaging procedures so can image a unique sample in 3D
- Helps to bridge the gap between light microscopy and protein structure determination methods

When to use tomography?



Hoffmann N et al, 2015, Nature Pfeffer S et al, 2015, Nat.Comm. Briggs JAG & Kraeusslich HG, 2011, J. Mol. Biol

Cryo-electron tomography

- Thin samples (< 300 nm)
 - Edges of cells
 - Micro-organisms
 - Sections of cells/tissue



Campylobacter jejuni

- Causes food poisoning, possibly paralysis if untreated
- Spiral shape with flagellum at each end



Bacterial flagella

- Long filamentous assembly of protein
- Attached by a motor complex
- Motor rotates to move flagella
- Different species have different structure



Principle of tomography



Figure 2 Principle of tomography. (*left*) Projections of the specimen were recorded from different directions by tilting the specimen holder. (*right*) The three-dimensional reconstruction of the sample is obtained most commonly by backprojection into a common three-dimensional reconstruction body.

Tilt series





Principle of tomography



Figure 2 Principle of tomography. (*left*) Projections of the specimen were recorded from different directions by tilting the specimen holder. (*right*) The three-dimensional reconstruction of the sample is obtained most commonly by backprojection into a common three-dimensional reconstruction body.









Not so pretty...







Data acquisition considerations

Dose

- 40-200 electrons/Å² has to be split over all tilts
- Higher contrast versus accumulative damage
- Magnification/pixel size
 - Higher mag = smaller field of view = tracking harder during data acquisition

Defocus

Low dose data acquisition



Image from Florian Schur

Missing wedge

5 deg increment





original image



2 deg increment

dimensional imaging of soft matter, 2011, Soft Matter (7)

Nudelman F, de With G, Sommerdijk NAJM , Cryo-electron tomography: 3-

Missing wedge





Tilt schemes



Do you need low dose at low tilt, or would more tomograms be better?

Energy filter



 \bigvee

Cryo-ET of viruses



- (a) Herpes simplex virus was studied by Grünewald et al. . The virus is bound by an envelope membrane (dark blue) studded with a number of different glycoprotein spikes (yellow), enclosing the proteinaceous tegument layer (orange) and the off-centre icosahedral capsid (blue) harbouring the DNA.
- (b) VV IMV was studied by Cyrklaff et al. The virion is composed of multiple layers: outer membranes (orange), enclosing the lateral bodies (red) and the dumbbell shaped core (dark blue), with a remarkably compact distribution of DNA (green) and a crystalline spike layer (light blue).
- (c) Human immunodeficiency virus studied by Briggs et al. consists of an envelope (blue), and an envelope-spanning core (red) of fullerene architecture, harbouring the RNA viral genome. The density marked yellow is probably Gagderived protein not incorporated into the core.

Structure of complex viruses and virus-infected cells by applies to all panels. electron cryo tomography. Curr Opin Microbiol. 2006 Aug;9(4):437-42. Grünewald K et al.

Actin filaments in a cell

Actin filaments were trapped using millisecond freezing methods and identified using structural information



 Medalia O, Weber I, Frangakis AS, Nicastro D, Gerisch G, Baumeister W. 2002. Science 298(5596):1209–13



Sub-tomogram averaging



Flagellar motors



Beeby et al 2016 https://doi.org/10.1073/pnas.1518952113

Deletion mutants



Beeby et al 2016 https://doi.org/10.1073/pnas.1518952113

4.9Å sub-tomogram average...





chings et al 2018 https://doi.org/10.1038/s41467-018-06577-4

Not easy...

Resolution trends for subtomogram averages 🛛 🚍



How long is a piece of string?



References

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- Macromolecular architecture in eukaryotic cells visualised by cryoelectron tomography. O Medalia et al., Science (2002) 298, 1209-1213.
- Visualising cells at the nanoscale. A Leis et al., TIBS (2008) 34, 60-70
- Studying intracellular transport using highpressure freezing and correlative light electron microscopy. E. Brown et al., Seminars in Cell and Developmental Biology (2009), 20, 910-919