

## The Winter-Spring 2022 EM Course

## Introduction to Cryo-electron Tomography

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The New York Times

Resolving Structures to Drive Scientific Discoveries during the Pandemic

## The Coronavirus Unveiled

By Carl Zimmer, Oct. 9, 2020







How does SARS-CoV-2 enter human cells? Wrapp D. *et al.*, Science 2020; Simulation by Amaro lab, UCSD







## Structures Resolved by Tomography in EMDB

EMDB current entry modality distribution



As of Feb. 4, 2022



## Outline

- What is cryo-electron tomography?
- Sample preparation: special considerations
- Data collection, alignment, and reconstruction
- Application of cryo-electron tomography in cell biology (structural cell biology)



## **Cryo-EM Single Particle Analysis**

The Nobel Prize in Chemistry 2017



Jacques Dubochet Prize share: 1/3



Elmehed

Joachim Frank

Prize share: 1/3

Rabed defa. II. N.

© Nobel Media. III. N. Elmehed Richard Henderson Prize share: 1/3



**O** Using thousands of **J** similar traces, the computer generates a high-resolution 2D image The computer 4 calculates how the different 2D images relate to each other and generates a high-resolution structure in 3D.



## Cryo-electron tomography (Cryo-ET)

On a TEM: 3D structures  $\rightarrow$  2D images



Baumeister W. 1999 Trends in Cell Bio.

On a computer: 2D images  $\rightarrow$  3D structures





## Why Cryo-electron Tomography (Cryo-ET)?

- Sample has a unique structure or heterogenous
- Sample in a complex environment





## Sample Preparation

- Preserving various structural elements of the specimen in native structure in aqueous solution
- Good concentration
- Good thickness & good contrast
- Target tracking in their native environment



## **Plunge Freezing**

To vitrify water:

- Temperature drop >  $10^5$ - $10^6$  K/s  $\rightarrow$  liquid ethane
  - Liquid N<sub>2</sub> has poor cooling capacity
  - Water is a poor thermal conductor so sample thickness < 5 μm</li>
- Gravity plunge at > 1 m/s









## Specimen Preserved by Plunge Freezing



R. F. Thompson, et al., 2016 Methods, Vol. 100, 3-15



### Preparing Intact Mammalian Cells For Cellular Tomography







## CryoET Data Collection

#### What is a "tilt-series"?

- Images taken when the sample is tilting about the tilt axis.

Tilt series of *C. glabrata* plasma membranes





## CryoET Data Collection

- There are many configuration parameters involved in data collection. Each is a balance between opposing considerations.
  - Defocus: contrast vs resolution
  - Total dose: signal vs radiation damage
  - Tilt range and increment:
    - goniometer mechanical limit (-70 <->+70)
    - goal of the project
    - sample geometry





## Data alignment and reconstruction

- Each image in a tilt series has to be "aligned"
  - x, y shift

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- Rotation (position of tilt axis)
- Tilt angle
- defocus



## Data alignment and reconstruction

- Each image in a tilt series has to be "aligned"
  - x, y shift

ITGERS

- Rotation (position of tilt axis)
- Tilt angle
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## Data alignment and reconstruction





#### Data visualization, analysis and subtomogram averaging











## Outline

- What is cryo-electron tomography?
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Cellular Tomography:

- Cytoplasm: too thick for electrons to penetrate;
- How to find targets within a crowded cell?





## Applying Cryo-ET to Reveal Protein Structure *in situ* – The Workflow

CelPress

Cell

Article

The In Situ Structure of Parkinson's Disease-Linked LRRK2

Reika Watanabe,<sup>1,6,7</sup> Robert Buschauer,<sup>1,6,8</sup> Jan Böhning,<sup>1,9,6</sup> Martina Audagnotto,<sup>1,10</sup> Keren Lasker,<sup>2</sup> Tsan-Wen Lu,<sup>3</sup> Daniela Boassa,<sup>4</sup> Susan Taylor,<sup>3,5</sup> and Elizabeth Villa<sup>1,11,\*</sup>



## Structure of LRRK2

- LRRK2: (Leucine-rich repeat kinase 2) the most mutated gene in familial Parkinson's disease
- Functions in neurite outgrowth, membrane trafficking, autophagy
- Mutations or pharmacological inhibition of kinase activity recruit LRRK2 to microtubules
- Multi-domain protein; structure of the full-length protein is not available.



Guaitoli, G. et al., PNAS 2016



## Workflow



Watanabe, R. et al., Cell 2020

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# Step 1: Design and Prepare Cells to Allow Detection of Targets in the Crowded Environment

- Add fluorescence tag; Increasing abundance for easy detection
- Correlative Light and Electron Microscopy (CLEM)





## Step 2: Focused Ion Beam Milling to Generate Thin Cell Lamella for Cryo-ET

- Cells on grids: 1 5  $\mu$ m
- Electron penetration power: 100–300 nm



<u>Gallium ion milling capability</u> 20 nm milling precision Fine milling (<1pA) to preserve specimen and high-current (>100nA) for large areas SEM column ~1nm resolution Beam deceleration



<u>Cryostage/cryotransfer</u> Accommodates autogrid cartridges for integration with cryoCLEM & cryoTEM Stable operation below the devitrification point of water Approaches liquid nitrogen temperature

Airlock for loading/unloading under cryo-conditions

<u>Detectors</u> Secondary electron Back-scattered electron incl. in-lens detectors



#### **Focused Ion Beam**



Rigort and Plitzko, 2015 Arch Biochem Biophys. 581: 122-130



## Step 2: Focused Ion Beam Milling to Generate Thin Cell Lamella for Cryo-ET

- Cells on grids:  $1 5 \,\mu m$
- Lamella: 100–150 nm





### Step 3: Cryo-ET Imaging and Tomogram Reconstruction

• Use CLEM to guide tilt series data collection



Watanabe, R. et al., Cell 2020



### Step 4: In situ Structure Analysis

• Distribution and dynamics in cells





## Step 5: Subtomogram Analysis

- Extraction
- Classification
- Averaging
- Model fitting



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## Step 6: Integrative Modeling

 Details in domain organization can be deduced from nanometer resolution maps



Watanabe, R. et al., Cell 2020



#### **Step 7: Functional Analysis**

**Disturbing structure** 

Variations of functions





## Summary

- Introduction to cryo-electron tomography, correlative light and electron microscopy and focused ion beam milling
- Sample preparation for cryo-electron tomography
- Structures and distribution of protein complexes or aggregates in neurodegenerative diseases by multimodal bioimaging combining CLEM, cryoFIB and cryoET.



#### References

1. Wrapp, D. *et al.* Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. *Science* **367**, 1260-1263, doi:10.1126/science.abb2507 (2020).

2. Yao, H. *et al.* Molecular Architecture of the SARS-CoV-2 Virus. *Cell* **183**, 730-738 e713, doi:10.1016/j.cell.2020.09.018 (2020).

3. Klein, S. *et al.* SARS-CoV-2 structure and replication characterized by in situ cryo-electron tomography. *Nat Commun* **11**, 5885, doi:10.1038/s41467-020-19619-7 (2020).

4. Deniston, C. K. *et al.* Structure of LRRK2 in Parkinson's disease and model for microtubule interaction. *Nature* **588**, 344-349, doi:10.1038/s41586-020-2673-2 (2020).

5. Watanabe, R. *et al.* The In Situ Structure of Parkinson's Disease-Linked LRRK2. *Cell* **182**, 1508-1518 e1516, doi:10.1016/j.cell.2020.08.004 (2020).

6. Jiménez-Ortigosa C., Jiang J., Chen M., Kuang, X., Healey K. R., Castellano P., Boparai N., Ludtke S. J., Perlin D. S., and Dai W. (2021), Preliminary structural elucidation of  $\beta$ -(1,3)-glucan synthase from candida glabrata using cryo-electron tomography. *JOF* 7 (2), 120.



## **Concept Checking Questions**

- Single particle vs Tomography
- Data collection configurations
- The missing wedge artifact
- Factors limiting the resolution of subtomogram averages
- Identifying objects in information-rich tomograms
- Factors affecting correlation in CLEM



## Single Particle *or* Tomography



41 https://clipart-library.com



## CryoET Data Collection

- There are many configuration parameters involved in data collection. Each is a balance between opposing considerations.
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• "Crowther criterion":



radius (Å)	res (Å)	# views	angular step (°)
125	3	259	0.69
125	10	79	2.292
125	40	20	9.167
10000	3	20944	0.009
10000	10	6283	0.029
10000	40	1571	0.115

Courtesy of Jason Kaelber



• The Missing Wedge Artifact



## Data alignment and reconstruction



- What is the "missing wedge"?
  - Missing data that are not recorded because of limited tilt range



## Dual tilt reduces missing wedge

A holder that "flips" in the microscope so x-tilt will image a second axis



https://www.wormatlas.org/EMmethods/ETmethods.htm

## Dual tilt reduces missing wedge

UTGERS



lancu, Wright &al. JSB 2005



# What are the factors limiting the resolution of subtomogram averages?



## Identifying objects in tomograms

- Structure signature
- CLEM

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- Perturbing abundance or structure
- Template matching
- Heavy metal tag

## CLEM:

- What are the advantages and disadvantages of doing light microscopy at room temperature and cryotemperature?
  - Room temperature: oil immersion objective lens, large NA
  - Cryo temperature: samples stop moving

## CLEM: many factors affect correlation



GFP RT 100x NA1.4 oil immersion objective lens

GFP 80K 60x NA 0.7 air objective lens

PA-GFP 80K cryo-PALM



Distance between EM/cryo-PALM bead centers around 9±2 nm

#### Fluorophore & objective lens

#### Correlation of images

Tomography - Identifying objects in tomograms concept check questions:

- What is "cryo-PALM"?
- PALM: photoactivated localization microscopy

## PALM (Photo Activated Light Microscopy)





In PALM, small bursts of UV light are used to excite subsets of fluorophores. Since these fluorophores are excited in small sets, their diffraction patterns are less likely to overlap, allowing the location of the actual molecules to be located through back calculation

http://huanglab.ucsf.edu/STORM.html