CRYOEM 001 : COLLECTING DATA AND OTHER MATTERS

February 8, 2023

New York Structural Biology Center

SIMONS ELECTRON MICROSCOPY CENTER



WHAT BROUGHT ABOUT THE RESOLUTION REVOLUTION

(~2012-2014)

Hardware



Microscopes

Direct Detectors



Computers





THREE-DIMENSIONAL RECONSTRUCTION:
STRUCTURES WITH HELICAL SYMMETRY. 1968 (sample prep: negative staining)
Pioneering work: 3D reconstruction of a bacteriophage tail using the Fourier-Bessel approach, 1968
Application of the Projection-Slice Theorem



Aaron Klug and David DeRosier, LMB/MRC Cambridge



DIRECTIONAL INFORMATION LOSS



Iterative angular refinement



NEW ERA (SINCE 2012): DIRECT ELECTRON DETECTING CAMERAS



Koning et al. Ann. Anatomy 2018







DETECTORS Detector Performance Characterization

MTF (Modulation Transfer Transform) contribute to signal envelope

DQE (Detector Quantum Efficiency) S/N over spatial frequency range





Detector Performance Characterization





dectris.com

DETECTORS

Ruskin, et al JSB

K3 SPECS



https://www.gatan.com/K3

Specifications

	КЗ	K3 Base
TEM operating voltage (kV)	200/300	
Sensor size (pixels)	5,760 x 4,096	3,456 x 4,096
Readout modes	Counting Super-resolution	Counting
Max. image size (pixels)	11,520 x 8,184 Super-resolution	3,456 x 4,096
Performance relative to physical Nyquist (DQE) Peak 0.5	>0.87 / >0.83 >0.53 / >0.53	>0.8 >0.5
Sensor read-out (full fps)	>1500	
Transfer speed to computer (full fps)	>75	>25
Motion correction	Inline	
Gatan Microscopy Suite® software	Included	
Automation support	Latitude and other third-party software	

Specifications are subject to change without notice.

COUNTING MODE











Electron enters detector.

Electron signal is scattered.

Charge collects in each pixel.

Events reduced to highest charge pixels.

https://www.gatan.com/improving-dqe-counting-and-super-resolution

K3 lowers Read Noise with Correlated Double Sampling (CDS)

Standard mode Reset Reset Read, Pixel charge Time Time Net readout = Read,

CDS mode Reset Read Read Pixel charge Time X 2 Net readout = Read, - Read,

https://www.gatan.com/

CTF: WHY IS MONITORING THE CTF IMPORTANT IN OUR DATA COLLECTION?



CTF

The **contrast transfer function** (**CTF**) mathematically describes how aberrations in a transmission electron microscope (TEM) modify the image of a sample

The phase shift (phase distortion function) due to the objective lens can be combined into a single phase factor χ , given by,

where,

Cs -- The spherical aberration coefficient, defining the quality of objective lens,

 λ -- The wave-length,

 Δf -- The defocus value,

lgl -- The spatial frequency,

 α -- The convergence semi-angle.

https://www.globalsino.com/EM/page4236.html

FOCUS





Most cryo-EM data are acquired using defocus contrast



- At high defocus, highresolution information in the image is strongly delocalized.
- Image processing can relocalize the signals, but at most only about half of the theoretical contrast is preserved by defocusing.
- "Underfocus" means decreasing the strength of the objective lens, effectively focusing above the specimen.





How to undo the CTF effects? 150 -5 -100 -100 Projection Point-spread function mage 0.3 0,2 0.1 R -0.1 -0.2 -0.2 FT of image, k = 0.3 CTF. 2 m, B=100Å² FT of Projection

- 1. Phase flipping
 - $\tilde{A} = \operatorname{sgn}(C)X$
 - 2. Wiener filter



How to undo the CTF effects in noisy images?



-100 -50 0 50 100 angstroms



Weher from 100 images

3. Wiener from multiple images

$$\tilde{A} = \frac{\sum_{i}^{N} C_{i} X_{i}}{k + \sum_{i}^{N} C_{i}^{2}} \qquad \qquad k = 1/\text{SNR}$$
$$= \frac{|N|^{2}}{|A|^{2}}$$



https://guide.cryosparc.com/processing-data/all-job-types-incryosparc/ctf-estimation

Thermo Fisher

ROUTINE USE OF SPA



Join a discussion on sub-2.5 Å cryo-EM structure determination of GPCRs for drug design

Wed, Sep 9, 2020, 8 p.m. EDT | 5 p.m. PDT | 10 a.m. AEST | 9 a.m. JST

Attend our upcoming Ask the Experts Q&A session on routine sub-2.5 Å cryo-EM structure determination of GPCRs for drug design. This rapidly developing field is constantly producing new and exciting biological and pharmacological discoveries. Ask questions and get answers from leading academic investigators in the field.

You'll learn about:

- GPCR biochemistry and purification for cryo-EM
- GPCR sample preparation for cryo-EM
- High-resolution single-particle cryo-EM imaging and 3D reconstruction of GPCRs

Today's Experts

Part -

- Patrick Sectors, PhD Monash Institute of Promessarbeal Sciences, Monash University
- PiQ Pharmacology, Unit of Malkooma (Australia)
- -30 years appendix a studying GPCRs
- With Devine Wooflan, Plant Centry +50 GPCR atturnees determined by tryn-CM (-25 4 2 5 Å)



Viewing Therme Pisher 5.

Practical tips for GPCR cryo-EM

- Centre Wootlen, PHO Monaith Institute of Pharmaceutical Sciences, Nonaith University
- IND Sochernity, Unix of Benerghan (United Hingdory)
- Boohamility and pharmacology of GPCPs
 With Patinuk Sectors. Plastic Genery >00 GPC01 absorbance determined by strys-EM (~25.4.2.5.4)

Radodis Dereix, PhD Greduale School of Medicine, The University of Tokyo 1900 Brophysics, National Institute for Physicsopical Ecleran, Japan

- · Oys-EMmetrod amergenet
- Well Public Station, Damas Wooten 100 GPCR structures determined by cryp EV (<25.5.2.5.4)

TIPS AND TRICKS FOR Cryo-EM sample preparation



- The quality of the cryo-EM sample governs the outcome of the experiment!
- We optimized the plunging parameters for ice thickness consistency and grid coverage
- Our blot time is relatively long: 10 s
- For every new sample, depending on the
- initial concentration, we prepare 2-3 grids
- a with 2x dilution in-between
- GPCR sample concentrations in the range
 3 7 mg/ml work best.
- Avoid as much as possible lower concentrations!
- Gold foil grids (UltrAuFoil) improved the consistency of getting uniformly thin ice and reduce beam-induced motion.



DATA COLLECTION

Cryo-EM data acquisition strategy



- Collect on the thinnest possible ice that still has good particle coverage !
- We used 3 x 3 = 9-hole beam-image shift data acquisition scheme, 1 image/hole, realized with homemade scripts in SerialEM
- \simeq Defocus range: 0.5 1.5 $\mu m.$ Start at the high end on
- the first hole and reduce the defocus step-wise for each
- $_{\mbox{\tiny el}}$ hole in the pattern, e.g. $1.4 \rightarrow 1.3 \rightarrow 1.2 \rightarrow \ldots \rightarrow 0.6$
- :: Use an energy filter with <15 eV slit
- Do not use super-res (K3), select pixel size ≈ 1/3 the resolution you are hoping to get. Use EER with Falcon 4.
- Throughput: 1 sample/day ≈ 1 structure/day; ~5,500 movies
- Collect non-gain-normalized compressed TIFFs/EER.
 prepare your own gain reference with Relion



WHAT FACTORS MATTER

Performance factors

Viewing Thermo Fisher S...

MONASH

University

東京大学

Do not use VPP; use zero-loss filtering; defocus <1.5 µm; total exposure ≥60 e/Å²



IMPACT OF GRIDS

Benefits of Au foil grids

Viewing Thermo Fisher S





More consistent grid quality – many squares with uniformly thin ice; support does not break

