

# NCCAT VIRTUAL TOMOGRAPHY SHORT COURSE

## APRIL 12-14, 2021 NEW YORK, USA

### INSTRUCTOR BIOS

#### MUYUAN CHEN (BAYLOR COLLEGE OF MEDICINE)



My work focuses on developing machine learning algorithms for a wide range of CryoEM applications, including protein structural variability analysis, de novo modeling tools, and structure determination from cellular tomography.

#### WEI DAI (RUTGERS UNIVERSITY)



Our research focuses on characterizing the structures of macromolecular machinery in their cellular context using three-dimensional (3D) cryo-electron tomography (cryoET) and correlative light and electron microscopy. Structures of intracellular macromolecular complexes are usually heterogeneous and dynamic, relying largely on interactions with other cellular components. Using cryoET to determine the structure of cellular machinery inside the cell avoids damage to the complexes during purification, captures snapshots of the complex while in action, and provides information on cross-talk of the complexes with their cellular partners during biological processes.

Our current research interest includes:

Huntington's disease:

*structure and organization of protein aggregates; 3D architecture of the diseased cells under misfolded protein aggregation stress*

Structural biology of phage/virus maturation.

## STEVEN LUDTKE (BAYLOR COLLEGE OF MEDICINE)



My group focuses on CryoEM/CryoET and quantitative image processing, applying these techniques to a wide range of biological systems ranging from individual macromolecules to whole cells. For the last 20 years my group has been developing the EMAN software suite for both high resolution single particle analysis as well as in-situ and in-vitro tomography. This software has been used on a large fraction of the structures in the EMDataBank, and with over 30,000 downloads is one of the most widely used in the field. In addition to developing new image processing methods such as deep learning applications and bispectral analysis, my group engages in a wide range of biological projects, from the high resolution structure and dynamics of individual molecules to the study of functioning macromolecular assemblies within the cell. This is an exciting time for the cryoET field, with many opportunities to substantially advance our fundamental understanding of biomolecular interactions in situ.

## ALEX NOBLE (NEW YORK STRUCTURAL BIOLOGY CENTER)



Alex is broadly interested in developing and applying methods for solving biomedical problems. He is the primary tomographer at SEMC. He works on several projects including cryo-FIB/SEM, tomography of cells, reconstituted systems, and purified protein samples, tomography software development (<https://github.com/nysbc/appion-protomo>), and mentoring deep learning projects in cryoEM.

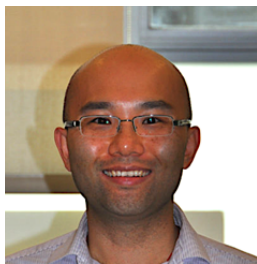
## WILLIAM RICE (NEW YORK UNIVERSITY)



I was a manager for CryoEM for over 10 years at the New York Structural Biology Center, where I saw first-hand the incredible improvements in cryo-EM. Over the past decade, single particle analysis has truly moved to become a mainstream structural biology technique, and I predict cryo tomography will become a mainstream technique in cell biology in the next decade. Since becoming cryo-EM Director at NYU in 2019, I have enjoyed several collaborations with structural biology labs there, and hope to expand more into cryo-ET in the future.

## SHORT COURSE ORGANIZERS AND STAFF

### ED ENG (NEW YORK STRUCTURAL BIOLOGY CENTER/NCCAT)



Ed leads the operations team at the Simons Electron Microscopy Center, a world leading cryoEM facility, and is the manager of NCCAT, a NIH cryoEM service center. The national service center program allows him to engage with scientists in an open and collaborative forum to advance biomedical research. By bringing the best practices in the field to assist researchers he acts as a champion of cryoEM. His mission is to lower the barriers of access to the cryoEM technology and cross-train researchers to have accelerated impact at their home institutions.

### ELINA KOPYLOV (NEW YORK STRUCTURAL BIOLOGY CENTER/NCCAT)



Elina is NCCAT's Traffic Controller (TC) and is the principal lead of the NCCAT User Office (NUO). The TC is one of NCCAT's most important staff members who not only serves as a project coordinator, but also ensures that users have all the information they need to access the Center (either in person or remotely), and follows up with users to gather feedback and address any issues. As part of the NUO she communicates with users, sets schedules, tracks samples and grids, and ensures that quality objectives are met in terms of both service and data.

### SWAPNIL BHATKAR (NEW YORK STRUCTURAL BIOLOGY CENTER/SEMC)



Swapnil Bhatkar is an AWS Solutions Architect and HPC Systems Engineer at the New York Structural Biology Center. He currently leads the AWS cloud initiative for the National Center for CryoEM Access and Training (NCCAT) funded by NIH. He is responsible for building a robust cloud-based CryoEM data processing pipeline for biomedical researchers. He also consults small businesses and NYU Startups to build highly scalable and resilient web applications using AWS stack. He is a member of the global AWS Community Builders program that provides technical mentorship and guidance to help individuals and companies get started with the cloud.

### CHRISTINA ZIMANYI (NEW YORK STRUCTURAL BIOLOGY CENTER/NCCAT)



Christina is NCCAT's embedded scientist liaison, serving as a main point of contact for our embedded trainees and cross-training programs. She works with visiting scientists to ensure that they meet their cross-training goals during their time at NCCAT. With over a decade of experience as a structural biologist, Christina is excited to broaden the impact of CryoEM in the biomedical sciences by coordinating specialized training to help scientists become independent CryoEM practitioners.

#### CATHLEEN CASTELLO (NEW YORK STRUCTURAL BIOLOGY CENTER/SEMC)



Cathleen is the Lab Administrator for the Simons Electron Microscopy (SEMC). She assists with purchasing as well as logistics for NCCAT's Workshops and Courses.

#### CHARLIE DUBBELDAM (NEW YORK STRUCTURAL BIOLOGY CENTER/NCCAT)



Charlie is a member of the NCCAT User Office (NUO). As a part of the NUO he ensures that your queries are responded to promptly, and that you have all the information you need to make your experience with NCCAT go as smoothly as possible. He also corresponds with users about session logistics, making sure your samples and grids are processed promptly upon arrival, that they are properly stored, and returned to you in a timely manner after your session is complete.

#### MAHIRA ARAGON (NEW YORK STRUCTURAL BIOLOGY CENTER/NCCAT)



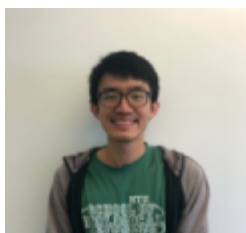
Mahira is NCCAT's research associate and lead teaching assistant (TA) for cross-training programs. For our instrumentation access she assists with our General User Proposal category 2 (GUP2) access which includes access for users in need of staff-assisted sample preparation using the Chameleon sample preparation instrument. Her experience with taking user projects from its initial stages to cryo data collection allows her to instruct users in the best practices in the field. As our lead TA she will be on hand to ensure all our trainees are always supported in their journey into the art and science of cryoEM.

#### MICAH RAPP (NEW YORK STRUCTURAL BIOLOGY CENTER/COLUMBIA UNIVERSITY)



Micah is a graduate student working jointly in Larry Shapiro's lab in the Department of Biochemistry and Molecular Biophysics at Columbia University and with Clint Potter and Bridget Carragher at the Simons Electron Microscopy Center. He is interested in studying macromolecular complexes in their native state, focusing on visualizing cell adhesion assemblies using cryo-EM, with experience in both single particle analysis and cryo-electron tomography. He has served as a teaching assistant for the SEMC Winter EM Course since 2018.

#### EUGENE CHUA (NEW YORK STRUCTURAL BIOLOGY CENTER/NCCAT)



Eugene is a scientist and teaching assistant (TA) for NCCAT cross-training programs. For our instrumentation access he provides staff-assisted access to Krios GUP1 and BAG categories. His main responsibility is to assist researchers with obtaining high resolution information on their biological objects of interest. His scientific interests include sample preparation for cryoEM and automation. He can usually be found operating a microscope, snacking at his desk, or trying to get some sun outside.