# NCCAT SINGLE-PARTICLE ANALYSIS SHORT COURSE MARCH 14-18, 2022 NEW YORK, USA

## INSTRUCTOR BIOS

### GIRA BHABHA (NEW YORK UNIVERSITY)

Gira Bhabha grew up in Mumbai, India. As an undergraduate, she attended the University of Chicago, where she had the best time ever, and discovered that she loved doing research. Her undergraduate theses in Elizabeth McNally's lab focused on using drosophila as a model system for understanding muscular dystrophy. As a graduate student in Peter Wright's lab at the Scripps research Institute, she used NMR and X-ray crystallography to probe the role of protein dynamics in enzyme catalysis. During her postdoc with Ron Vale and Yifan Cheng at UCSF, she used cryoEM and other techniques to understand the mechanism of motility in the motor protein dynein, and worked on a family of lipid transporters called the MCE proteins. Gira's lab focuses on understanding the structural basis of protein machines involved in transport and motility.

http://bhabhaekiertlab.org/

### YINGJIE VICTOR CHEN (PURDUE UNIVERSITY)

Yingjie Victor Chen is an Associate professor at Purdue University in the Department of Computer Graphics Technology. His experience is in Human-Computer Interaction, Virtual Reality,  visualization, and interaction design. He leads Purdue's Laboratory of Intelligent Visualization and Interaction Lab. His research focuses on utilizing modern technologies to model, design, and construct new forms of visualization and interaction that enable computing systems to become a free extension of the human brain and hand. He and Dr. Wen Jiang are developing the virtual reality-based training application, CryoVR, to provide low-cost, low-risk, easy-to-access hands-on training to CryoEM device operation.

## OLI CLARKE (COLUMBIA UNIVERSITY)

The ultimate goal of our research is a structural understanding of how the voltage gated Ca2+ channels on the plasma membrane mechanically couple to the ryanodine receptor and directly control gating of the receptor, and how adjacent RyRs in the paracrystalline arrays that have been observed at the terminal cisternae interact with one another and signal cooperatively. Intracellular calcium signaling, mediated by release of calcium from intracellular stores, is involved in many fundamental biological processes, amongst which perhaps most prominent is the coupling of nervous excitation to muscle contraction (E-C coupling). A key goal of the laboratory is to understand the mechanism by which intracellular calcium release is triggered, modulated and terminated. We use X-ray crystallography and cryoelectron microscopy (CryoEM) to investigate the structure and dynamics of the molecular machines involved in such process, including amongst others the ryanodine receptor (RyR), which mediates intracellular Ca2+ release during E-C coupling.

https://www.anesthesiology.cumc.columbia.edu/research/basic-science-research/oliver-clarke-phd

## AMEDEE DES GEORGES (ASRC/CITY UNIVERSITY OF NEW YORK)

Amédée des Georges received his B.S. and M.S. in Biochemistry from Université Pierre and Marie Curie in Paris before obtaining his Ph.D. degree from the University of Cambridge in 2008 for his work with Linda Amos at the MRC-Laboratory of Molecular Biology. He then joined the lab of Joachim Frank at Columbia University as a postdoctoral researcher. He uses the ability of single-particle cryo-electron microscopy to sort electron microscopy images into different sub-populations in order to obtain high resolution structures of samples conformationally or compositionally heterogeneous, such as the mammalian translation initiation complex or the largest known membrane channel called the ryanodine receptor. He established a research group at the ASRC Structural Biology Initiative and the City College Department of Chemistry and Biochemistry to explore with cryo-electron microscopy the regulatory mechanisms of such large protein and RNA complexes.

https://asrc.gc.cuny.edu/people/amedee-des-georges/

## DAMIAN EKIERT (NEW YORK UNIVERSITY)

My lab uses structure-driven approaches to understand how pathogens establish infection and persist in the host, with the goal of applying these insights to developing new treatments for infectious disease.
Powerful new methods in structural biology—including X-ray crystallography and cryoelectron microscopy—have improved our ability to determine the structure of membrane proteins and large macromolecular assemblies. This in turn has led to new mechanistic understanding and new hypotheses we can test in cell-based models of infection.
We are particularly interested in pathogens that present ongoing challenges to global public health, such as those that cause tuberculosis and malaria. We are also interested in understudied or “orphan” pathogens, particularly those with complex invasion machinery, unique cell biology, or an unusual infectious lifestyle.

http://bhabhaekiertlab.org/

## JOACHIM FRANK (COLUMBIA UNIVERSITY)

Joachim Frank is a Professor of Biochemistry and Molecular Biophysics and of Biological Sciences at Columbia University, and Distinguished Professor of the State University of New York at Albany. Born and educated in Germany, he received his Diplom in physics from the University of Munich. In his doctoral research, conducted at the Max Planck Institute for Biochemistry, Martinsried, and at the Technical University of Munich, he developed methods of digital image analysis as applied to electron microscopy. In his postdoctoral research, in the United States and at the Cavendish Laboratory in Cambridge, U.K., he worked on problems of electron optics and image processing. In 1975 Dr. Frank joined the Wadsworth Center in Albany, New York, as a senior research scientist, where he developed the single-particle reconstruction approach and applied it to the ribosome. He moved in 2008 to take on his current position at Columbia University. Dr. Frank shared the Elizabeth Robert Cole Award of the Biophysics Society with David DeRosier for developing methods of three-dimensional reconstruction of biological macromolecules. He is a Fellow of the American Association for the Advancement of Science and the Biophysical Society, and was invited by the Biophysical Society to give the National Lecture in 2005. In 2006 he was elected to the National Academy of Sciences, the American Academy of Arts and Sciences, and the American Academy for Microbiology. He was honored for his contributions to the development of cryogenic electron microscopy of biological molecules and the study of protein synthesis with the 2014 Franklin Medal in Life Science. Om 2017 he shared the Wily Prize in Biomedical Sciences with Richard Henderson and Marin van Heel, and the Nobel Prize in Chemistry with Richard Henderson and Jacques Dubochet.

http://franklab.cpmc.columbia.edu/franklab/

## RICH HITE (MEMORIAL SLOAN KETTERING CANCER CENTER)

Richard Hite is an Assistant Member in the Structural Biology Program at Memorial Sloan Kettering Cancer Center. Richard started his lab in 2016 and it primarily focused on characterizing the molecular mechanisms of intracellular ion channel function. Richard received his Ph.D. from Harvard Medical school working in the laboratory of Thomas Walz in 2010 and performed his postdoctoral studies at Rockefeller University in the laboratory of Roderick MacKinnon.

https://www.mskcc.org/research/ski/labs/richard-hite

## WEN JIANG (PURDUE UNIVERSITY)

Dr. Wen Jiang is a professor at Purdue University in the Department of Biological Sciences. He is also the scientific director of the Purdue Cryo-EM Facility. Since his Ph.D. studies, Dr. Jiang's research focus has been on method developments and applications of cryo-electron microscopy (cryo-EM) to structural studies of viruses, protein complexes and more recently protein filaments implicated in neurodegenerative diseases. He and Dr. Yingjie Victor Chen have been leading the development of CryoVR that utilizes virtual reality to augment hands-on training of cryo-EM operations.

## CATHY LAWSON (RUTGERS UNIVERSITY)

Cathy Lawson's research explores the diverse landscape of biological structure-function relationships, with the goal of improving our fundamental understanding of life processes. Her current projects involve structure database development (EMDataResource, Nucleic Acid Database, Protein Data Bank), with emphasis on improving representation of large biological assemblies. They have developed an online curriculum, "PDB and Data Archiving," that introduces best practices in data resource management based on the extensive experience accumulated by the Research Collaboratory for Bioinformatics team.

## FRED SIGWORTH (YALE UNIVERSITY)

Fred Sigworth studied applied physics at Caltech and was a graduate student at Yale, working in the neuroscience laboratory of Charles F. Stevens. He received the PhD in physiology from Yale in 1979 and was a postdoc in the laboratory of Erwin Neher in Göttingen, Germany where he was a co-developer of patch-clamp techniques for single-channel electrophysiology. He returned to Yale as a faculty member at Yale in 1984. His current research is in the structural biology of ion-channel proteins, making use of novel cryo-EM methods. "How do I see the scientific enterprise? An old book puts it this way: one generation commends God's works to another. It is a great privilege to unravel the workings of ion channels, and to pass on the excitement about these molecular machines to students, colleagues and anyone else who will listen!"

## TOM WALZ (ROCKEFELLER UNIVERSITY)

Tom Walz uses cryoEM to study the structure and dynamics of proteins within the membrane, and to visualize the effects that lipids and other membrane characteristics exert on these proteins. His earlier work includes the use of electron crystallography to determine the structure of the archetypal water channel, aquaporin-1, and as an approach to study how membrane proteins interact with their annular lipids.

His research group uses nanodiscs to visualize lipid-induced conformational changes in membrane proteins, asking, for example, whether the thinning of a membrane is sufficient to open certain channels. He is also investigating other membrane-related processes, such as membrane repair and vesicular transport. For example, they are exploring how multisubunit tethering complexes help ensure that transport vesicles fuse with the appropriate target membrane.

https://www.rockefeller.edu/our-scientists/heads-of-laboratories/1124-thomas-walz/

## ORGANIZERS AND CENTER STAFF

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

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.

https://nccat.nysbc.org

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

Christina is NCCAT's embedded scientist liaison, which serves as a main point of contact for our visiting embedded trainees and cross-training programs, ensuring 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 further the mission of training researchers to be independent users of EM techniques, with broad impact in the biomedical sciences.

https://cryoemcenters.org

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

Mahira is NCCAT's research associate and lead teaching assistant (TA) for our embedded cross-training programs. For our instrumentation access she assists with our General User Proposal programs which includes Krios data collection access and staff-assisted use of Chameleon, a blot-free sample preparation device. 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 one of our TAs for the short course she will be on hand to ensure all our trainees are always supported in their journey into the art and science of cryoEM.

## WILLIAM “CHASE” BUDELL (SEMC/NEW YORK STRUCTURAL BIOLOGY CENTER)

Chase is the lead application scientist for the National Resource for Molecular Microscopy (NRAMM). He is focused on new applications in automating sample preparation to ensure high throughput and reproducibility. His toolkit includes assaying EM readiness of samples though mass photometry (Refeyn), multi-specimen screening within a single grid (Scorpion), and time resolved cryoEM (Spotiton). By leveraging his molecular biology and biochemical background he is able to accelerate the research for scientists in all scientific fields through electron microscopy. Have a biological question that needs the rigor of EM? You’ve found your champion!

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

Elina is NCCAT’s Traffic Controller (TC), user coordinator 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.

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

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.