NCEMS

National Synthesis Center for Emergence in the Molecular and Cellular Sciences

First Annual Summit Meeting

October 6th – 9th 2024

Chicago, USA

INDEX

INTRODUCTION

It is our pleasure to welcome you to the first annual NCEMS Summit meeting.

Our goal at this Summit is to identify the most critical questions surrounding emergent phenomena at the mesoscale. We have brought together a diverse group of scientists & trainees with unique perspectives and expertise. Your participation is crucial in making this a productive meeting that builds the foundations of NCEMS and its future activities.

We encourage you to engage actively with your fellow attendees, share your ideas, and participate fully in each session. This is an opportunity to shape the future directions of research into emergence at the mesoscale.

The key outcomes of this Summit meeting are team-based "proto-proposals" to address research questions that are primed for community-scale synthesis efforts, and community input on the NCEMS strategic plan. We hope that you will make new connections to form teams around specific questions, and, after the meeting, that you will take those proto proposals and apply to form an NCEMS-supported Working Group (deadline January 2025), with the first Working Groups starting in March 2025.

Thank you for joining us at this important Summit. We look forward to stimulating and productive sessions, and to the collaborations and new science that will emerge from our collective efforts.

Kim Reynolds, Organizing Committee, UT Southwestern

Dave Thirumalai, Organizing Committee, UT Austin

Sucheol Shin, Organizing Committee, UT Austin

Jerry Dinan, Organizing Committee, UT Southwestern

Ed O'Brien, NCEMS Director, Penn State University

CODE OF CONDUCT

Dear NCEMS Summit 2024 participants,

We are thrilled to welcome you to the first annual NCEMS Summit! We look forward to your active participation and hope that this event will be an enriching experience for all. As a community committed to fostering collaborative and innovative scientific dialogue, we are dedicated to ensuring a respectful and productive environment for every attendee.

The NCEMS community is committed to providing a safe and productive environment that promotes idea generation and rigorous scientific discussion amongst all participants. This means that our meeting must be free of harassment and provide equal opportunity and treatment for all participants. Behavior that is acceptable to one person may feel unacceptable or uncomfortable to another, including harassment intended in a joking manner. Please choose your actions to indicate respect.

While you are attending the NCEMS Summit, you may discuss any issues you encounter with our ombudsmen. They are available to assist with non-urgent matters, such as interpersonal conflicts, concerns about respectful behavior, or questions regarding event policies. Please note that the ombudsmen are not emergency responders but are here to support you in maintaining a positive experience during the Summit.

Ombudsmen: Melanie McReynolds (mcreynolds@psu.edu), Rick Gilmore (rog1@psu.edu)

In joining us for this meeting, you agree to abide by the below code of conduct and confidentiality statements:

This event is supported by the NSF under Award No. 2335029 and is governed by the NSF PAPPG 23-1, which came into effect on January 30, 2023. This guide requires that we provide all event participants with information on Penn State University policies on sexual harassment, other forms of harassment, and sexual assault, as well as information about how to report any violations of such policies. For purposes of this requirement, “other forms of harassment” is defined as “non-gender or non-sex-based harassment of individuals protected under federal civil rights laws, as set forth in organizational policies or codes of conduct, statutes, regulations, or executive orders.”

Penn State University is committed to maintaining a community that is dedicated to the advancement of knowledge and creative endeavors through academic excellence, where all individuals who participate in Penn State activities can work and learn in an environment free of harassment, exploitation, or intimidation.

CODE OF CONDUCT (CONTINUED)

Policy AD91 Discrimination and Harassment prohibits discrimination and/or harassment against any person because of their actual or perceived age, race, color, ancestry, national origin, sex, sexual orientation, gender, gender identity, physical or mental disability, religion, creed, service in the uniformed services, veteran status, marital or family status, pregnancy-related conditions, genetic information, or political ideas.

Policy AD85 Title IX Sexual Harassment prohibits sexual harassment and misconduct, including sexual violence, domestic violence, and stalking, in accordance with Title IX of the Education Amendments of 1972.

These policies apply to all Penn State University campuses, programs, and activities, including this Summit. Penn State University will respond promptly and effectively to reports of Prohibited Conduct and take action to prevent, stop, and remedy conduct violations.

Resources are available to report different types of misconduct; most reporting options offer the ability to remain anonymous. If you feel you or someone else is in immediate danger, please call 911. Anyone may report sexual harassment, discrimination, or sexual violence to the Office of Ethics and Compliance.

Finally, maintaining confidentiality is crucial to fostering open and candid discussions at the Summit. The use of electronics to record presentations and other sessions is prohibited, including audio, video, and photographic means. Posting the ideas discussed at the meeting on the internet, social media, or referencing such results in publications is prohibited, as it may compromise the intellectual property of participants and the collaborative nature of the event.

We thank you for your cooperation in upholding these standards and for contributing to a respectful, productive, and inspiring environment. We look forward to the ideas and collaborations that will emerge from this Summit and are excited to see the impact of your participation.

SUNDAY, OCTOBER 6TH

TIME	EVENT	LOCATION
12:00 – 1:00 pm	**Trainee Lunch**	On your own
1:00 – 4:00 pm	**Build a Better Network** **Presented by: Brian Uzzi**	Coleman B/C
4:00 – 5:00 pm	**Break**	Any
5:00 – 6:00 pm	**Opening Ceremony** **Presented by: Melanie McReynolds, Ed O'Brien, Kim Reynolds, & Dave Thirumalai**	Coleman B/C
6:00-6:30 pm	**Reception** *Drink tickets*	International Ballroom
6:30 – 8:00 pm	**Dinner** *Assigned seating*	International Ballroom

MONDAY, OCTOBER 7th

TIME	EVENT	LOCATION
7:30 – 8:45 am	**Breakfast**	International Ballroom
9:00 – 9:15 am	**Opening Remarks** **Presented by: Kim Reynolds**	International Ballroom

Posing the Problem Sessions 1-5

	1	2	3	4	5
9:15 – 11:15 am	*Comprehensive identification of metabolic drivers of aging* **Melanie McReynolds**	*Reconstruction of quinary interaction networks* **Eugene Shakhnovich**	*Towards integrative analyses of multi-omics data* **Vasant Honavar**	*Emergent cytoskeletal dynamics: integrating data from molecules to tissues* **Adriana Dawes**	*Probing biomolecular condensates across spatiotemporal scales* **Jerelle Joseph**
	Coleman B	Coleman A	Orchard	Lakeshore	Chicago

11:15 – 11:45 am	**Coffee Break**	Coleman C

Strategic Implementation Plan Sessions 1-3

	1	2	3
11:45 am – 1:00 pm	*Team science best practices* **Brian Uzzi, Brian Manata, & Ed O'Brien**	*Open science implementation best practices* **Nirav Merchant & Justin Petucci**	*Inclusive communities outreach activities* **Justin Graham & Camelia Kantor**
	Inclusive communities outreach activities **Justin Graham & Camelia Kantor**	*Team science best practices* **Brian Uzzi, Brian Manata, & Ed O'Brien**	*Open science implementation best practices* **Nirav Merchant & Justin Petucci**
	Chicago	Orchard	Coleman B

MONDAY, OCTOBER 7th (CONTINUED)

TIME	EVENT					LOCATION
1:00 – 2:00 pm	**Lunch**					International Ballroom
2:00 – 4:00 pm	**Posing the Problem Sessions 6-10**					
	6	**7**	**8**	**9**	**10**	
	Enhancing data reuse through quality certification of public datasets	*Learning cell dynamics from quantitative imaging*	*Genome organization*	*Integrative modeling of evolutionary and ecological dynamics in emerging high throughput data*	Protein structure, dynamics, networks and expression across cells and species	
	Wout Bittremieux	**Margaret Gardel**	**Bin Zhang**	**Soojin Yi**	**Ed O'Brien**	
	Coleman B	Coleman A	Orchard	Lakeshore	Chicago	
4:00 – 5:00 pm	**Break**					Any
5:00 – 6:30 pm	**Social Hour & Entertainment** *Orchestrating Leadership* **Presented by: Dr. Stephen Alltop**					Coleman B/C
6:30 – 8:00 pm	**Dinner**					International Ballroom

NCEMS Summit 2024 - Program

TUESDAY, OCTOBER 8th

TIME	EVENT	LOCATION
7:30 – 8:45 am	**Breakfast**	International Ballroom
9:00 – 9:15 am	**Opening Remarks** **Presented by: Dave Thirumalai**	International Ballroom

Posing the Problem Sessions 11-15

9:15 – 11:15 am	11	12	13	14	15
	Physicochemical adaptation of intrinsically disordered regions to distinct environments	*Empirical laws in bacteriology*	*Foundation models in molecular biology*	*Systematic reanalysis of the crosslinking mass spectrometry universe*	*Learning and comparing biological networks across cell types, tissues, organs, and species*
	Dave Thirumalai	**Kim Reynolds & Jeremy Schmit**	**Vasant Honavar**	**Stephen Fried**	**Anshul Kundaje**
	Coleman B	Coleman A	Orchard	Lakeshore	Chicago

11:15 – 11:45 am	**Coffee Break**	Coleman C

Strategic Implementation Plan Sessions 4-6

11:45 am – 1:00 pm	4	5	6
	Authorship credit best practices	*Data integration best practices*	*National remote research experience logistics*
	Nicole Lazar & Camelia Kantor	**Tyson Swetnam & Justin Petucci**	**Melanie McReynolds & Ed O'Brien**
	Data integration best practices	*National remote research experience logistics*	*Authorship credit best practices*
	Tyson Swetnam & Justin Petucci	**Melanie McReynolds & Ed O'Brien**	**Nicole Lazar & Camelia Kantor**
	Chicago	Orchard	Coleman B

TUESDAY, OCTOBER 8th (CONTINUED)

TIME	EVENT	LOCATION
1:00 – 2:00 pm	**Lunch**	International Ballroom
2:00 – 2:45 pm	**Round Robin of Top Questions**	Coleman B/C
2:45 – 3:00 pm	**Participants Select #1 Question** *Form groups*	Coleman B/C
3:00 – 3:30 pm	**Groups Create Pitch Slides**	Coleman A, Coleman B/C, Chicago, Orchard, Lakeshore
3:30 – 3:45 pm	**Break**	Any
3:45 – 5:00 pm	**Pitch Presentations** *15 min per pitch*	Coleman A, Coleman B/C, Chicago, Orchard, Lakeshore
5:00 – 6:30 pm	**Social Hour & Entertainment** *Drink tickets*	Coleman B/C
6:30 – 8:00 pm	**Dinner**	International Ballroom

WEDNESDAY, OCTOBER 9th

TIME	EVENT	LOCATION
7:30 – 8:30 am	**Breakfast**	Food in Orchard Dining in Coleman B/C
9:00 – 9:15 am	**Opening Remarks** **Presented by: Kim Reynolds**	Coleman B/C
9:15 – 9:30 am	**Last-Minute Pitch Presentations**	Coleman B/C
9:30 – 10:30 am	**Write Proto-proposal**	Coleman B/C
10:30 – 11:15 am	**Give Written Proto-proposal Feedback**	Coleman B/C
11:15 – 11:45 am	**Coffee Break**	Coleman B/C
11:45 am – 12:45 pm	**Lunch**	Food in Orchard Dining in Coleman B/C
12:45 – 1:30 pm	**Update Proto-proposals**	Coleman B/C
1:30 – 1:45 pm	**Next Steps & Closing Remarks** **Presented by: Ed O'Brien, Kim Reynolds, Dave Thirumalai**	Coleman B/C

DETAILED SESSION DESCRIPTIONS

POSING THE PROBLEM FORMAT

Each participant will take part in three Posing the Problem sessions. The purpose of each brainstorming session is to identify the set of key open questions in each area that are primed for community-scale synthesis efforts. During your discussions, do not worry if you are unsure if certain data exists – NCEMS can help determine this after the Summit if you choose to apply to form a Working Group. Instead, focus on determining the synthesis research questions that would most significantly drive the field forward and the data you would need to answer them. Each Posing the Problem session will have the following schedule:

5 min	**Introduction**	Session lead provides a brief overview of the format, goals, and topics for this session.
3 min	**Transition to Triads**	Participants are randomly broken into groups of three.
10 min	**Brainstorming**	Each triad rapidly generates as many possible synthesis research questions as possible and then selects their top 1 or 2 questions.
15 min	**Report Back**	Each triad shares their top 1 or 2 questions with the entire group. One person from each triad writes these top 1 or 2 questions on sticky notes and turns them in to the session lead.
15 min	**Break**	Participants take a 15-min break while the session lead identifies four themes emerging from the questions.
3 min	**Transition into 4 Groups**	Participants choose one of 4 groups, with one group per theme
47 min	**Idea Refinement**	Participants answer the following questions: (1) What are the key synthesis questions in this theme? (2) How will the answers to these questions advance the field? (3) What computational methodologies could be used to answer these questions? (4) What datasets are available or needed to address these questions? Each research question and additional details will be written on a notecard, with each group producing 2-3 notecards.
22 min	**Idea Sharing, Feedback, and Action**	*Sharing*: One person from each group takes 3.5 minutes to present no more than 2 key questions. *Feedback*: All participants have 90 s to ask questions. *Action*: One group member uploads the 1-2 refined questions, significance statements, and potential data to Qualtrics.

DETAILED SESSION DESCRIPTIONS (CONTINUED)

POSING THE PROBLEM SESSIONS 1-15

1 - Comprehensive identification of metabolic drivers of aging – Led by Melanie McReynolds. This session will explore computational strategies for analyzing multi-omics and single-cell data to identify common metabolic drivers of aging and disease, with the goal of identifying targetable metabolic vulnerabilities. How such data can answer new questions into the origins of aging and disease will be discussed.

2 - Reconstruction of quinary interaction networks – Led by Eugene Shakhnovich. AlphaFold's success in using evolutionary covariation to predict protein structures raises the question of whether similar sequence covariations across different proteins can reveal quinary-level organization. Systematic proteome-wide alignments, especially in bacteria, could offer new insights into evolutionary inter-dependencies, interaction networks, and opportunities for identifying and optimizing metabolic circuits.

3 - Towards integrative analyses of multi-omics data – Led by Vasant Honavar. Current multi-omics approaches often analyze data modalities separately, ignoring the intricate interactions within biological systems. This session will explore the computational methodologies required to truly combine omics data, overcoming key computational challenges to obtain insights from all data modalities jointly.

4 - Emergent cytoskeletal dynamics: integrating data from molecules to tissues – Led by Adriana Dawes. This session will discuss integrating research on cytoskeletal dynamics across scales from single molecules to tissues to explore how continuous variables from diverse data sources reveal emergent structures essential for cell and tissue function. Key aspects include: How to extract continuous variables from disparate data sources across scales, how these variables inform the formation of large-scale emergent cytoskeletal structures, and how these structures function to ensure proper cell and tissue function.

5 - Probing biomolecular condensates across spatiotemporal scales – Led by Jerelle Joseph. In this session, we will define synthesis questions about the spatiotemporal dynamics of biomolecular condensates, focusing on their formation, regulation, and functional implications through advanced imaging, biophysical approaches, and computational modeling.

6 - Enhancing data reuse through quality certification of public datasets – led by Wout Bittremieux. The aim of this session is to identify specific opportunities to develop and implement data quality badges for quality assurance and quality control across omics and other data modalities to enhance the visibility and standardized evaluation of underutilized but high-quality datasets, promoting their broader reuse and improving research integrity.

7 – Learning cell dynamics from quantitative imaging – Led by Margaret Gardel. Many of our most powerful methods for probing cells at the mesoscale involve imaging. This session will examine how images can be mined to create multidimensional datasets suitable for quantitative, top-down modeling of cells.

8 - Genome organization – Led by Bin Zhang. This session will explore opportunities for synthesis of genome organization data and models across spatial and temporal scales for multiple species spanning yeast to human genomes, and how multiple scales, various modeling and experimental approaches, and the combination of modeling and experimentation must be synthesized and combined to deduce genome structures, dynamics, and biological mechanisms.

DETAILED SESSION DESCRIPTIONS (CONTINUED)

9 - Integrative modeling of evolutionary and ecological dynamics in emerging high throughput data – Led by Soojin Yi. This session will discuss bridging the gap between evolutionary and ecological models by integrating population genetics and ecological approaches to better understand microbial evolution, leveraging data including community abundance time-series, lineage tracking, and 16S rRNA profiling.

10 - Protein structure, dynamics, networks and expression across cells and species – Led by Ed O'Brien. This session will explore how we can utilize the diverse data on protein structure, function, dynamics, and expression levels across cell types and species to uncover conserved features, causal mechanisms, and develop models linking these diverse multiscale data.

11 - Physicochemical adaptation of intrinsically disordered regions to distinct environments – Led by Dave Thirumalai. This session will explore the conservation of physicochemical properties in intrinsically disordered regions (IDRs) across organisms, focusing on their ecological adaptation to different environments. Addressing community-scale synthesis questions in this area will need diverse expertise including biophysicists, computational biologists, and evolutionary/ecological scientists, potentially aligning with NSF's NEON and WALII programs.

12 - Empirical laws in bacteriology – Led by Kim Reynolds & Jeremy Schmit. Recent years have seen an expansion in quantitative microbial physiology data, including growth rate measurements, transcriptomics, metabolomics and ribosome profiling across varied media types and stress conditions. This session will identify community-scale synthesis questions concerning how these dense, multidimensional microbial data can reveal emergent principles in bacterial function, metabolism, and growth.

13 - Foundation models in molecular biology – Led by Vasant Honavar. Foundation models like AlphaFold, ProteinBERT, and DNABERT are trained on relatively unstructured data to capture core features of complex phenomena. In this session, we will identify opportunities to create and integrate foundation models across various biological scales to address domain-specific problems and reduce training costs.

14 - Systematic reanalysis of the crosslinking mass spectrometry universe – Led by Stephen Fried. Crosslinking mass spectrometry (XL-MS) data remain underutilized despite their availability in proteomics repositories. This session will discuss leveraging new approaches and algorithms that make systematic reanalysis feasible, potentially uncovering global protein interactions, new sub-networks, condensates, and metabolons across species.

15 - Learning and comparing biological networks across cell types, tissues, organs, and species – Led by Anshul Kundaje. This session will explore what new insights community-scale synthesis might reveal by utilizing broad classes of models, including statistical and machine learning approaches, to compare biological systems across conditions, tissues, and species.

DETAILED SESSION DESCRIPTIONS (CONTINUED)

BUILD A BETTER NETWORK: RAISE WHAT YOU KNOW TO THE POWER OF WHO YOU KNOW.

Presented by: Brian Uzzi

Personal expertise is a cornerstone of scientific success, yet it overlooks the value of social capital. The powerful, unseen resource through which thriving leaders in science access unique resources, innovate, deepen collaborations, and mobilize support for their best ideas. Nevertheless, many leaders inadvertently build weak networks. This presentation explains the scientifically grounded principles for developing an influential network by "Raising what you know to the power of who you know."

ORCHESTRATING LEADERSHIP

Presented by: Dr. Stephen Alltop, Bienen School of Music

The interactive experience of *Orchestrating Leadership* offers perspectives on leadership and communication from the context of the professional symphony orchestra. Conductors must inspire highly skilled musicians toward unified goals using a wide variety of skills, knowledge and insights. Important topics will include the critical roles that preparation and vision play in the work of orchestral conductors, and the many parallels that exist between musical ensembles and other organizations. A chamber orchestra of accomplished musicians will add perspectives about leadership traits that allow them to perform at their highest level.

STRATEGIC IMPLEMENTATION PLAN FEEDBACK SESSIONS 1-6

Each participant will take part in four sessions over two days to provide feedback and input on specific aspects of the NCEMS Strategic Implementation Plan. This document will be updated and finalized based on this feedback. The strategic plan is a critical document with both public and internal components that describes the mission, vision, and values of the Center in addition to all of NCEMS' specific goals and timelines surrounding its activities.

1 – Team science best practices – led by Brian Uzzi, Brian Manata, & Ed O'Brien. Team science is at the heart of NCEMS' approach to synthesis research. This session will present plans for team science standards, management, and logistics within the Center.

2 – Open science implementation best practices – led by Nirav Merchant & Justin Petucci. Open science is a key part of NCEMS' mission. In this session, participants will provide feedback on the Center's plans for open science training, standards, and incentives.

3 – Inclusive communities outreach activities – led by Justin Graham & Camelia Kantor. One of the key aspects of NCEMS' training and teaching goals is providing opportunities to underserved groups. Participants will provide feedback on the plan for incorporation of minority-serving institutions and the undergraduate summer research experience at Penn State into NCEMS.

DETAILED SESSION DESCRIPTIONS (CONTINUED)

4 – Authorship credit best practices – led by Nicole Lazar & Camelia Kantor. In this feedback session, participants will have the opportunity to provide suggestions and ideas for NCEMS' proposed authorship credit policies before the formation of the first Working Groups.

5 – Data integration best practices – led by Tyson Swetnam & Justin Petucci. NCEMS seeks to provide harmonized data from diverse sources to lower barriers to synthesis research. In this session, you will provide feedback on current plans for making intermediate data products available on CyVerse.

6 – National remote research experience logistics – led by Melanie McReynolds & Ed O'Brien. The national remote research experience will incorporate students from across the USA into synthesis research projects. This session will provide a mechanism for feedback on logistical plans for the recruitment and matching of undergraduate students with mentors as well as the management of research activities.

ROUND ROBIN OF TOP QUESTIONS

Each Posing the Problem session will generate a set of 4-8 key synthesis questions, for a total of 60-120 questions across all 15 sessions. Participants will vote online for their top questions, and the 20-30 questions that emerge from this voting process will then move forward to the Round Robin. The 20-30 questions will be written on easel boards spread around Coleman B/C and participants converge on their top question in two phases:

Phase 1 (45 min): Participants spend 15 min at each of their top 3 questions and discuss with participants at that easel.

Phase 2 (15 min): Participants go to their #1 question and discuss if they are interested in that question as posed, or whether some are interested in further refining the question. Based on this discussion, the group decides if they should prepare a pitch slide as one group or split into two or more groups.

PITCH SLIDES AND PRESENTATION

After choosing their top question during the Round Robin, participants can join a group and begin working on pitch slides to present to the Summit. These slides will follow the below template to provide a brief summary of the proposed synthesis question, the potential impacts of answering it, and any missing expertise in their nascent team. These slides are then presented during the pitch presentations (10 min + 5 min Q&A.)

PROTO-PROPOSALS

After presenting their pitch slides on Tuesday, groups will then write a 1–2 page proposal outlining their idea in more detail on Wednesday morning. These proto-proposals will follow the template linked below. Other attendees will then provide written feedback on three proto-proposals. The Summit will conclude with a 45-min update period for groups to receive feedback from other participants. These proto-proposals, which may form the beginnings of a formal NCEMS Working Group proposal, are the key outcome of the Summit.

PARTICIPANT INFORMATION

INDEX	NAME	AFFILIATION	EXPERTISE	EMAIL
1	Ashif Akram	Kansas State University	Thermodynamics, biophysics, spacer-sticker theories	akram.a0@gmail.com
2	Kaustubh Amritkar	University of Wisconsin-Madison	Protein structure evolution	amritkar@wisc.edu
3	Samina N. Assanie-Shivji	Claflin University	Apoptosis, CRISPR-Cas editing, knockout, miRNA therapeutics	shassanali@claflin.edu
4	Ferhat Ay	La Jolla Institute for Immunology	Bioinformatics, epigenetics, genome organization	ferhatay@lji.org
5	Priyanka Banerjee	Iowa State University	Artificial intelligence	pb11@iastate.edu
6	Jeff Barrick	UT Austin	Synthetic biology, experimental evolution	jbarrick@cm.utexas.edu
7	Victoria Baskerville	Penn State University	Metabolomics, aging, NAD+	vrb5159@psu.edu
8	Wout Bittremieux	University of Antwerp	Mass spectrometry, proteomics, metabolomics	wout.bittremieux@uantwerpen.be
9	David Blehi	Penn State University	Event coordinator	dmb385@psu.edu
10	Steven Boeynaems	Baylor College of Medicine	Condensates, tandem repeats, stress response, neurodegeneration	steven.boeynaems@bcm.edu
11	Dante Bolzan	La Jolla Institute for Immunology	Bioinformatics, deep learning, epigenomics	dbolzan@lji.org
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16	Ananya Chakravarti	Princeton University	Biomolecular condensates, computer simulations	ananyac2000@princeton.edu
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21	Valerie de Crecy-Lagard	University of Florida	Bioinformatics, unknowns, genetics	vcrecy@ufl.edu
22	Jerry Dinan	UT Southwestern Medical Center	Protein design, evolution, proteomics	jerry.dinan@utsouthwestern.edu
23	Laura Domínguez	Universidad Nacional Autónoma de México	Simulation, proteins, biophysics	lauradd@unam.mx
24	Maowei Dong	Penn State University (NCEMS)	Project management, communication, organization	mvd6246@psu.edu

PARTICIPANT INFORMATION (CONTINUED)

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26	Stephen D Fried	Johns Hopkins University	Protein folding, mass spec proteomics	sdfried@jhu.edu
27	Iddo Friedberg	Iowa State University	Protein function, bacterial genomics	idoerg@gmail.com
28	Margaret Gardel	University of Chicago	Mechanobiology, cell dynamics, cytoskeleton	gardel@uchicago.edu
29	Kelsey Gasior	University of Notre Dame	Phase separation, cellular dynamics, epithelial mesenchymal transition	kgasior2@nd.edu
30	Anupam Gautam	University of Tübingen	Microbiome, algorithms, metagenomics, bioinformatics	anupam.gautam@uni-tuebingen.de
31	Rick Gilmore	Penn State University	Open science, data sharing, reproducibility, Quarto	rog1@psu.edu
32	Muskan Goel	Purdue University	Membrane proteins, translocon	goel107@purdue.edu
33	Theresa Good	National Science Foundation	Molecular and Cellular Biosciences Division	tgood@nsf.gov
34	Vera Gorbunova	University of Rochester	Aging, longevity, comparative biology	vera.gorbunova@rochester.edu
35	YiFei Gou	Clemson University	Bioinformatics, machine learning, PPI	ygou@clemson.edu
36	Justin Graham	Fayetteville State University (NCEMS)	Microbiologist	jwgraham01@uncfsu.edu
37	Danielle Graham	Fayetteville State University	Microbiology	degraham@uncfsu.edu
38	Janne Heirman	University of Antwerp	Computational mass spectrometry, ML	janne.heirman@uantwerpen.be
39	Chris Henry	Argonne National Laboratory	Comparative genomics, metabolic modeling, cellular community modeling	chenry@anl.gov
40	Henning Hermjakob	EMBL-EBI	Biomolecular networks, proteomics, databases	hhe@ebi.ac.uk
41	Manju Hingorani	National Science Foundation	Molecular and Cellular Biosciences Division	mhingora@nsf.gov
42	Antentor "AJ" Hinton	Vanderbilt University	Mitochondria, imaging, electron microscopy	antentor.o.hinton.jr@vanderbilt.edu
43	Vasant G Honavar	Penn State University (NCEMS)	AI, ML, data science, bioinformatics	vuh14@psu.edu
44	David Hubert	Oregon State University	Molecular biology, experimental evolution	david.hubert@oregonstate.edu
45	Ankur Jain	Whitehead Institute	RNA biology, phase separation, fluorescence microscopy	ajain@wi.mit.edu
46	Ivana Jelic	Chan Zuckerberg Initiative	Machine learning, AI, biology, evals	ijelic@chanzuckerberg.com
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PARTICIPANT INFORMATION (CONTINUED)

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49	Graham Johnson	Allen Institute for Cell Science	Generalist, multiscale modeling, FAIRness	grahamj@alleninstitute.org
50	Jerelle Joseph	Princeton University	Biomolecular condensates, molecular simulations	jerellejoseph@princeton.edu
51	Suckjoon Jun	UC San Diego	Single-cell physiology, imaging	s2jun@ucsd.edu
52	Betül Kaçar	University of Wisconsin - Madison	origins of life, metabolism, ancestral sequences, molecular evolution	bkacar@wisc.edu
53	Camelia Kantor	Penn State University (NCEMS)	Assessment, education, broader impacts, management	cmk6719@psu.edu
54	Kalli Kappel	Broad Institute of MIT and Harvard	Computational modeling, RNA structure, disordered proteins, condensates	kkappel@broadinstitute.org
55	Natalia Kravtsova	The Ohio State University	Applied mathematics, data science, optimal transport	kravtsova.2@buckeyemail.osu.edu
56	Anshul Kundaje	Stanford University	Regulatory genomics, deep learning	akundaje@stanford.edu
57	Stewart Lamerdin	National Science Foundation	Division of Biological Infrastructure	slamerdi@nsf.gov
58	Keren Lasker	The Scripps Research Institute	Condensates, microbiology, bioengineering, cryo-EM	klasker@scripps.edu
59	Nicole Lazar	Penn State University (NCEMS)	Statistics, data science, open science	nfl5182@psu.edu
60	Zilong Li	New York University	Chromatin modeling, Brownian dynamics	zl3765@nyu.edu
61	Junlang Liu	Harvard University	Experimental & theoretical biophysics	junlangliu@fas.harvard.edu
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