Society of Biomolecular Imaging & Informatics 2026

SBI2's 13th Annual Conference

Renaissance Boston Waterfront, Boston, MA, USA

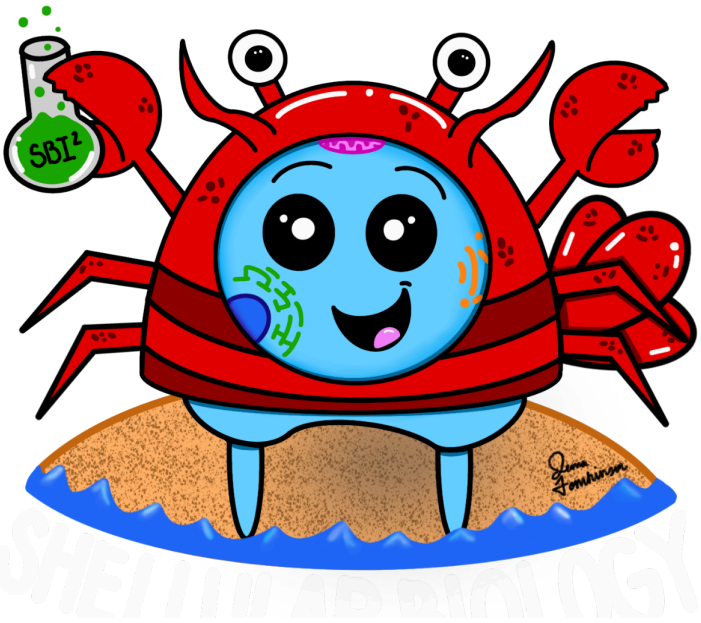
November 2nd-4th, 2026

Program & Events Guide



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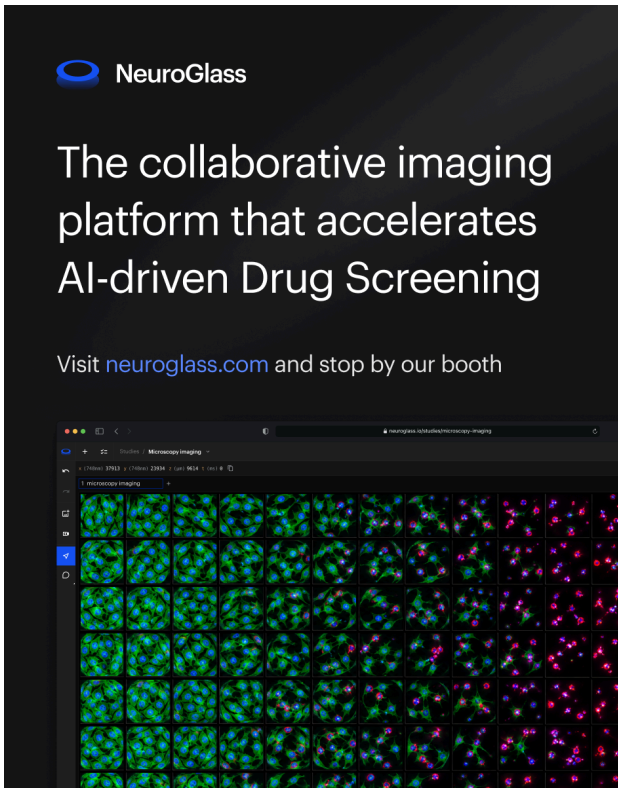
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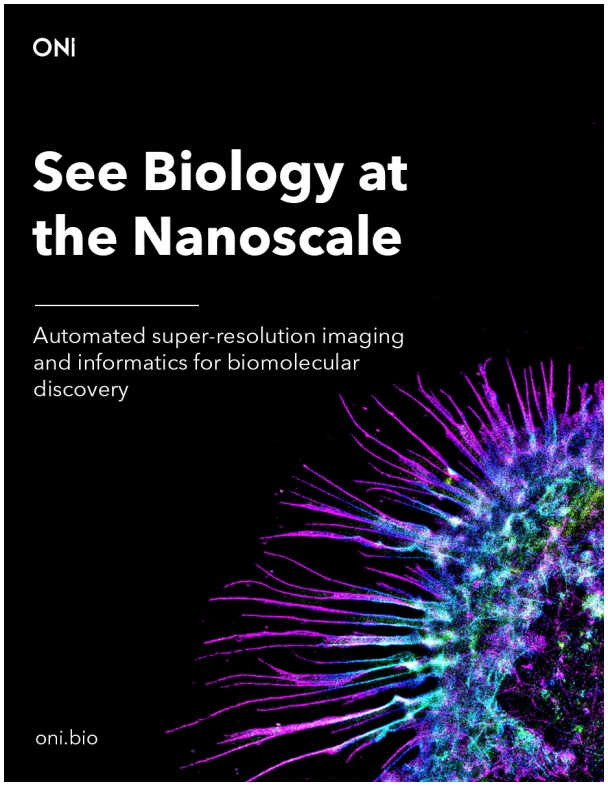
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Glencoe SOFTWARE	Glencoe Software builds and delivers innovative, scalable, easy-to-use scientific imaging solutions for its clients and partners. Our proven image database technology, OMERO Plus, makes the viewing, sharing, analysis and management of large sets of images and metadata easy and accessible to everyone in a group, team, project or organization.
SAGUARO Biosciences	Saguaro is the leading platform for high-fidelity cell data. Our proprietary non-toxic dyes deliver deeper biological insights through rich, unperturbed images of cells, and our live-cell profiling platform combining wet lab imaging and AI-powered analysis helps pharma, biotech, and AI labs better prioritize drug candidates with the richest cell data.
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NeuroGlass	MetaCell builds life science software trusted by the Allen Institute, CZI, Natus, Biogen and J&J. Our platform, NeuroGlass, makes terabyte-scale high-content imaging data AI-ready. Open your studies in the browser, annotate, filter, review and collaborate with your team from anywhere. No downloads, no bottlenecks. Just faster drug screening decisions.
cellanome	Cellanome develops tools that enable researchers to observe how living cells behave, interact, and change over time, while connecting those dynamics with molecular measurements from the same cells.


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President's Welcome

Dear Colleagues and Friends,

Welcome to the 13th Annual Conference of the Society of Biomolecular Imaging and Informatics in Boston, MA! On behalf of the SBI² Board members, councilors, and volunteers, I am delighted to welcome you back for another exciting year of scientific discovery, collaboration, and connection.

This year's program reflects how quickly our field continues to evolve. Our educational courses and hands-on workshops cover everything from the fundamentals of high content imaging to advanced bioimage analysis, complex biological models, and emerging AI-driven tools. Our scientific sessions will follow the discovery process, from advances in cellular models and imaging technologies to image analysis and translating increasingly rich biological data into meaningful insights. We're especially excited to welcome back the CytoData Hackathon and introduce a new colloquium, "AI Today: The Good, The Bad, and The Ugly," which promises to spark some interesting conversations! We're also honored to welcome keynote speakers Dr. Emma Lundberg and Dr. Derek Lowe, bringing perspectives on bioimaging, AI, and modern drug discovery.

Beyond the annual conference, this has been an exciting year for SBI²! In July, we hosted our **first-ever European Regional Meeting** in Cambridge, UK. The enthusiasm, scientific discussions, and new connections were a wonderful reminder of the global reach of the SBI2 community. I'm incredibly grateful to our European organizing committee and volunteers for making this inaugural event possible and excited to build on this momentum!

We've also been working to strengthen SBI²'s future by expanding corporate sponsorships. These relationships help us support educational initiatives and create opportunities for scientists at every career stage. I want to extend a special thank you to our longstanding corporate partners, the new organizations joining our community, and the volunteers building these relationships.

At its heart, SBI² remains a Society built on the passion and generosity of its volunteers and a shared commitment to advancing science through collaboration, innovation, and education. As we continue to grow, preserving that sense of community remains incredibly important. Whether this is your first SBI² conference or you have been part of our community for years, I hope you take full advantage of the opportunities to learn, share ideas, reconnect with colleagues, and make new friends. Some of the most valuable parts of these meetings happen in the conversations between sessions, over posters, or in the exhibit hall!

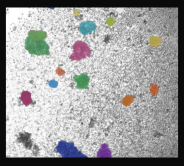
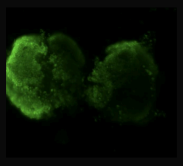
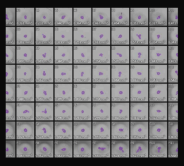
Thank you to everyone who has contributed to making this year such an exciting one for SBI², and thank you all for being here. I look forward to another wonderful conference and to seeing what we accomplish together in the year ahead!

Kind Regards,
Kristin Halfpenny, PhD
SBi2 2026 President

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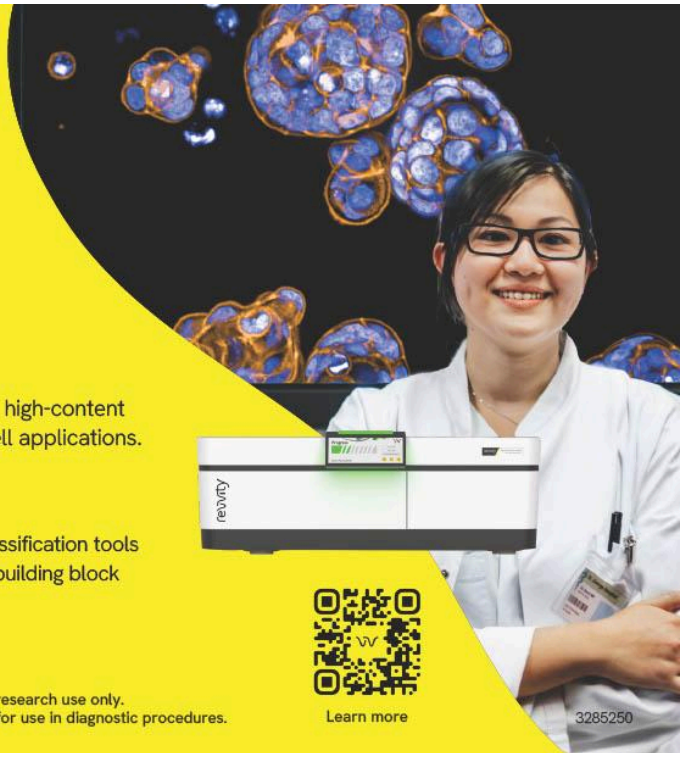
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About SBI2

The Society of Biomolecular Imaging and Informatics (SBI2) is an international community of leaders, scientists, and students promoting technological advancement, discovery, and education to quantitatively interrogate biological models to provide high-context information at the cellular level.

SBI2 Founders Message - a nod to history, State of the Society, and Welcome *Paul A. Johnston, Joe Trask, Mark Collins and Steve Haney*

Inaugural SBI2 High Content Cellular Imaging Symposium

North Carolina Biotech Center, RTP, NC, 11/10/2012



Left to right: Paul Johnston, Joe Trask, Mark Collins, Steve Haney

As founding members who participated in establishing SBI2 and leading its early development we've been asked to provide our perspective. SBI2 was boot-strapped by a grassroots movement of early adopters and experts in High Content Screening (HCS) technologies in the scientific community that routinely attended commercial scientific tradeshows or HCS specialized sessions at SLAS and ISAC (CYTO). Although these events helped highlight and bring the High Content community together it became apparent that the continued evolution of HCS would be better served by a professional society dedicated to highlighting the best and innovative science while providing educational resources to the community. In 2012 SBI2 was founded as a not-for-profit organization (501(c)3 status) with a culture grounded in the following core principles.

- **Volunteering & Affordability.** SBI2 was shaped by the passion of volunteer scientists and leaders who contributed their time and effort to emphasize high-quality cutting-edge

science while maintaining affordability for the community of students, young investigators, and professionals.

- **Rigor & scientific content**. In a rapidly evolving field encompassing multiple complex technologies (cellular technologies, microscopy principles, image analysis, assay validation, informatics, and data sciences), establishing and maintaining best practices was critical to advancing HCS science and its application to preclinical drug discovery. SBI2 addresses these needs through the educational programs and plenary sessions of its annual conferences, curated website content, and by peer-reviewed contributions to scientific literature.
- **Informatics.** When naming the society, initial emphasis was placed on biological aspects—hence terms like “Society of Biomolecular Imaging”. However, after some lively discussions (& a few beverages), we recognized the critical role of data analysis and added what has arguably become the most essential part of the SBI2 name: “informatics”. Since founding SBI2, informatics has evolved dramatically and now stands as a cornerstone of the entire HCS workflow.
- **Highlighting innovation**. SBI2 was founded with a commitment to drive innovation in the rapidly evolving fields of imaging and informatics. Our members actively champion the adoption and integration of emerging technologies, methodologies, and analytical approaches that push the boundaries of HCS. Through rigorous scientific exchange at annual conferences, publication of peer-reviewed research, and the development of accessible online resources, SBI2 serves as a catalyst for translating cutting-edge advancements into practical applications. This commitment ensures that SBI2 remains at the forefront of scientific discovery and technological progress.
- **Community & networking.** A founding strength of SBI2 is fostering collaborative networking alliances to advance science with global leaders of HCS technologies. These relationships have facilitated partnerships between academia, the pharmaceutical industry, and vendors, supporting career development for students and professionals in finding new positions or jobs and align with agencies to participate in “the standards” for the community.
- **Guidance & Educational Resources**. The SBI2 community offers guidance and educational materials to address many basic and fundamental questions in HCS. These include but are not limited to: how to design, develop, optimize and implement (automate) HCS assays; selection of appropriate HCS platforms and evaluation of what features or capabilities will be needed; considerations for using integrated image analysis software versus open-source image processing for data generation and analysis; best practices for applying appropriate statistical methods and quality control measures in HCS.
- **The Evolution of HCS.** The HCS field continues to evolve to more fully embrace and realize the “High Content” potential of these technologies. This progression includes the application of more complex cellular models, 3D biology, physiologically relevant primary cells, iPSCs, patient derived cells and organoids, spatial biology, digital histopathology, and the generation of big data from single cell analyses in HCS studies. Advanced microcopy techniques are being deployed to enable these analyses. Furthermore, image-based phenotypic and molecular profiling for drug discovery and toxicology are leveraging machine learning and AI-driven deep learning algorithms to analyze multiparametric data, address high dimensionality, and provide advanced visualization tools for interpretation.

A final message from the Founders. As founders, we take great pride in the remarkable growth and success of SBI2 and extend our deepest gratitude to the many individuals who have

generously volunteered their time and expertise since its inception. Their dedication has been instrumental in shaping SBI2 while upholding its core mission and principles.

Looking ahead, we must remain steadfast in ensuring that SBI2 continues to deliver access to high-quality, innovative science at a reasonable cost, while embracing the diversity of disciplines and contributors that make our community so vibrant.

Based on the commitment of our volunteers serving on the SBI2 Board and committees, the thoughtful planning of the 2026 Annual Conference, and the exceptional quality of the scientific program and educational offerings, we are proud to affirm that “the state of the society is strong.”

We warmly invite you to join us and contribute to the continued growth and future success of the SBI2 family.

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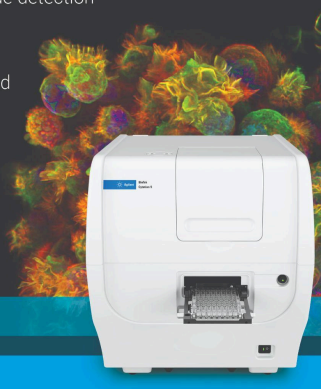
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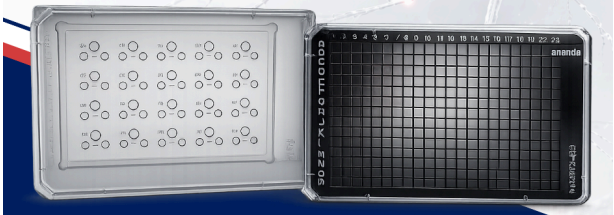
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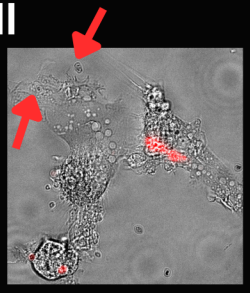
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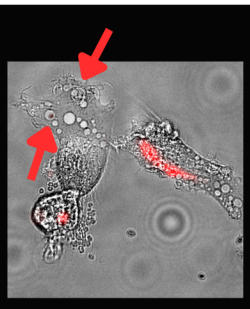
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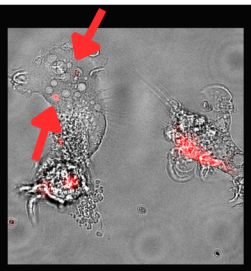
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Minute 40



Minute 44



Minute 48

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SBI2 Leadership

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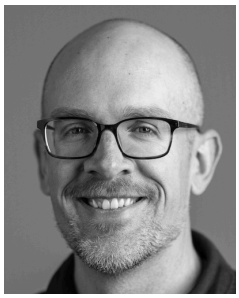
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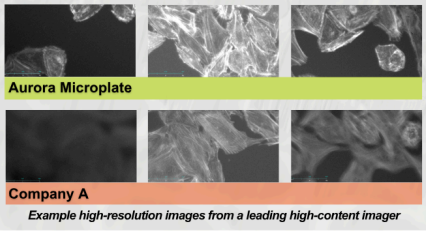
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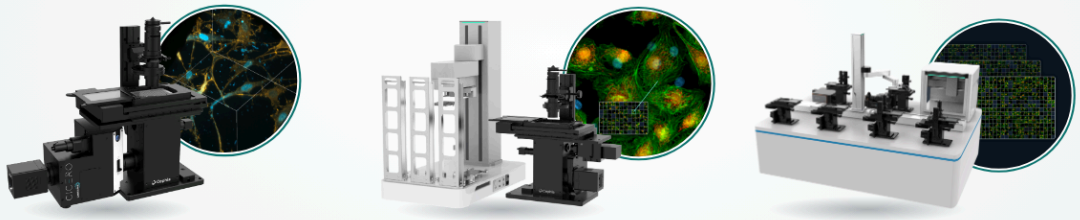


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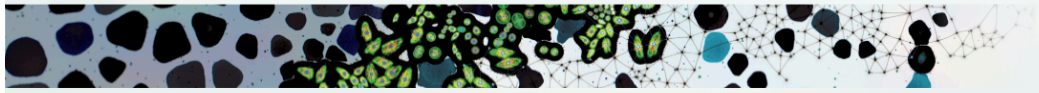


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Conference at-a-Glance

Sunday, November 1st, 2026	
7:30 AM – 9:00 AM *Caspian*	**Registration (Hackathon only)**
9:00 AM – 9:00 PM *Caspian*	**Cytodata Hackathon: Using Scverse to analyze phenomics data**
Monday, November 2nd, 2026	
7:30 AM	**Check-in opens**
8:00 AM – 9:00 AM	**Registration, Coffee and Carbs**
9:00 AM – 9:00 PM *Caspian*	**Cytodata Hackathon: Using Scverse to analyze phenomics data**
9:00 AM – 12:00 PM *Salon F* *Salon G* *Salon H*	**Education sessions:** ● *Image-based Assays for Screening and other applications* ○ *Unlocking the Principles of Assay Development - **OJ Trask*** ○ *HCS/HCI/HCA Its all about the Models - **PA Johnston*** ○ *From Ideation to Application: A Case History of Establishing An Imaging-Based Phenotypic Profiling Assay for Chemical Hazard Screening - **Joshua A. Harrill.*** ● *Optical microscopy for complex biological models* ○ *Introduction to High Content Light-Sheet Microscoopy - **Chris Dunsby*** ○ *Optical Pooled Screening: Linking Genetic Perturbations to Cellular Phenotypes - **Louise Morlot*** ○ *A Closed Loop Phenomics Engine for Disease-Relevant Screening: Modeling and Pharmacological Rescue of a Fibrotic Phenotype with Cell PAinting - **Jordi Carreras-Puigvert*** ● *Bioimage analysis* ○ *Processing and Evaluating High-Content Morphological Profiles - **John Arevalo*** ○ *Learning cellular representations that matter: deep learning for morphological profiling - **Runxi Shen and Alán F. Muñoz.*** ○ *Innovating and Operationalizing OME-Zarr for Bioimaging in the Cloud - **Erin Diel***
12:00 PM – 1:00 PM	**Lunch**

1:00 PM – 3:00 PM *Salon F* *Salon G* *Salon H*	**Workshops** ● *Deep learning on morphology data within the Scverse ecosystem* ○ *Led by **Tim Treis** and **Ilan Gold*** ● *AI Pair Programming* ○ *Led by **Jonny Sexton*** ● *Getting Started in Image Analysis with CellProfiler* ○ *Led by **Beth Cimini** and **Erin Weisbart***
1:00 PM – 3:00 PM *Atlantic Ballroom*	**SBI2 Career Panel - A guided discussion** Panelists: David Egan, Paul Johnston, Steve Haney, Debby Nickischer, Joe Trask and Jenna Tomkinson Moderator: Kristin Halfpenny
3:00 PM – 4:00 PM *Atlantic Ballroom*	**Keynote Address:** Emma Lundberg, Stanford University
4:00 PM – 5:30 PM *Atlantic Ballroom*	**Colloquium:** *AI Today: The Good, The Bad, and the Ugly.* *A guided discussion on the benefits and pitfalls of Pattern Recognition, Machine Learning and Large Language Models in imaging assays.* *Panelists: Emma Lundberg, Johnny Sexton, Runxi Shen, Shalin Mehta, Jenna Tomkinson.* *Moderators: Ilya Goldberg and Paul Johnston*
5:30 PM – 7:30 PM *Pacific Ballroom*	**Reception and Poster Viewing** ODD number Poster Presentations
Tuesday, November 3rd, 2026	
7:30 AM	**Check-in opens**
8:00 AM – 8:30 AM	**Registration, Coffee and Carbs, Exhibit Hall Opening** *All keynotes and scientific sessions take place in the Atlantic Ballroom*
8:30 AM – 8:45 AM	**Opening Remarks:** Kristin Halfpenny, SBI2 President.
8:45 AM – 9:45 AM *Atlantic Ballroom*	**Session 1: The Evolving Importance of Complex Model Systems (Part 1)** ● Jonny Sexton (UMich) ● Jenny Tam (Wyss Institute)
9:45 AM – 11:00 AM	**Coffee Break, Poster and Exhibit Viewing**
11:00 AM – 12:00 PM *Atlantic Ballroom*	**Session 1: The Evolving Importance of Complex Model Systems (Part 2)** ● Max Winkelman (Emulate Bio) ● Exhibitor Spotlight: NeuroGlass ● Selected Poster Talks

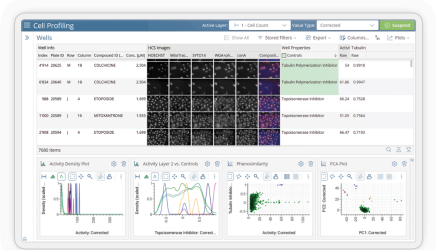
12:00PM - 12:15PM	**Pick Up Lunch**
12:15 PM – 1:15 PM *Salon F* *Salon G*	**Lunch & Learn Sponsored Sessions** ● Cephla ● Ananda Devices
1:15 PM – 2:30 PM *Atlantic Ballroom*	**Session 2: Acquisition: The Next Frontier of Imaging Technologies (Part 1)** ● Akaash Kumar (Cambridge University) ● Exhibitor Spotlight: Molecular Devices ● Adam Glaser (The Allen Institute)
2:30 PM – 3:45 PM	**Coffee Break, Poster & Exhibit Viewing**
3:45 PM – 4:30 PM *Atlantic Ballroom*	**Session 2: Acquisition: The Next Frontier of Imaging Technologies (Part 2)** ● Alfred Millett-Sikking (Calico Labs) ● Vendor Spotlight: Revvity
4:30 PM – 5:30 PM *Atlantic Ballroom*	**Keynote Address:** Derek Lowe, Novartis *Drug Discovery: How We Got Here and Where We Might Be Going*
5:30 PM – 7:30 PM *Pacific Ballroom*	**Poster and Exhibit Viewing Reception** EVEN number poster presentations
Wednesday, November 4th, 2026	
7:30 AM	**Check-in opens**
8:00 AM	**Registration Coffee and Carbs, Exhibit Hall Opening** *All keynotes and scientific sessions take place in the Atlantic Ballroom*
8:30 AM – 10:00 AM *Atlantic Ballroom*	**Session 3: Analysis - From Observations to Novel Phenotypes (Part 1)** ● Avtar Singh (Genentech) ● Laura Heiser (OHSU) ● Vendor Spotlight: Cellanome ● Selected poster talks
10:00 AM – 11:00 AM	**Coffee Break, Poster and Exhibit Viewing**
11:00 AM - 12:15 PM *Atlantic Ballroom*	**Session 3: Analysis - From Observations to Novel Phenotypes (Part 2)** ● Shalin Mehta (CZI) ● Exhibitor Spotlight: Saguaro ● Hackathon Wrap-up
12:15PM -12:30PM	**Pick Up Lunch**

12:30 PM- 1:30 PM *Salon F*	**Lunch & Learn Sponsored Sessions** ● Element
1:30 PM - 2:45 PM	**Session 4 - Application: Novel Phenotypes to Decisions (part 1)** ● Emery Smith (UF-Scripps) ● Jonne Rietdijk (EMBL-EBI) ● Exhibitor Spotlight: Glencoe Software
2:45 PM – 3:30 PM	**Coffee Break, Poster & Exhibit Viewing**
3:30 PM – 4:15 PM	**Session 4: Novel phenotypes to decisions (part 2)** ● Max R Salick (insitro) ● Selected poster talks
4:15 PM – 4:45 PM	**Awards Ceremony and President's Award Presentation** ● President's Innovation Award and Presentation ● Award Ceremony: Best Posters
5:00 PM – 6:00 PM	**SBI2 Annual General Meeting (AGM)** *The AGM will cover the Society's current status, finances, and open Board positions. The public is encouraged to attend and join as members.*
	End of Conference

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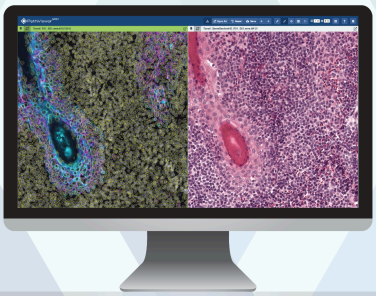
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Program Agenda: Day 1

Monday, November 2nd

EDUCATION SESSIONS
9:00 AM – 12:00 PM (noon)

Track I	**Image-based Assays for Screening and other applications**
Room: Salon F 3rd floor	*Unlocking the principles of Assay Development* **Joe Trask,** SBI2 Founder, Retired

Abstract: Unlock the full potential of high-content screening in this fast-paced, engaging session built for scientists driving innovation in basic research, phenotypic drug discovery, and targeted therapeutic development. Whether you're refining established workflows or stepping into next-generation technologies, this session equips you with the tools, insights, and strategies to elevate your HCS capabilities. You'll learn impactful assay-development approaches grounded in best practices from the NIH/NCATS Assay Guidance Manual, giving you a trusted framework to strengthen your assays long after the session ends. We'll start with the essential foundations of high-content assay design and then move into advanced territory—3D imaging, complex cellular models, and modern phenotypic discovery strategies. You'll gain practical guidance on both fixed and live-cell imaging, learn how to navigate and overcome common experimental challenges, and explore how AI, machine learning, and deep learning are transforming assay optimization and data interpretation. Throughout the session, we'll highlight proven best practices from the NIH/NCATS Assay Guidance Manual, ensuring you leave with actionable knowledge, stronger workflows, and the confidence to push your HCS programs forward.
By the end of this session, you will be able to:

- Confidently navigate the principles and workflows of high-content screening.
- Design robust, reproducible assays tailored to complex biological systems.
- Optimize imaging and analysis parameters for maximum scientific impact.
- Troubleshoot real-world challenges with proven strategies.
- Apply statistical and quality-control metrics that ensure data integrity and assay reliability.

Room: Salon F 3rd floor	*HCS/HCI/HCA It's all about the Models* **Paul A. Johnston,** Dept. Pharmaceutical Sciences, School of Pharmacy, University of Pittsburgh

Abstract: Implementing image-based assays involves numerous critical decisions that impact how they will be performed and what outcomes are achievable. Sample preparation typically begins with the selection of an appropriate physiologically relevant biological model that expresses the target protein(s) of interest or that exhibits appropriate phenotypes and functions that can be modulated. The choice of model and/or cells profoundly impacts the biological responses that can be measured, the type of assay that can be implemented, and the data that can be extracted. In this course we will showcase several cellular models that utilize different cell types, detection modalities, and reagents to quantify modulation of signaling pathways and cellular phenotypes. The models include: the use of specific antibodies to quantify JAK-STAT pathway activation in head and neck cancer cell lines; the utilization of a tetracycline repressed glucocorticoid nuclear receptor-GFP fusion system in a mouse mammary adenocarcinoma cell line to study transcriptional regulation; and the application of adenovirus encoded

fusion protein biosensors to study protein-protein interactions between nuclear receptors and coactivators in the U2 OS sarcoma cell line. A C. elegans model that provided an HCS assay for a protein misfolding disorder of the human secreted Serpin α1-antitrypsin will be presented. The production of Multicellular Tumor Spheroid (MCTS) models produced in hydrogel microwell arrays, by magnetic bioprinting, or in ultra-low attachment (ULA) microplates and their ability to phenocopy the microenvironments of solid tumors will be discussed. Several imaging-based assay formats implemented in patient derived hepatocellular carcinoma tumor organoids will also be discussed.

Room: Salon F
3rd floor

From Ideation to Application: A Case History of Establishing Phenotypic Profiling Assays for Chemical Hazard Screening.
Joshua Harrill, Corteva Agriscience

Abstract: Traditionally, chemical hazard characterization is based upon information obtained from *in vivo* toxicity studies performed using rodent and non-rodent models. Such studies are time-consuming, expensive, use many dozens-to-hundreds of animals and at times do not generate information that can be used to discern a chemical's molecular mechanism-of-action. In recent years, a variety of stakeholders including government, industry, academia and non-governmental organizations (NGOs) have invested time and resources developing and evaluating new approach methodologies (NAMs) for chemical hazard characterization that avoid the use of *in vivo* animal models. In this course, a case history for implementation of a NAM, high-throughput phenotypic profiling (HTPP) with the Cell Painting assay, for chemical hazard screening will be reviewed and discussed from the initial ideation to downstream applications that have the potential to inform chemical risk assessment. The presentation will be divided into two overarching sections. The first section will describe steps in HTPP assay development and optimization, study design considerations and data analysis strategies pertinent to estimating chemical potency and quality control procedures used to evaluate assay performance and reproducibility. The second section will describe how information from the HTPP assay has been used in downstream applications relevant to chemical risk assessment. Topics will include screening level assessment and prioritization using *in vitro* to *in vivo* extrapolation and bioactivity-to-exposure ratio (BER) analysis, chemical grouping for read-across and mechanistic inference and evaluating the impact of xenobiotic metabolism on assay readouts. The session will conclude with an overview of how HTPP (and other molecular profiling assays) are being incorporated into toolbox approaches for evaluating systemic toxicity. Attendees will gain a broader understanding of imaging-based phenotypic profiling assay development and downstream applications that transform the assay outputs into actionable information for next generation chemical risk assessment.

Track II — Optical microscopy for complex biological models

Room: Salon G
3rd floor

Introduction to high-content light-sheet microscopy
Chris Dunsby, Imperial College, London

Abstract: Light-sheet fluorescence microscopy (LSFM) provides low out-of-plane photobleaching and phototoxicity and is therefore well suited to high-speed optically-sectioned imaging of biological specimens in 2D or 3D. Conventional LSFM configuration employs two microscope objective lenses orientated at 90° to one another – the first is used to generate an illumination light sheet and the second is used to collect fluorescence from the illuminated plane – but this places restrictions on how the sample can be mounted. Oblique plane microscopy (OPM) uses a single high numerical aperture microscope objective to provide both fluorescence excitation and detection whilst maintaining the advantages of LSFM, enabling it to provide high-speed 3D imaging for a range of applications on a conventional fluorescence microscope frame. The speed of OPM imaging can also be applied to image samples arrayed in multiwell plates in 3D over time with 10s of volumes imaged in multiple colour

channels on a timescale of 10 minutes. This tutorial will introduce the basics of LSFM and OPM, and go on to give examples of the application of OPM, including high-content analysis of cells, spheroids, organoids and tissue slices imaged in multi-well plate arrays.

Room: Salon G
3rd floor

Optical Pooled Screening: Linking Genetic Perturbations to Cellular Phenotypes
Louise Morlot, University of Copenhagen

Abstract: Optical pooled screening (OPS) has emerged as a powerful technology for systematically linking genetic perturbations to optical phenotypes at single-cell resolution. By combining pooled genetic perturbation, high-content microscopy, and optical genotyping, OPS enables researchers to interrogate how genetic perturbations influence complex spatial, morphological, and cellular phenotypes across millions of cells.
This session will provide an overview of OPS workflows, with a focus on their technical principles, opportunities, and challenges. We will first introduce the fundamentals of OPS, from library design to data analysis, and examine how genetic perturbations can be decoded directly in individual cells using in situ sequencing and microscopy. We will explore how phenotypic imaging and genotyping are integrated within a single workflow, and how image-based data analysis can connect the molecular identity of each perturbation to the phenotype of the corresponding cell.
The session will then cover approaches for extracting and interpreting phenotypic features, including cellular and nuclear morphology, and discuss how these features can be used to characterize the effects of genetic perturbations at the single cell level. We will also explore different phenotyping strategies, including live-cell imaging, Cell Painting, and multiplexed staining, and consider how these approaches are incorporated into OPS workflows to broaden the phenotypic space interrogated with optical screens.
By the end of the session, participants will have a practical understanding of the key steps and considerations involved in designing and analyzing optical pooled screens, as well as the strengths and limitations of OPS for connecting gene perturbations to cellular phenotypes.

Room: Salon G
3rd floor

A closed-loop phenomics engine for disease-relevant screening: modelling and pharmacological rescue of a fibrotic phenotype with Cell Painting
Jordi Carreras-Puigvert, Pixl Bio

Abstract Phenotypic screening in disease-relevant models requires imaging platforms that deliver consistent, high-quality data at scale, together with analytics that capture both efficacy and undesired compound effects. Here we present the Pixl Bio phenomics engine, which integrates automated plate handling, two Squid microscopes and a multivariate analytics pipeline in a closed-loop configuration. The dual-microscope set-up enables continuous, unattended acquisition. Its modular design allows imaging parameters to be adapted to each assay, while robust autofocus and illumination keep image quality consistent across plates and batches. We applied the engine to an in vitro model of idiopathic pulmonary fibrosis. TGF-β stimulation of lung fibroblasts induced a distinct fibrotic morphology and increased collagen expression, and both were reversed by a reference ALK5 inhibitor. We then screened a focused compound library in dose-response. Morphological profiles were projected onto a disease axis defined by the fibrotic and healthy states, which yields two complementary scores: on-target rescue and off-target deviation. The screen recovered reference inhibitors of the TGF-β pathway with high precision. It also identified compounds with distinct mechanisms of action that reverse the fibrotic phenotype, and resolved dose windows that separate efficacy from undesired

morphological effects. An independent validation screen reproduced the primary results. These data show that a closed-loop, dual-Squid phenomics engine supports

Track III	**Bioimage analysis**

Room: Salon H
3rd floor

Processing and Evaluating High-Content Morphological Profiles
John Arevalo, Genetech

Abstract Image-based phenotypic profiling converts microscopy images into feature vectors for biological discovery. However, raw profile datasets are impacted by technical noise, such as spatial well-position effects, plate-to-plate variance, and batch effects that hinder real biological signals.

This talk covers practical computational steps to improve and standardize morphological profiles. We will walk through common pipeline stages, including outlier detection, spatial artifact mitigation, profile normalization, feature selection, and batch correction, discussing the practical trade-offs involved when removing technical variation without wiping out subtle biological differences.

To judge whether processing decisions actually benefit the profile quality, this session will review an information retrieval framework based on mean Average Precision (mAP). We will explore how mAP evaluates both phenotypic activity (how well replicate profiles separate from negative controls and non-replicates) and phenotypic consistency (whether distinct perturbations sharing a mechanism of action or target retrieve one another). Tracking mAP across pipeline configurations gives practitioners a quantitative way to confirm that preprocessing reduces technical noise while preserving underlying biological relationships.

Room: Salon H
3rd floor

Learning cellular representations that matter: deep learning for morphological profiling
Runxi Shen, Purdue University
Alán F. Muñoz Purdue University

Abstract: Rather than identifying a single universally optimal model, our studies show that different representations preserve different aspects of biology. I will discuss how foundation models, self-supervised learning, and increasingly transferable representations can support analyses across assays, perturbations, and cell systems. Together, these advances are moving morphological profiling beyond cellular description toward biological explanation and action, helping us interpret genetic variants, uncover disease mechanisms, generate therapeutic hypotheses, and develop safer medications.

Room: Salon H
3rd floor

Innovating and Operationalizing OME-Zarr for Bioimaging in the Cloud
Erin Diel, Glencoe Software, Inc.

Abstract: Further, Glencoe has extended OMERO, a widely adopted standard for image data management, with scalable, cloud-native data services to consume NGFF. These enhancements have been adopted by projects such as the Image Data Resource (OME) and BIOMERO (NL-Bioimaging). Guidance on managing, viewing, and analyzing imaging datasets in the cloud will be shared, including AI-powered workflows.

12:00pm – 1:00 PM **Lunch**

Workshops
1:00PM – 3:00 PM

Workshop I

Room: Salon F
3rd Floor

Deep learning on morphology data within the Scverse ecosystem
Led by Tim Treis, Helmholtz Munich and **Ilan Gold**, Memorial Sloan Kettering

Abstract: High-content imaging routinely captures millions of cells, yet in many cases phenotypic profiling still stops at handcrafted features. The scverse ecosystem offers an open, interoperable Python stack to go further, from CellProfiler-style features to learned representations, end-to-end and at screen scale. This hands-on workshop tours two complementary pipelines on real high-content image data: A) extracting morphological features with cp_measure (a fast, CellProfiler-compatible featurizer), storing them in AnnData, and training a variational autoencoder with scVI; B) segmenting and extracting single cells directly with scPortrait, then training a deep-learning model on the single-cell crops through its built-in PyTorch dataloader, with annbatch streaming data at scale. Both build on spatialdata and squidpy for scalable handling and tiling, so the same code runs from a single well up to genome-wide optical pooled screens. Taught from a method-development and infrastructure perspective, the emphasis is reproducible pipelines you can adapt to your own screens. Aimed at beginner-to-intermediate users comfortable with basic Python; prior image-analysis experience helps but isn't required.

Workshop II

Room: Salon G
3rd Floor

AI Pair Programming
Led by Jonny Sexton, University of Michigan

Abstract: This hands-on workshop will demonstrate how AI coding assistants such as Claude, Gemini, and Codex can accelerate the development of high-content imaging analysis workflows. Using a real antiviral assay, participants will take extracted CellProfiler measurements from SQLite databases, perform quality control and normalization with Pycytominer, develop single-cell infection classifiers, and generate efficacy and cytotoxicity scores. The session will highlight practical approaches for using AI to write, debug, and validate scientific code while maintaining reproducibility and analytical rigor. Advanced topics may include machine learning–based assay scoring, model interpretation, and unsupervised analyses such as UMAP and clustering.

Workshop III

Room: Salon H
3rd Floor

Introduction to CellProfiler
Led by Beth Cimini and Erin Weisbart, Broad Institute

Abstract: We will introduce participants to CellProfiler, a no-code image analysis workflow tool that allows users to create end-to-end reproducible image analysis pipelines. Participants will use CellProfiler to find objects (such as Cell, Nucleus and Nucleoli) using classical segmentation methods and learn how to relate those objects and make measurements in their images and objects.

1:00 PM – 3:00 PM	**Career Panel** **Moderator:** Kristin Halfpenny (SBI2 President) **Panelists:** David Egan, Paul Johnston, Steve Haney, Debby Nickischer, and Jenna Tomkinson

Navigating the current job market can be challenging, so let's talk about it! Join us for an engaging discussion about career paths, opportunities, and navigating these turbulent times in biomolecular imaging and informatics.

KEYNOTE
Atlantic Ballroom
3:00 PM – 4:00 PM



Dr. Emma Lundberg
Associate Professor of Bioengineering and Pathology at Stanford University &
Professor at KTH Royal Institute of Technology
Decoding human cell architecture – from spatial proteomics to cell modeling

Abstract: Biological systems are functionally defined by the nature, amount, and spatial location of their proteins. We have generated an image-based map of the subcellular distribution of the human proteome and showed that there is great complexity to the subcellular organization of the cell giving rise to potential pleiotropic effects. As much as half of all proteins localize to multiple compartments and around 20% of the human proteome shows temporal variability. Our temporal mapping results show that cell cycle progression explains less than half of all temporal protein variability and that most cycling proteins are regulated post-translationally, rather than by transcriptomic cycling. This work is critically dependent on computational image analysis, and I will discuss machine learning approaches for embedding spatial subcellular patterns, and how such embeddings as well as generative AI can be used to build multi-scale models of cell architecture. In summary, I will demonstrate the importance of spatial proteomics data for improved single-cell biology and present how the freely available Human Protein Atlas database (www.proteinatlas.org) can be used as a resource for life science.

4:00 PM – 5:30 PM	**Colloquium: AI Today: The Good, The Bad and the Ugly.** A guided discussion on the benefits and pitfalls of Pattern Recognition, Machine Learning and Large Language Models in imaging assays. ***Moderators:*** *Ilya Goldberg and Paul Johnston* ***Panelists:*** *Emma Lundberg, Johnny Sexton, Runxi Shen, Shalin Mehta, Jenna Tomkinson.*
5:30 PM – 7:30 PM	**Reception**

Program Agenda: Day 2

Tuesday, November 3rd

8:30AM - 8:45AM *Atlantic Ballroom*	**Opening Remarks** Kristin Halfpenny, SBI2 PResident
Scientific Session I: The Evolving Importance of Complex Model Systems **Session Chair:** **9:00 AM – 12:00 PM (noon)** **Atlantic Ballroom**	
8:45 - 9:15 AM	*Ten Percent Yield: Mitigating Drug Discovery's Worst Adverse Event with Patient-Derived Liver Organoids* **Jonny Sexton, University of Michigan**

Abstract

Drug-induced liver injury (DILI) remains a leading cause of clinical trial failure and drug withdrawal. Preclinical liver models often rely on a single donor and cell death as the primary endpoint, limiting their ability to capture variation in susceptibility and sublethal injury. We tested whether morphological profiling of liver organoids from patients with DILI improves hepatotoxicity prediction.

We generated induced pluripotent stem cell lines from six Drug-Induced Liver Injury Network patients with high single-drug causality scores and one healthy donor, then differentiated them into human liver organoids containing hepatocyte- and stellate-like cells. Organoids in 384-well plates were exposed to 74 compounds (54 hepatotoxicants and 20 non-hepatotoxic controls) at five concentrations for 72 hours. Multiplex imaging captured nuclear, lipid, mitochondrial, HNF4α, and cytoplasmic features.

Machine learning with compound-grouped cross-validation achieved AUROCs of 0.88–0.91 across individual lines. Averaging predictions across all seven lines outperformed each line alone, yielding 94.4% sensitivity and 85.0% specificity. Morphological profiling was more accurate than cytotoxicity (84.6% versus 43.8%) and the same pipeline applied to cancer cell lines (73.3%). Donor responses were correlated (r = 0.66–0.85), but benchmark-concentration modeling identified reproducible differences in sensitivity: a median fourfold difference, exceeding twentyfold for some drugs. Clustering identified mechanism-associated phenotypes, including phospholipidosis, while TNFα co-treatment revealed sulindac’s inflammation-dependent toxicity.

These findings support multi-donor organoid profiling as a scalable first-tier hepatotoxicity screen for lead optimization. Differences among donors may guide panel selection, while integration with drug exposure data could help estimate clinical DILI risk.

9:15 - 9:45 AM	*Brain Organoid-Based Platform for Drug Discovery in Bipolar Disorder* **Jenny Tam, Wyss Institute**

Abstract
Organoids have the potential to reduce reliance on animal models by enabling the study of complex cellular responses in three dimensions within a human-relevant context. Leveraging recent advances in stem cell technology, we developed cortical and midbrain organoids from human induced pluripotent stem cells (hiPSCs) derived from patients with bipolar disorder (BD) and healthy controls to study neurodegeneration and neuropsychiatric disease. To reduce variability and increase throughput in organoid production, we implemented automated liquid handling and high-content imaging, and we established quality control metrics to identify organoids unsuitable for further study. We analyzed transcriptomic differences in neuronal and progenitor cell types using Light-Seq and differential protein expression using mass spectrometry. Neural activity was assessed by calcium imaging and high-density microelectrode arrays (MEAs). Compared with controls, individual BD organoids showed significantly elevated neuronal activity, including increased mean firing rate, mean amplitude, and conduction velocity, as well as extended axonal and dendritic growth. Treatment with AI-predicted drug candidates for BD normalized both neural hyperactivity and protein dysregulation.

9:45 - 11:00AM	**Coffee Break, Poster and Exhibition Viewing**

11:00 - 11:30 AM	*A Real-Time Window into Human Biology: Advancing Organ-on-a-Chip Technology from Validation to Routine Use* **Max Winkelman, Emulate Bio**

Abstract
A regulatory turning point is underway in biomedical research and drug development. As agencies, policymakers, and industry leaders increasingly prioritize human-relevant New Approach Methodologies (NAMs), there is now an urgent need for scalable, reproducible, and biologically relevant models that can better predict human response.
Organ-on-a-Chip technology offers a powerful path forward. By recreating key aspects of human tissues, Organ-Chips are designed to bridge the translational gap between conventional in vitro systems and human outcomes. The dynamic microenvironments of Organ-Chips promote more physiologically relevant tissue organization than conventional in vitro systems while remaining optically accessible. This provides a real-time window into human biology that enables researchers to visualize tissue architecture, monitor morphological changes over time, and observe interactions across tissue interfaces alongside biochemical and functional readouts.
This presentation will introduce the key concepts of Organ-on-a-Chip technology and how it provides a more in vivo-relevant platform for predicting clinical outcomes, including the use of Emulate's Liver-Chip for predicting drug-induced liver injury. The discussion will highlight how Liver-Chips can better identify hepatotoxic risk and support more predictive preclinical safety assessment.
The session will also explore how Emulate is turning the promise of Organ-Chip technology into routine practice through its AVA™ Emulation System. By integrating incubation, microfluidic culture, imaging, and automation-compatible workflows in a high-throughput platform, AVA is designed to overcome key barriers that have historically limited Organ-Chip adoption. Together, the Liver-Chip and AVA represent a path toward making Organ-Chip assays standard tools in pharmaceutical development, and ultimately supporting more human-relevant decision-making."

11:30 - 11:45AM	*Exhibitor Spotlight*

NeuroGlass

The annotated image: a shared, structured layer for review in image-based screening

Matteo Cantarelli, Neuroglass (by MetaCell)

Abstract

Image-based screening is well served by tools that link wells, segmentation and readouts. What they miss is the judgement applied on top: why one call was accepted and another overruled, where two scientists disagreed, which model outputs were corrected and how. That review happens in meetings, chat and email, and is often lost. As AI-proposed readouts become routine, that judgement is the most valuable data a screening group produces, and the least likely to be kept.We describe an approach where the image itself carries the review. The whole plate is on screen at once, hundreds of fields in 2D or full 3D volumes, and scientists jump instantly between wells at full resolution without leaving the view. Annotations from scientists and models sit as a live layer on the images, each anchored to an exact location and tagged with shared ontology terms rather than free text: Cell Ontology for cell types, Uberon for anatomy, and the Cellular Microscopy Phenotype Ontology for phenotypes. With a vocabulary shared across people, plates and projects, annotations can be reviewed, filtered and aggregated in real time: every disputed call, every instance of a phenotype, every correction to model output, while the screen runs. Reviewed hits keep full provenance, from the call back to the pixels and the person who made it, and corrections accumulate as validated ground truth for the next screen.The platform, NeuroGlass, runs inside the organisation's own cloud or on premise and also serves in production for whole-brain reconstruction.

11:45AM - 12:00PM Selected Poster Talks (Ivana Mikic, Son C. Nguyen)

12:00 PM – 1:15 PM	**Lunch & Learn Sponsored Sessions**

Room: Salon F

Cephla

A closed-loop phenomics engine for disease-relevant screening: modelling and pharmacological rescue of a fibrotic phenotype with Cell Painting

Jordi Carreras-Puigvert, PixlBio

Abstract

Phenotypic screening in disease-relevant models requires imaging platforms that deliver consistent, high-quality data at scale, together with analytics that capture both efficacy and undesired compound effects. Here we present the Pixl Bio phenomics engine, which integrates automated plate handling, two Squid microscopes and a multivariate analytics pipeline in a closed-loop configuration. The dual-microscope set-up enables continuous, unattended acquisition. Its modular design allows imaging parameters to be adapted to each assay, while robust autofocus and illumination keep image quality consistent across plates and batches. We applied the engine to an in vitro model of idiopathic pulmonary fibrosis. TGF-β stimulation of lung fibroblasts induced a distinct fibrotic morphology and increased collagen expression, and both were reversed by a reference ALK5 inhibitor. We then screened a focused compound library in dose-response. Morphological profiles were projected onto a disease axis defined by the fibrotic and healthy states, which yields two complementary scores: on-target rescue and off-target deviation. The screen recovered reference inhibitors of the TGF-β pathway with high precision. It also identified compounds with distinct mechanisms of action that reverse the fibrotic phenotype, and resolved dose windows that separate efficacy from undesired morphological effects. An independent validation screen reproduced the primary results. These data show that a closed-loop, dual-Squid phenomics engine supports reproducible, disease-relevant screening that measures efficacy and liability in a single assay.

Room: Salon G



High Content Analysis of NAM MPS Devices for Live Cell Analysis of 3D Human Neuromuscular Junctions

Keith Olson, Ananda Devices

Abstract
There is a drastic need for improved model systems (NAMs) in the neuroscience field to address the industry challenges around high value compounds failing in the clinic at a rate approaching 96%. Ananda Devices' mission has been to develop and launch these models using novel MPS devices and human cells, addressing the market challenges mentioned above. Our products include both a human neuromuscular junction (NMJ) MPS used for disease modeling and neurotoxin testing as well as a human neuronal MPS used with high content analysis to model neurotoxicity, neurological disease phenotypes and axonal regrowth following injury. In the case of the NMJ model system we will also show data on a novel brightfield imaging approach using our machine learning algorithm to automatically detect muscle contraction without force measurement or any fluorescent labeling. The Ananda Devices MPS products are designed in a 384-well footprint for universal adoption on any imaging platform. Each device contains multiple MPS chips on each plate and allows users to approach NAM systems with an easy to use, accessible format that allows higher throughput analysis and lower cost for broader adoption in the market.

Scientific Session II: Acquisition: the Next Frontier of Imaging Technologies
Session Chair:
1:30 PM – 5:30 PM
Atlantic Ballroom

1:15 PM - 1:45 PM

Multispectral Live Imaging and the Path Toward Predicting T Cell Killing

Akaash Kumar, Cambridge University

Abstract
The hallmark of life is that it is animate. Decoding the complexity of cells requires watching many molecular players at once, but conventional live fluorescence microscopy is fundamentally limited in how many fluorophores it can resolve simultaneously in a living cell. This longstanding issue has prevented the complexity of live biology from being observed without a tradeoff in spatial, spectral or temporal resolution.
To overcome this barrier I developed a novel imaging platform, consisting of both hardware and software, enabling simultaneous imaging of eight or more spectrally distinct fluorophore species in live cells over 10000x faster than commercial alternatives. I will describe the underlying optical and computational architecture, and how it has been deployed on state-of-the-art microscopes to shed light on intracellular trafficking.
More recently, I have applied this platform to a long-standing question in cellular immunology: how cytotoxic T lymphocytes (CTLs) coordinate their internal architecture to kill target cells. Using simultaneous multi-organelle imaging, we uncover a staged programme of organelle delivery to the immune synapse, with implications for immune cell biology and CAR T immunotherapies. Finally, I will discuss how this rich, multi-dimensional imaging data creates an opportunity for new computational approaches, with the goal of identifying early, predictive signatures of a cell's

functional outcome. I will outline this direction and its implications for mechanistic potency profiling of engineered T cell and NK cell therapies.

1:45 PM - 2:00 PM

Exhibitor Spotlight

Screen Smarter and faster with the new HCS.ai High-Content Screening System

Angeline Lim, Molecular Devices

Abstract
The increasing adoption of new approach methodologies (NAMs) presents challenges in acquiring, interpreting, and managing multidimensional high-content imaging data at scale. This session will examine how the ImageXpress® HCS.ai High-Content Screening portfolio, combined with artificial intelligence (AI)–enabled image analysis, can help address these challenges. The discussion will focus on acquisition strategies to improve the efficiency of complex screening workflows and on image segmentation and phenotypic analysis to support the interpretation of imaging data. AI-based prediction of cell viability from imaging data will be used to illustrate the connection between image acquisition, computational analysis, and the assessment of a biologically relevant endpoint.

2:00 PM - 2:30 PM

How to see the big and the small? New technologies for mapping centimeter scale tissues with nanoscale resolution
Adam Glaser, The Allen Institute

Abstract
The brain is the most complex system under study. It relies on precise wiring and signaling across billions of neurons. Studying the structure and spatial organization of neurons, their tiny synaptic connections, and the underlying biomolecular components, will shed light on the mechanisms of brain function. However, mapping these neural circuits in three dimensions (3D), which I will refer to as molecular cartography, is extremely challenging. Neurons span centimeters, communicating with one another via a sea of sub-micrometer synapses and nanoscale proteins. At the same time, neurons have distinct cell types, stemming from their unique expression of thousands of genes, and can assemble into spatial gradients spanning entire brain regions. Decoding the spatial organization of these cells, their genetic identities, and how they communicate therefore requires imaging molecular moieties at a brain-wide scale. These examples highlight an important technical requirement. Molecular cartography requires seeing the big (i.e., the entire brain) and the small (i.e., individual synapses, proteins, and RNA transcripts) in a highly multiplexed manner (i.e., many molecular markers). Here I will present my group's effort to develop new imaging technologies that enable charting these vast maps of the brain and other organs at scale.

2:30 PM - 3:45 PM

Coffee Break, Poster and Exhibit Viewing

3:45 PM - 4:15 PM

Snouty light-sheet microscopy
Alfred Millett-Sikking, Calico Labs

Abstract
Snouty light-sheet microscopy is a fast, high resolution and versatile 3D microscopy technique that is compatible with standard microscope platforms and sample formats (e.g. multiwell plates). Here we give an overview of how it works, some attractive upgrade options, and why it's a compelling microscope to build and use.

4:15 PM - 4:30 PM

Exhibitor Spotlight

From Plate to Cloud to Universe: A Complete High-Content Imaging Workflow Solution Featuring Opera Phenix OptIQ, Harmony 6, Image Artist 1.6 and PhenoVue Reagents

Steve Straub, Revvity

Abstract
Complex 3D cell models, microphysiological systems and live-cell assays demand imaging platforms that combine sensitivity, speed and intelligent analysis. Building on over two decades of innovation, Revvity continues to push the boundaries of high content imaging with the introduction of the Opera Phenix OptIQ, Harmony 6, and Image Artist 1.6. The Opera Phenix OptIQ provides increased detection sensitivity compared to Opera Phenix Plus coupled with Phenologic.AI pretrained deep learning segmentation models enabling scientists to quickly extract the maximum amount of information from precious samples. A reengineered autofocus system and multilayer plate definition wizard simplifies setup and imaging of multilayer organ-on-chip type samples while the Find Organoids building block enables robust detection of organoids using only brightfield images. Harmony 6 extends the open data format of Harmony 5.3, allowing Harmony to interact directly with popular external segmentation tools such as Cellpose. To simplify cloud-based image analysis, Image Artist 1.6 is available as a fully Revvity-hosted solution, allowing scientists to leverage the power of cloud computing without the need for internal IT support or infrastructure. When combined with our library of PhenoVue high content reagents and antibodies as well as our PhenoPlate microplates, Revvity provides solutions across every step of the high content imaging workflow.

KEYNOTE
Atlantic Ballroom
4:30 - 5:30 PM

Picture

Derek Lowe
Position Title, Novartis
Drug Discovery: How We Got Here and Where We Might Be Going

Abstract
This talk will present a brief background of some ways that drug discovery has evolved over the last 30 years, with particular attention to recent developments in AI/ML techniques and their applicability to longstanding problems.

5:30 - 7:30PM
Foyer, Exhibit Hall

Poster Sessions, Exhibit Viewing, & Reception

Program Agenda: Day 3

Wednesday, November 4th

Scientific Session III: Analysis: From Observations to Novel Phenotypes
Session Chair: Brian Feng
8:30 - 12:15PM
Atlantic Ballroom

8:30 - 9:00AM

Toward Interpretable and Predictive Image-Based Screening
Dr. Avtar Singh, Genentech

Abstract
Microscopy provides an information-rich readout of cellular state, resolving the abundance, localization, and organization of molecules in single cells. Optical pooled screening (OPS) brings this readout to pooled genetic screens, using in situ sequencing of perturbation barcodes to connect phenotype and genotype at scale. As OPS has become more widely adopted, two limitations stand out: image features are difficult to interpret biologically, and their ability to predict orthogonal molecular readouts is unclear.
To address the first, we extended OPS to highly multiplexed antibody-based phenotyping of subcellular compartments. Systematic in silico subsetting showed that markers recover non-redundant classes of gene-gene relationships and that detection breadth increases with panel complexity. We then decomposed phenotypic space into discrete archetypes and annotated them using multimodal language models, yielding interpretable descriptions of individual phenotypes. Integrating archetypes across markers defined morphological programs: coordinated, modular reorganization across multiple compartments. Functionally distinct perturbation classes combined these programs in different ways to mount tailored cellular responses.
To address the second, we performed parallel OPS and Perturb-Seq in LPS-stimulated primary macrophages. The modalities were broadly concordant but complementary. Imaging was more sensitive to weak perturbations and post-transcriptional effects, while RNA better captured perturbations to the gene-expression machinery and connected to cell atlases and human genetics. Using imaging embeddings as empirical priors, we imputed and denoised transcriptomes, tripling the number of perturbations with RNA profiles, and validated these predictions in a secondary screen.

Together, these directions suggest a path toward imaging as a scalable, interpretable foundation for mapping perturbation response.

9:00 - 9:30 AM	*Morphology in motion: Predicting gene expression from live-cell dynamics* **Dr. Laura Heiser, OHSU**

Abstract
Extracellular signals drive continuous changes in cell phenotype, but how these dynamic states relate to the molecular programs underlying them remains poorly understood. MMIST (molecular and morphodynamics-integrated single-cell trajectories) addresses this gap by linking live-cell "morphodynamics", single-cell trajectories of shape and motility extracted from time-lapse imaging, to snapshot gene expression measurements. Using morphodynamic trajectories as a scaffold for cell state, MMIST reconstructs a continuous landscape of epithelial-mesenchymal transition (EMT) and its reverse, MET, revealing distinct sequences of intermediate states that connect epithelial and mesenchymal endpoints. This landscape enables prediction of expression dynamics for thousands of RNA transcripts across EMT/MET with near-continuous time resolution, even though the underlying molecular data consist only of static snapshots. These results demonstrate that coupling live-cell imaging with molecular profiling can recover dynamic, single-cell-resolved views of gene expression from data that are individually static or population-averaged. The MMIST framework generalizes broadly across imaging approaches, molecular snapshot modalities, and biological systems beyond EMT/MET, offering a general strategy for connecting phenotypic dynamics to the molecular programs that drive them.

9:30 - 9:45 AM cellanome	*Exhibitor Spotlight* *Paired longitudinal live-cell imaging and transcriptomics enable deeper characterization of cellular states* **Pier Federico Gherardini, Cellanome**

Abstract
Single-cell RNA sequencing has transformed how we map molecular states, but a transcriptomic map is not necessarily a functional one. Cells with similar expression profiles can behave very differently, and similar behaviors can arise from distinct molecular programs. Because conventional workflows typically measure phenotype and transcriptome in different cells, the link between what a cell expresses and what it actually does is lost.In this talk, Pier Federico Gherardini, Head of Computational Biology at Cellanome, will show how CellCage technology preserves the identity of each individual cell from live observation through molecular readout. On a fully automated platform, cells can be cultured, perturbed and imaged over days before transcriptomic profiling of those very same cells, connecting observed behavior, experimental context and gene expression in a single dataset. Through examples in immune function, drug response and viral infection, we will show what following the same cells over time reveals that RNA alone cannot.

9:45 - 10:00AM	Selected Poster Talks (Alexandr Kalinin)
10:00 - 11:00 AM	**Coffee Break, Poster and Exhibit Viewing**
11:00 - 11:30 AM	*Dynamic Cell Profiling* **Dr. Shalin Mehta, CZI Biohub**

Abstract

Label-free images of cells, i.e., images of intrinsic properties of cells without chemical dyes or fluorescent proteins encode a surprising amount of functional information as illustrated by recent reports of perturbation screens of mammalian cells (https://www.biorxiv.org/content/10.64898/2026.06.01.728087v2.full) and genome scale profiling of microbiome (https://www.biorxiv.org/content/10.64898/2026.08.30.748126v1.full), among other reports. Models that decode architectural and functional information encoded in such large scale label-free imaging datasets is an active area of research. We will share our work at Biohub in establishing robust virtual staining and representation learning methods for profiling cell state dynamics from label-free data.

11:30 - 11:45 AM	*Exhibitor Spotlight*
SAGUARO Biosciences	*Benchmarking Live-Cell Profiling with ChromaLIVETM Against Fixed Cell Painting for Early Drug Discovery* **Mike Veling, Merck & Co (MSD)**

Abstract
N/A

11:45 - 12:15 PM	**Hackathon Wrap Up**
12:30 PM – 1:30 PM	**Lunch & Learn Sponsored Sessions**

Room: Salon F

Element Biosciences	*Bridging Imaging and Omics: Multimodal Screening at Single-Cell Resolution* **Michael Previte, Element Biosciences**

Abstract
High-content image-based screening has become a cornerstone of phenotypic drug discovery, yet conventional approaches remain limited to morphological readouts alone, leaving mechanistic and molecular context largely inferred rather than measured. Cytos is a multimodal single-cell screening technology, performed on the Element Biosciences AVITI24 platform, that simultaneously captures protein expression, transcriptomic profiles, cellular morphology, and guide RNA identity from the same individual cells in a single experimental run. By unifying these four data layers at single-cell resolution, Cytos eliminates the need for parallel or serial assays and preserves the direct correlation between a cell's genetic perturbation, its molecular state, and its phenotypic outcome.This talk will introduce the Cytos screening technology and demonstrate how its multimodal data structure is paired with AI-driven computational models to integrate imaging and omics readouts into a unified phenotypic signature. These models enable deeper resolution of mechanism of action, more accurate clustering of phenotypic subpopulations, and improved detection of subtle or heterogeneous cellular responses that single-modality screens may miss. We will present example workflows illustrating how this integrated approach supports target identification, mechanism-of-disease studies, and compound screening, and discuss how combining rich multimodal data with computational modeling is reshaping the resolution and scale at which phenotypic screening can be applied to drug discovery.

Scientific Session IV: Applications: Novel Phenotypes to Decisions
Session Chair: Shuyan Lu (J&J) and Debby Nickischer (Arvinas)
1:30 - 2:45PM

Atlantic Ballroom

1:30PM-2:00PM

Ultra High Content Analysis For Cancer Cell Differentiation Effectors

Emery Smith, Herbert Wertheim UF Scripps Institute for Biomedical Innovation and Technology

Abstract

Drug-tolerant persister (DTP) cells survive cancer therapy and drive relapse and resistance. We hypothesize that exploiting DTP plasticity to reprogram these cells into a benign adipocyte-like state may represent a novel therapeutic strategy. To address this, we developed a phenotypic high-content imaging assay in HER2+ breast cancer DTP models and performed an unbiased screen of the Wertheim UF Scripps Drug Discovery Library (~665,000 compounds). This was done using a fully automated HTS platform inclusive of the Araceli Endeavor high content reader, whose unique combination of speed, sensitivity, and image quality supports ultra-high-throughput imaging at unprecedented scale. We completed the full 665K-compound screen in less than six weeks, a record-setting high content imaging campaign for our program and, to our knowledge, one of the fastest high-content phenotypic screens reported at this scale. The platform maintained the image quality required for robust phenotypic analysis while dramatically accelerating throughput. The screen identified multiple candidate compounds capable of inducing adipogenic reprogramming phenotypes in DTP cells which have been advanced to confirmation and mechanistic studies. In doing so we have demonstrated how next-generation ultra-high-throughput imaging can transform phenotypic drug discovery that has vastly accelerated the discovery of chemical probes which may redirect drug-tolerant cancer cells toward a benign fate.

2:00PM-2:30PM

Multimodal Profiling for Mechanistic and Translational Prediction of Hepatotoxicity

Jonne Rietdijk, EMBL-EBI

Abstract

Predicting hepatotoxicity remains a major challenge in pharmaceutical and chemical safety assessment, particularly using non-animal methods. The emergence of toxicogenomics shifted toxicology from traditional endpoints towards broad molecular profiling to identify biomarkers, predict toxicity, and provide mechanistic insights into toxic responses. However, gene expression captures only one aspect of cellular responses. High-content image-based profiling and proteomics provide complementary phenotypic and molecular readouts that can improve mechanistic understanding and translation to human toxicity.

As part of the OASIS Consortium, we have generated a harmonised dataset of 160 compounds integrating Cell Painting, targeted high-throughput transcriptomics, and extracellular protein profiling in HepaRG cells. We systematically compare the bioactivity captured by each modality and assess their complementary ability to characterise compound-induced responses. We then use these profiles to predict toxicity across biological levels, from mechanisms of action to in vivo animal and human hepatotoxicity endpoints.

Preliminary results show that Cell Painting, transcriptomics, and proteomics have comparable overall bioactivity rates but differ in the responses and endpoints they capture, with certain endpoints better predicted by one modality than another. Integration through weighted co-expression network analysis identifies cross-modal relationships linking cellular responses to in vivo hepatotoxicity outcomes. Together, these results provide an initial benchmark for comparing profiling approaches and can help build confidence in the use of multimodal profiling for toxicity prediction.

2:30 - 2:45 PM	*Exhibitor Spotlight*
Glencoe SOFTWARE	*OMERO Plus Hosted is the data architecture behind AI-ready imaging*
	Erin Diel, Glencoe

Abstract
Research organizations face growing challenges in managing, processing, and sharing large and complex imaging datasets. To enable AI-readiness, data architecture matters more than ever. Glencoe Software's OMERO Plus sets the standard for how data is stored, described and accessed, and these architectural commitments serve many simultaneous human users (researchers, pathologists, image analysts, data scientists, IT administrators) and AI agents alike.OMERO Plus Hosted is a fully managed service designed to simplify image data management and workflow orchestration for organizations of any size. Streamline the process of importing, converting, analyzing and managing your complex screening and spatial biology data in the cloud, including co-registration of multi-omic results. Visualization and data mining interfaces within OMERO Plus Hosted are fully web-based, enabling seamless remote workflows, or use the open API to build a custom data dashboard.Reduce manual effort, improve traceability, and accelerate your AI-ready imaging workflows with Glencoe Software's OMERO Plus Hosted.

2:45 - 3:30 PM	**Coffee Break, Poster and Exhibit Viewing**
3:30 -4:00 PM	*Pooled screening and tool building for ML-enabled phenotypic rescue in iPSC-derived models of ALS cryptic splicing and TSC mTOR hyperactivation* **Max R Salick, insitro**

Abstract
The functional genomics toolkit has continued to expand over the past decade, with the advancements such as optical pooled screening (OPS), perturb-seq, CRISPRa/i, and in vivo screening; meanwhile, computational methods to interrogate these rich perturbational datasets rapidly progress with advancements in computer vision and machine learning. Here we'll describe how insitro has developed, automated, and industrialized several of these technologies in order to identify new targets for our therapeutic pipelines. In this presentation, we will share examples of our advancements, focusing on foundational model development and applications in Amyotrophic Lateral Sclerosis (ALS) and Tuberous Sclerosis (TSC). For ALS, we will describe these screens, including the design of robust data pipelines and production-ready machine learning models, illustrating their critical role in tackling the complexities of neurological diseases. We'll next describe TSC, a genetic disease in which somatic loss of heterozygosity leads to dysfunctional TSC1/TSC2, mTOR hyperactivation, and intractable epilepsy and autism spectrum disorder. For this disease, we developed a similar iPSC-based genetic model of the disease and conducted an OPS for revertants of mTOR-hyperactivity phenotypes, while also capturing general morphology via CellPaint and Quantitative Phase Imaging. Lastly we'll describe how Self-DIstillation with NO Labels (DINO) embeddings of the phenotypic images were utilized to identify label-free temporal and dose-responsive reversion of the disease phenotype, along with novel mTOR biology.

4:00 PM - 4:15 PM	Selected Poster Talks (Mou Deb, Pavana Gururaj Rotti)
4:15 PM – 4:45 PM	**Awards Ceremony and President's Award**

4:15 PM – 4:35 PM	President's Innovation Award
4:35 PM – 4:45 PM	Award Ceremony: Best Posters
5:00 PM - 6:00 PM	**SBI2 Annual General Meeting (AGM)** The AGM will cover the Society's current status, finances, and open Board positions. The public is encouraged to attend and join as members.
6:00 PM	**End of Conference**

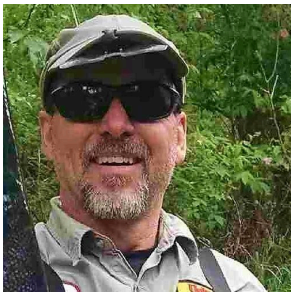
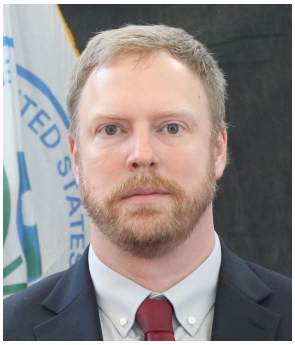
Speaker Bios

Hands-On Workshops & Education Sessions



Paul A. Johnston, Ph.D.
Professor, Department of Pharmaceutical Sciences, School of Pharmacy
University of Pittsburgh

Paul A. Johnston is a professor of Pharmaceutical Sciences, School of Pharmacy at the University of Pittsburgh. He obtained a B.Sc. with Honors (2.1) and Ph.D. in Biochemistry, from the University of East Anglia, Norwich, England. Postdoctoral positions at UNC, Duke University, and Howard Hughes Institute UT Southwestern provided expertise in biochemistry, molecular biology, cell biology, immunology, recombinant protein expression and purification. He has 35 years of drug discovery experience in the Pharmaceutical (American Cyanamid, Sphinx Pharmaceuticals, & Eli Lilly), Biotechnology (Embrex), and academic sectors (Pitt). An innovator of cell-based lead generation he pioneered high content imaging technology applications in drug discovery. In 2005, he built the Pitt Molecular Library Screening Center (School of Medicine) where he led 21 HTS campaigns and reconfigured the NCI 60 assays for drug combination screening. In 2011, Dr. Johnston established an independent chemical biology laboratory focused on applying novel drug discovery strategies to identify new and effective drugs or drug combinations for cancer. He provides expertise in HTS/HCS assay development and implementation in other therapeutic areas. A founding member (2012) and former president of SBI2, Dr. Johnston teaches biochemistry and drug discovery courses in the Pharm.D. and Ph.D. programs of the School of Pharmacy.

 **Joe Trask** Emeritus Research Scientist & Founding President, SBI2	Joe Trask is a co-founder and the founding president of the Society for Biomolecular Imaging and Informatics (SBI2) and serves as an associate editor for the NIH/NCATS Assay Guidance Manual. Over three decades, he advanced drug discovery through cellular technologies including high content imaging, confocal microscopy, and flow cytometry, contributing to research in cancer, immunology, neurodegeneration, and toxicology. He is recognized for driving strategic collaborative engagement through teaching, training, and partnerships. His career includes positions in academia (Duke University; The Ohio State University), the pharmaceutical industry (Abbott Laboratories; Eli Lilly), nonprofit research (Hamner Institute for Health Sciences), and the life sciences sector (PerkinElmer/Revvity).
 **Joshua A. Harrill** Senior Investigative Toxicologist Corteva Agriscience	Dr. Joshua Harrill is a Senior Investigative Toxicologist at Corteva Agriscience in Indianapolis, Indiana. He received his doctorate in Toxicology from the University of North Carolina at Chapel Hill in 2008 and most recently was a Cellular and Molecular Toxicologist at the US EPA Center for Computational Toxicology and Exposure prior to joining Corteva. Dr. Harrill's expertise includes the development and use of high-content imaging and molecular profiling assays to characterize the biological activity of chemicals in human and animal-derived cell models and application of such data for predictive safety assessment. Dr. Harrill has previously served as a project leader and technical expert in omics for the OECD Advisory Group on Emerging Science in Chemicals Assessment and the Health and Environmental Sciences Institute Emerging Systems Toxicology for the Assessment of Risk Committees. He currently serves on the steering committee of the Omics for Assessing Signatures for Integrated Safety (OASIS) Consortium, which aims to advance the use of omics technologies, including phenomics, for chemical safety assessment and toxicity prediction. Dr. Harrill has co-authored > 70 research publications in peer-reviewed toxicology journals as well as six book chapters on a variety of topics including imaging-based assay development for toxicology.
 **Chris Dunsby** Professor Imperial College London	Chris Dunsby works on quantitative fluorescence imaging techniques for applications in biomedicine, including Förster resonant energy transfer microscopy, automated multiwell plate imaging and fluorescence lifetime imaging. He has also worked on super-resolution fluorescence imaging techniques. He collaborates with colleagues in Bioengineering to translate developments in optical super-resolution imaging to super-resolved ultrasound imaging. He invented and patented oblique plane microscopy, which is a form of light sheet fluorescence microscopy that can be implemented on a conventional microscope frame to provide high speed 2-D and 3-D imaging. He has also led projects to develop and apply multiphoton imaging and FLIM for clinical applications and developed novel multiphoton endoscopes.

 **Louise Morlot** PhD fellow Danish Cancer Institute	Louise Morlot is a PhD fellow at the Danish Cancer Institute and the University of Copenhagen where she develops optical pooled screening approaches to interrogate cellular and nuclear processes involved in genome stability.
 **Jordi Carreras-Puigvert** CSO Pixl Bio	Jordi Carreras-Puigvert, PhD, is Chief Scientific Officer and co-founder of Pixl Bio, a biotechnology company combining automated phenomics, iPSC-derived human cell models, and artificial intelligence for predictive biology. Jordi holds a MSc in Biotechnology by the Universitat Autònoma de Barcelona, Catalonia, and a PhD in Life Sciences by Leiden University, Leiden, the Netherlands. With a prolific scientific publication record, and over a decade of experience in high-content imaging and cell-based phenotypic screening, Jordi is considered a key opinion leader in the field and has been leading the application of Cell Painting and morphological profiling for drug discovery and toxicity assessment. In parallel, Jordi holds an Associate Professor and Senior Lecturer position at Uppsala University, Sweden, affiliated with the Pharmaceutical Bioinformatics group. Prior to this position, Jordi gained a solid scientific background during two postdoctoral periods at the Leiden University Medical Center, Leiden, the Netherlands, and Karolinska Institutet, Stockholm, Sweden, where he was also Assistant Professor. His research sits at the intersection of quantitative imaging, chemical biology, and machine learning, with a strong focus on translating phenotypic data into actionable insights for early drug development and safety prediction.
 **John Arevalo** Principal ML Scientist Genentech	John Arevalo is a Principal Machine Learning Scientist at Genentech, where he develops machine learning methods for multimodal perturbation data in computational biology and drug discovery. During his postdoctoral research at the Broad Institute of MIT and Harvard, he led data processing and batch correction benchmarks for the JUMP Cell Painting consortium and co-authored evaluation frameworks based on mean Average Precision (mAP) for phenotypic profiling pipelines. Previously, he built computer vision and natural language processing systems at the AI Fund. He holds a Ph.D. cum laude from Universidad Nacional de Colombia, where he developed multimodal data fusion architectures widely used across academia and industry.

 **Runxi Shen** Research Assistant Professor Purdue University	Runxi Shen, Ph.D., is a computational biologist whose research combines quantitative genetics, cellular imaging, and machine learning to understand human disease and advance drug discovery. His work uses rich cellular phenotypes to study how genetic variation and chemical exposure alter protein localization, cellular organization, and biological state. By connecting imaging profiles with genomic, molecular, and clinical evidence, he seeks to clarify the functional consequences of genetic variants and uncover mechanisms that link genotype to disease. He also studies how cellular responses to chemical exposure can reveal mechanisms of toxicity and support more predictive, human relevant approaches to chemical safety assessment. His research spans rare disease, cancer, functional genomics, predictive toxicology, and therapeutic discovery, with a consistent focus on translating complex multimodal measurements into interpretable biological insights. He is particularly interested in approaches that move beyond describing cellular differences to explain why they occur, determine whether they matter for disease or human health, and reveal how harmful phenotypes might be prevented or corrected. Across these efforts, his broader goal is to make cellular profiling a practical bridge from biological observation to safer medicines, more precise interventions, and improved human health.
 **Erin Diel** President Glencoe Software, Inc.	Erin Diel is President of Glencoe Software. She has worked with imaging data directly and in the context of educating and supporting users of imaging data for over 15 years. She has extensive experience translating community-developed open-source technologies into sustainable and scalable software ecosystems for global biopharma.
 **Tim Treis** scverse core developer / PhD student Helmholtz Munich	Tim Treis is a final-year PhD candidate in the lab of Fabian Theis at Helmholtz Munich and TUM, and a Visiting Scientist in the Carpenter-Singh Lab at the Broad Institute. He is a core developer of the scverse open-source ecosystem, where he contributes to squidpy and the SpatialData framework. He also works on cp_measure, a Python library exposing CellProfiler features for programmatic morphological profiling. His research focuses on spatial omics, including histopathology, and on integration and evaluation methods for image-based profiling.

 **Ilan Gold** scverse core developer / Computational Biologist Memorial Sloan Kettering	Ilan Gold is a Computational Biologist at Memorial Sloan Kettering and a core developer for scverse. He has worked across the open source single-cell stack, from GPU accelerated visualization to high performance file formats. His work on Viv provided a widely-used building block for web based viewers of OME data without needing a server. Now he focuses more on scverse's data structures and has recently extended the foundational anndata to deep learning with annbatch. His approach is rooted in a commitment to open source community and development, leading to roles in other projects like zarr-python and deck.gl.
 **Jonny Sexton, Ph.D.** Associate Professor, Internal Medicine University of Michigan	Jonny received his PhD in chemistry from the University of California, San Diego and moved to Stanford University as a postdoctoral fellow in Roger Kornberg's laboratory studying the structural biology of transcription complexes. During his time in the Kornberg lab, Roger was awarded the 2006 Nobel Prize in Chemistry for his studies of the molecular basis of eukaryotic transcription. Jonny then moved to North Carolina and helped to start the BRITE institute and ultimately became the director of drug discovery. He moved his laboratory to the University of Michigan in 2018 in the department of internal medicine, division of gastroenterology and hepatology, where his research focuses on drug-induced liver injury and liver organoids as a platform for drug discovery. His laboratory specializes in image-based high-content screening, cell painting, and AI/ML and machine vision to enhance drug discovery. He is also the director of the U-M Center for Drug Repurposing, founded in 2019.
 **Beth Cimini** Associate Director, Bioimage Analysis The Broad Institute of MIT and Harvard	Dr. Beth Cimini is the Director for Bioimage Analysis at the Imaging Platform at the Broad Institute in Cambridge, MA. The Cimini lab (est 2021) focuses on bioimage analysis tool creation (Piximi, Bilayers) and maintenance (CellProfiler), as well as on applying open source tools to novel biological problems; they collaborate with 20-30 outside labs a year (ranging from small academic labs through large pharmaceutical companies). She co-created and directs the Platform's Postdoctoral Training Program in Bioimage Analysis, and also leads the Broad efforts on community engagement and technology development for the Center for Open Bioimage Analysis (COBA). She is a proud recipient of both the Association of Biomolecular Resource Facilities Alan Smith "Mentor of the Year" award as well as BioImaging North America's Michael W Davidson award for contributions in "Inclusion, Education, Mentorship, Standardization, and/or Advocacy".

 **Erin Weisbart** Senior Computational Biologist Broad Institute of MIT and Harvard	Erin Weisbart, Ph.D., is a Senior Computational Biologist and the Head of Image Analysis in the Cimini Lab, in the Imaging Platform at Broad Institute of MIT and Harvard. She is an expert in image analysis at scale, particularly the Cell Painting assay and pooled optical screening. She is lead curator of the Cell Painting Gallery, a petabyte-scale public image data repository, and contributes to CellProfiler software. Erin is particularly passionate about metadata and documentation.
 **Emma Lundberg** Associate Professor Stanford University	Dr. Emma Lundberg is Associate Professor of Bioengineering and Pathology at Stanford University & Professor at KTH Royal Institute of Technology, where she directs the Cell Atlas of the Human Protein Atlas program. Her research sits at the intersection of bioimaging, proteomics, and artificial intelligence, mapping the spatiotemporal organization of the human proteome to understand how protein localization shapes cellular function and disease. A strong advocate for open science, she champions the generation and sharing of high-quality biological data as the foundation for building trustworthy AI models of the cell. She also advises biotech and AI companies, aiming to leverage her interdisciplinary expertise to underpin discoveries in biology and medicine.

Scientific Session I - The Evolving Importance of Complex Model Systems

 **Jonny Sexton, Ph.D.** Associate Professor, Internal Medicine University of Michigan	Jonny received his PhD in chemistry from the University of California, San Diego and moved to Stanford University as a postdoctoral fellow in Roger Kornberg's laboratory studying the structural biology of transcription complexes. During his time in the Kornberg lab, Roger was awarded the 2006 Nobel Prize in Chemistry for his studies of the molecular basis of eukaryotic transcription. Jonny then moved to North Carolina and helped to start the BRITE institute and ultimately became the director of drug discovery. He moved his laboratory to the University of Michigan in 2018 in the department of internal medicine, division of gastroenterology and hepatology, where his research focuses on drug-induced liver injury and liver organoids as a platform for drug discovery. His laboratory specializes in image-based high-content screening, cell painting, and AI/ML and machine vision to enhance drug discovery. He is also the director of the U-M Center for Drug Repurposing, founded in 2019.

 **Jenny Tam** Director - Synthetic Biology, Wyss Institute for Biologically Inspired Engineering	Jenny M. Tam, PhD, is Director of Synthetic Biology at the Wyss Institute for Biologically Inspired Engineering at Harvard University and Lecturer in Genetics at Harvard Medical School. Her career has centered on building optical instrumentation and imaging-based molecular readout systems, from single-molecule detection to whole-organoid transcriptomics. During her PhD, she developed high-density fiber-optic microwell and nanowell arrays resolving tens of thousands of individually addressable sensors per square millimeter, enabling attomolar- and femtomolar-sensitivity single-molecule detection. As a postdoctoral fellow at Massachusetts General Hospital and Harvard Medical School, she designed and built a custom optical-trap and confocal microscopy system for real-time imaging of host-pathogen interactions and intracellular signaling. At the Wyss Institute, in collaboration with George Church, she co-developed BOLORAMIS, a high-sensitivity variant of Fluorescence In Situ Sequencing (FISSEQ), to profile transcripts within intact iPSC-derived brain organoids. Currently, she directs a large team spanning molecular engineering, imaging, and translational neuroscience, and leads CircaVent, a drug-discovery program pairing high-density microelectrode array (HD-MEA) recordings with multi-omic organoid profiling to study bipolar disorder, for which she serves as lead PI on a funded award through BD^2.
 **Max A. Winkelman** Senior Scientist Emulate, Inc.	Dr. Max Winkelman is an accomplished scientist with over twelve years of Organ-Chip experience dedicated to improving the efficacy of human translational research through the routine adoption of microphysiological systems. In his role as a Senior Scientist at Emulate, Dr. Winkelman drives the development and validation of biological models for Emulate's Organ-on-a-Chip technology. He has contributed to the successful launch of numerous models across Emulate's platforms, including the Zoë-CM2® Culture Module and the AVA™ Emulation System. In addition to his development work, Dr. Winkelman has helped lead Emulate's Liver-Chip qualification work through the FDA's ISTAND program. Dr. Winkelman earned his Ph.D. in Bioengineering from Northeastern University, where his doctoral dissertation focused on the development of brain microvascular networks in microfluidic devices. Prior to his doctorate, he completed a M.Eng. in Biomedical Engineering at Rensselaer Polytechnic Institute and a B.S. in Biomedical Engineering from the University of Rochester.



Matteo Cantarelli
CEO & Co-founder
Neuroglass (by MetaCell)

Matteo Cantarelli is CEO and co-founder of MetaCell and the mind behind NeuroGlass, the collaborative platform where research teams review massive imaging datasets together, straight from their own cloud.

Trained as an electronic and systems engineer (University of Cagliari; École Normale Supérieure Paris-Saclay), Matteo has spent fifteen years where software architecture meets biology. At University College London he helped build Open Source Brain, a community resource for sharing computational models of neurons. He also co-founded the OpenWorm Foundation, the open-science project building a digital worm. His work has been published by the Royal Society and featured in The Economist.

Since co-founding MetaCell in 2011, Matteo has built its engineering and design team from the ground up and worked side by side with scientists in pharma, biotech and academia. After years as CTO, he was recently appointed CEO and continues to shape NeuroGlass and to serve customers including the Allen Institute, Calico Life Sciences, MIT and Harvard Medical School.

Find Matteo at the NeuroGlass booth to talk about large-scale image review, cloud data strategy, and where collaboration and AI fit in screening.

Lunch & Learn

 **Jordi Carreras-Puigvert** CSO Pixl Bio (for Cephla)	Jordi Carreras-Puigvert, PhD, is Chief Scientific Officer and co-founder of Pixl Bio, a biotechnology company combining automated phenomics, iPSC-derived human cell models, and artificial intelligence for predictive biology. Jordi holds a MSc in Biotechnology by the Universitat Autònoma de Barcelona, Catalonia, and a PhD in Life Sciences by Leiden University, Leiden, the Netherlands. With a prolific scientific publication record, and over a decade of experience in high-content imaging and cell-based phenotypic screening, Jordi is considered a key opinion leader in the field and has been leading the application of Cell Painting and morphological profiling for drug discovery and toxicity assessment. In parallel, Jordi holds an Associate Professor and Senior Lecturer position at Uppsala University, Sweden, affiliated with the Pharmaceutical Bioinformatics group. Prior to this position, Jordi gained a solid scientific background during two postdoctoral periods at the Leiden University Medical Center, Leiden, the Netherlands, and Karolinska Institutet, Stockholm, Sweden, where he was also Assistant Professor. His research sits at the intersection of quantitative imaging, chemical biology, and machine learning, with a strong focus on translating phenotypic data into actionable insights for early drug development and safety prediction.
 **Keith Olson** CEO Ananda Devices	Dr. Olson brings extensive leadership experience in the life sciences sector and a strong track record of helping organizations translate innovative technologies into real-world impact. Throughout his career, he has supported companies in advancing scientific innovation into scalable, commercially and strategically viable solutions. At Ananda Devices, Dr. Olson advises on corporate strategy, industry partnerships, and growth initiatives, strengthening the company's ability to collaborate with pharmaceutical, biotechnology, and research organizations. His expertise supports the expansion of Ananda's next-generation microfluidic platforms across drug discovery, toxicology, and translational research applications. Dr. Olson's leadership reinforces Ananda's mission to accelerate the development of safer, more effective therapies through human-relevant testing platforms.

Scientific Session II - Acquisition: The Next Frontier of Imaging Technologies



Akaash Kumar
Research Fellow
Cambridge Institute for Medical Research & MRC Laboratory of Molecular Biology

Akaash Kumar is an Isaac Newton Trust Research Fellow in Science, Technology, Engineering and Mathematics based at the Cambridge Institute for Medical Research (CIMR), the MRC Laboratory of Molecular Biology (LMB), and Fitzwilliam College, Cambridge. Akaash's research is highly interdisciplinary, operating at the intersection of engineering, biophysics, and cell biology. His work is dedicated to solving complex biological problems with two core long-term aims: first, to shed light on dynamic, 'systems-level' biology, and second, to use these fundamental insights to improve therapeutic approaches, such as 'living drugs'.

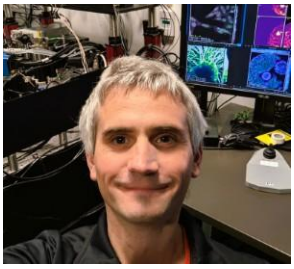
His research aims to decode how immune cells, such as cytotoxic T cells, execute their functions. To study this, Akaash has developed novel, custom imaging hardware and software. These technologies can improve any camera-based microscope, yielding significantly more information much faster than pre-existing approaches and enhancing our ability to visualise complex biological processes in live cells. He is an inventor on the patent for these technologies, which is undergoing commercialisation.

His work has culminated in publications in leading scientific journals (such as Nature Photonics) and has been recognised with several awards, including the Royal Microscopical Society Early Career Award, the Max Perutz Award, and the Cambridge Society for the Application of Research Award.



Angeline Lim
Product Manager
Molecular Devices

Dr. Angeline Lim is a Product Manager (Imaging) at Molecular Devices, where she drives innovation in high-content imaging and automation. With over a decade of research experience and a PhD in Molecular Cell and Developmental Biology from UC Santa Cruz, she has authored patents and publications in 3D cell culture and phenotypic analysis.

 **Adam Glaser** Senior Scientist Allen Institute	Adam Glaser joined the Allen Institute for Neural Dynamics in 2021. He works in the multi-scale molecular neuroanatomy group, focusing on the development of hardware and software tools for large-scale imaging projects. He is a recipient of the K99/R00 Pathway to Independence award from the NIH/NCI and DP2 New Innovator award from the NIH/OD. His imaging systems have led to the co-founding of two companies (Dose Optics and Alpenglow Biosciences) and have been licensed to multiple other companies. Prior to joining the institute, he worked as a postdoctoral research associate in the Department of Mechanical Engineering at the University of Washington, where he is now an Affiliate Assistant Professor. There he worked in Jonathan Liu's laboratory, leading the development of open-top light-sheet microscopy systems for three-dimensional clinical pathology. He earned his Ph.D. in Engineering Sciences from Dartmouth College in 2015, and B.S. in Mechanical Engineering from Tufts University in 2010.
 **Alfred Millett-Sikking** Senior Staff Engineer Calico Life Sciences LLC	Alfred Millett-Sikking is a hybrid physicist and engineer who is fascinated by the notion of optimal designs. He has spent his career assembling expertise in applied physics, optics, mechanics, electronics, and programming to drive innovation in microscopy. As a Senior Staff Engineer at Calico Life Sciences, Alfred has specialized in element- and system-level advancements, most notably through the invention of the "Snouty" objective lens and the development of AIRR microscopy. He is dedicated to improving existing technologies and inventing new ones that bridge the gap between complex optical engineering and practical biological application. https://amsikking.github.io/
 **Steven Straub** Principal Product Specialist Revvity	Steve Straub is a Principal Product Specialist for High Content Imaging and Cellular Analysis at Revvity, where he applies his scientific and technical expertise in imaging, image analysis, and automation to support drug discovery and research efforts across a diverse user base. Before joining Revvity, Steve was a Senior Scientist in the Cardiovascular, Metabolic, and Endocrine Diseases Research Group at Pfizer in Groton, CT, where he established an imaging and electrophysiology lab to support the development of novel therapeutics for the treatment of diabetes and obesity. Steve obtained his Ph.D. in Pharmacology from the University of Rochester School of Medicine and performed his postdoctoral training in the lab of Dr. Mark Nelson at the University of Vermont School of Medicine. His academic research focused on elucidating the mechanisms by which intracellular calcium signaling and ion channels control various physiological processes including matching blood flow to neuronal activity in the cerebral cortex, cerebral vascular function, and exocrine cell secretion.



Derek Lowe
Director, Exploratory Chemical Biology
Novartis

Derek Lowe has worked in drug discovery since 1989 for a series of biopharma companies across several therapeutic areas, most recently for Novartis doing exploratory chemical biology research. He is known for his "In the Pipeline" blog that covers drug discovery, chemistry, and science in general and has now been running since 2002.

Scientific Session III - Analysis: From Observations to Novel Phenotypes



Avtar Singh
Principal Scientist
Genentech

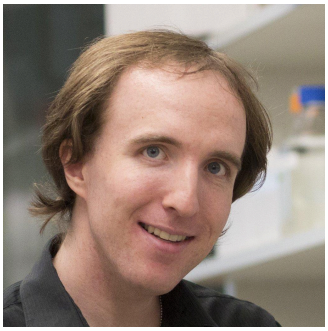
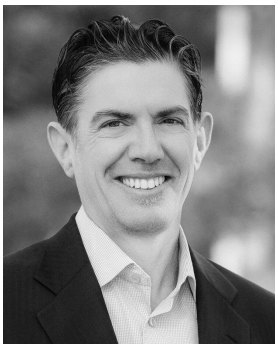
Avtar Singh is a Principal Scientist in the Discovery Omics Technology Department at Genentech, where he develops and applies image-based screening methods to identify new therapeutic targets and understand how drug molecules function.

He previously co-invented optical pooled screening (OPS) at the Broad Institute, a method that links image-based phenotypes to pooled genetic perturbations through in situ sequencing. OPS has made it possible to perform genome-scale imaging screens, with rich single-cell phenotypes resolved in space and time. It has since been applied to map regulators of NF-κB signaling, profile the morphological effects of genetic perturbations, and identify host factors governing viral infection. More broadly, OPS has been adopted by groups across academia and industry, and extended to new phenotypes, cell types, and biological questions.

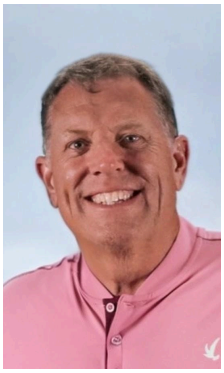
His current interests include pairing imaging with transcriptomic readouts, leveraging highly multiplexed phenotypic panels to dissect perturbation responses across diverse biological processes, and measuring live-cell dynamics to study responses over time.

Avtar previously received his PhD in Applied Physics from Cornell University, where he developed novel approaches for single-molecule and super-resolution microscopy.

 **Laura M. Heiser** Professor OHSU	Dr. Laura Heiser is Professor and Vice Chair of the Department of Biomedical Engineering and Co-Leader of the Knight Cancer Institute Quantitative Oncology Program at OHSU. In 2025, she was elected Fellow to the American Institute of Medical and Biological Engineering (AIMBE). The long-term goal of the Heiser Lab is to design smarter therapies that improve outcomes for patients with hard-to-treat cancers. Toward that goal, her research program integrates cutting-edge imaging, single-cell sequencing, and computational modeling to develop frameworks for predicting and overcoming therapeutic resistance in cancer. A central focus has been on cellular heterogeneity and tumor–microenvironment interactions, areas that are critical for advancing precision medicine in aggressive cancers such as triple-negative breast cancer. These contributions span both methodological innovation and translational impact, establishing new paradigms that advance fundamental science while informing therapeutic development.
 **Pier Federico Gherardini** VP Computational Biology Cellanome	Pier Federico Gherardini, PhD, is Vice President of Computational Biology at Cellanome, where he leads the development of advanced analytical frameworks and data integration strategies for the company's multimodal cellular analysis platform. With nearly 20 years of experience in bioinformatics and single-cell technologies, Pier Federico's vision is to harness longitudinal imaging data paired with transcriptomics to decode the complex "choreography" of cell behavior and interactions. Before joining Cellanome, he was Director of Informatics at the Parker Institute for Cancer Immunotherapy, where he led the design and development of the CANDEL platform to integrate clinical and molecular data for oncology research. Pier Federico holds a PhD in Cellular and Molecular Biology from the University of Rome Tor Vergata and completed his postdoctoral training in the laboratory of Garry Nolan at Stanford University. He has authored over 55 peer-reviewed papers in prestigious journals such as Science, Cell, and Nature Methods.
 **Alexandr Kalinin** Senior Machine Learning Scientist Biohub San Francisco	Alexandr Kalinin is a Senior Machine Learning Scientist in the Computational Imaging group at Biohub San Francisco, where his research focuses on foundation models for virtual staining and dynamic profiling of cells across biological scales and states. He previously worked as a Computational Scientist II at the Imaging Platform of the Broad Institute of MIT and Harvard, an International Postdoctoral Fellow jointly at the Shenzhen Research Institute of Big Data and the University of Michigan, and a Fulbright Visiting Graduate Researcher at UCLA. He holds a PhD in Bioinformatics from the University of Michigan and an MSc in Applied Mathematics and Computer Science from Novosibirsk State Technical University. He has authored over 35 peer-reviewed articles, cited more than 10,000 times according to Google Scholar.

 **Shalin Mehta** Senior Manager, AI/ML Biohub	We build computational imaging and AI methods that robustly profile dynamic cell systems across the scales of organelles to organs. Our interdisciplinary team of AI and imaging scientists and engineers develops and deploys computational imaging and deep-learning technologies that accelerate dynamic imaging and image-based profiling across the spatial scales spanning organelles to living tissues. The expertise of the group spans computational imaging, deep learning, live cell microscopy, and software engineering. We collaborate closely with other technology developers and biologists to address open questions in systems cell biology, host-pathogen interaction, immunology, and developmental biology.
 **Mike Veling** Senior Data and Imaging Scientist Merck (MSD)	Mike Veling, PhD is a Senior Data and Imaging Scientist at Merck & Co., where he develops image analysis and data science approaches for high-content imaging and image-based phenotypic profiling in drug discovery. At Merck, he has applied Cell Painting and transcriptomics to link organelle morphology with production performance in CHO recombinant clones (Biotechnology and Bioengineering, 2023). More recently, he led the analysis of a large-scale benchmark comparing live-cell profiling with ChromaLIVE™ against fixed-cell Cell Painting. His earlier research covered mitochondrial disease genetics, multi-omics, and multispectral imaging analysis. Mike earned his PhD from the University of Wisconsin–Madison and was a postdoctoral researcher at Harvard Medical School. He holds a BS in Biochemistry and Molecular Biology from UMass Amherst, where he was a Goldwater Scholar.
Lunch & Learn	
 **Michael Previte** CTO, SVP R&D & Co-Founder Element Biosciences	Michael co-founded Element Biosciences and brings more than 10 years of innovation and discovery in the field of genomics. Previously, Michael was an Associate Principal Scientist at Illumina. While at Illumina, Michael pioneered innovations in advanced sequencing technologies for both single molecule and ensemble-based methods. He also worked developing high throughput assays for protein evolution and discovery. Prior to Illumina, Michael worked at Life Technologies innovating new single molecule sequencing technologies. During his almost 10 years of work in the sequencing industry, Michael holds four independent sequencing technology patents and has published one of those technologies in Nature Communications. Michael holds his PhD from Boston College in physical chemistry and received his postdoctoral training from MIT, where he trained in combining advanced microscopy techniques with high throughput assays to study complex biochemical systems. Over his 25 years of work in science and discovery, Michael has over 35 publications and has filed over 25 patents in the areas of plasmonics, sequencing, enzymology, instrumentation, surface chemistry, DNA amplification, high throughput assay discovery, and microscopy.

Scientific Session IV - Application: Novel Phenotypes to Decisions



Emery Smith
Senior Scientist
Herbert Wertheim UF Scripps Institute for Biomedical Innovation and Technology

Senior scientist for the Department of molecular medicine at UF-Scripps. Been with Scripps since 2006. I have background in cell-based and biochemical assay development and HTS screening for the purpose of branching basic discovery and therapeutic treatment of diseases. I am a world leader in HTS screening technologies. Utilizing luminescence, fluorescence, TR-FRET, and high content analysis to find lead molecules for drug discovery. Previous to this, I worked in an infectology lab at Scripps, under Dr Charles Weissmann, working on prions. Prior to that, I spent 7 years in industry at Athersys, Inc Biotech company. My focus started with cell culture and process development for transfected cell lines. I then worked on a platform that eventually led to Multistem, a pluripotent cell line derived from bone marrow. I spent the time characterizing the cell line and differentiating it into different lineages as a proof of concept. From this, I worked on SOP generation for pre-clinical use of the stem cells.



Jonne Rietdijk, Ph.D.
Postdoctoral fellow
EMBL-EBI

Jonne is a Postdoctoral Fellow at EMBL-EBI and a data analyst for the OASIS Consortium, focusing on integrating Cell Painting, transcriptomics, and proteomics to advance toxicity prediction.

 **Erin Diel** President Glencoe Software Inc.	Erin Diel is President of Glencoe Software. She has worked with imaging data directly and in the context of educating and supporting users of imaging data for over 15 years. She has extensive experience translating community-developed open-source technologies into sustainable and scalable software ecosystems for global biopharma.
 **Max R. Salick** Director insitro	Max Salick, PhD, is the director of the Integrated Technology eXploration (ITX) department at insitro. Max holds a BS/MS in Engineering Mechanics and Astronautics, and a PhD from the Materials Science Program at the University of Wisconsin - Madison. During his 12 years in the pharma and biotech industries, he has developed numerous technologies that bridge the gap between wet lab and dry lab, with an emphasis on high throughput and pooled methodologies. Max completed his postdoctoral work at the Novartis Institutes for Biomedical Research (NIBR), where he conducted CRISPR screens on Zika virus tropism, developed human cerebral organoid models of epilepsy, and built one of the first industrial wet lab and computational droplet-based scRNAseq pipelines. At insitro, Max leads a cross-functional team of engineers and scientists that conduct research spanning imaging, transcriptomics, functional genomics, and computational biology. The tools and platforms developed by the team are directly translated into machine learning model development, target discovery, and therapeutic screening campaigns at insitro.

Poster and Speaker Information

Poster titles, abstracts, and placement numbers accessible below.	
SBI2 2026 Posters:	SBI2 Posters 2026

SBI2 Board Member Nominations

The Society invites those interested in supporting its Mission to participate in upcoming elections and Board member nominations.	
Feel free to nominate yourself or someone you believe will be a great fit for the board!	SBI2 Nominations 2027

Conference and Exhibit Hall Map

SBI2 13th Annual Conference
November 2-4, 2026

Renaissance
Boston Seaport District

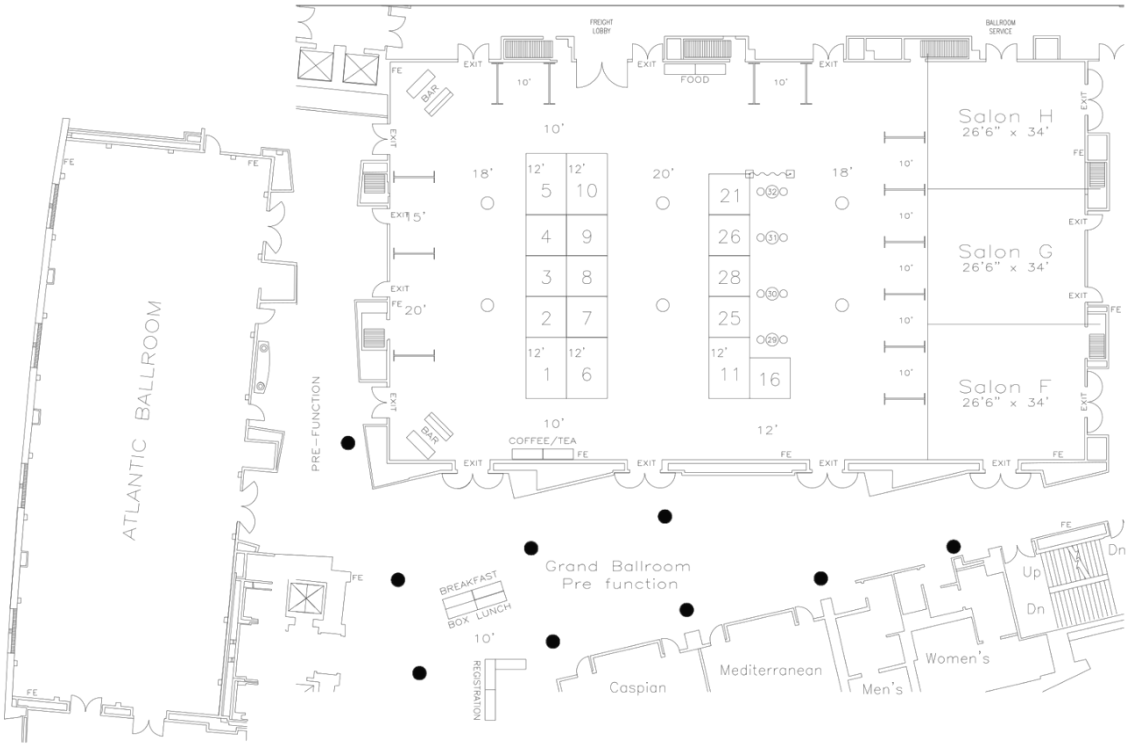


Exhibit Hall and Foyer
● Posters
● Exhibit booths
● High tops + EH map
● Food/Beverage stations
● SBI2 Registration Desk

Exhibitor Booths			
Cephla	1	Saguaro	2
Agilent	3	ONI	4
Yokogawa	5	Araceli Biosciences	6
Glencoe	7	Aurora	8
NeuroGlass	9	Revvity	10
Molecular Devices	11	Genedata	16
Ramona Optics	21	Tomocube	25
ibidiUSA, Inc.	26	Element Biosciences	28
Cytely	29	Oxxius	30
Okolab	31	Luminos	32