Society of Biomolecular Imaging & Informatics 2024

SBI2's 11th Annual Conference

WESTIN COPLEY PLACE, BOSTON, MA, USA
SEPTEMBER 18 - SEPTEMBER 20, 2024

Program & Events Guide

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Sponsors Description

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Lunch and learn by Dr. Leticia Montoya, Friday, Sept. 20, 1:00–1:45 p.m.

See program for location

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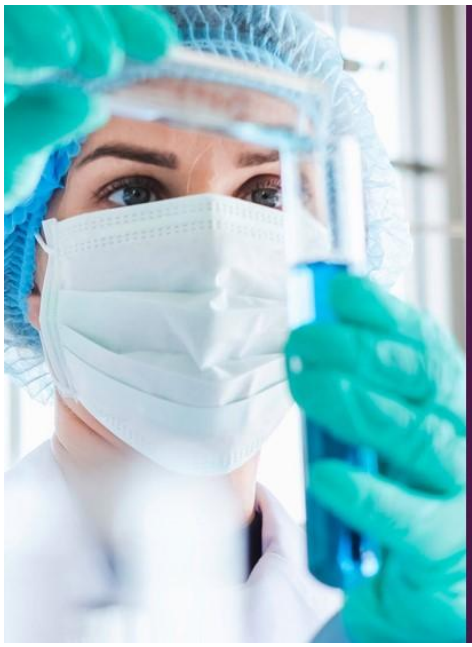


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President's Welcome

Dear Colleagues,

Welcome to the 11th Society of Biomolecular Imaging and Informatics Annual Conference in Boston, MA! On behalf of all the SBI2 Board members, councilors, and volunteers, we sincerely hope you will find this to be another fantastic year to share innovations in imaging and informatics.

The three full days of the program start with the Education Sessions led by experienced instructors that will provide both foundational concepts and the current state-of-the-art on topics ranging from HCI/HCS, large-capacity computational infrastructure, to 3D model systems and volumetric imaging. The Hands-on workshop led by Beth Cimini (the 2023 SBI2 President) will provide a practical introduction to HCS image analysis and tools. The workshop filled to capacity quickly, indicating the strong interest of scientists in learning HCS analytic workflows. The Colloquium, co-hosted with the CytoData Society (https://www.cytodata.org/), includes perspectives from speakers that will lead to a round table discussion on the future of image-based profiling with artificial intelligence. The Main Sessions offer compelling presentations by expert speakers that cover developments in artificial intelligence applied to imaging datasets, complex organoids, model systems, challenges associated with imaging biology in 3D, novel imaging modalities and multiplex techniques, and spatial-omics. We are delighted to host our Keynote Speakers: Daphne Koller of Insitro to offer compelling perspectives on the digital innovation and transformation of AI within the drug discovery process; Hongkui Zeng of the Allen Institute for Brain Science to share how the complexities of cellular diversity of the mammalian brain underly its organization and function.

This event has become a premier opportunity to discuss high-content imaging, screening, and emerging developments for scale and throughput in this field. The amalgamation of imaging platforms, biological model systems, and computational analytics and visualization highlights the expertise of academic, non-profit, industrial and commercial scientists across all levels and geolocations. Attendees from 16 countries reflect the international appeal of this community. Importantly, we can find delight in meeting up with colleagues and friends and making new connections through the scientific and social interactions offered at this event.

SBI2 is entirely volunteer-led, and this fantastic program is made possible through the dedication and personal efforts of the Board members, councilors, and volunteers. The Society invites those interested in supporting its Mission to participate in upcoming elections as a Board member, committee, or volunteer. You can also obtain insights at the SBI2 booth on how to get involved or speak to any of the Board members. I hope the conference will provide new insights, knowledge, and friendships that you can take back to continue your imaging innovation journey. Enjoy and have fun!

Katherine Hales
President, SBI2 2024

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.

A very brief history, a mission statement, a welcome

Paul A. Johnston, Joe Trask, Mark Collins, and Steve Haney

As founders and early members who participated in the driving force to set SBI2 in motion, we have documented the history and aims of this endeavor in introductory articles in scientific journals, ADT, and SLAS Discovery. While we encourage readers to delve deeper into the history of SBI2, this briefly highlights the key issues that have shaped the society.

SBI2 grew from the grassroots sentiments held by several early adopters of HCS technologies in the scientific community. This included recurring attendees at scientific tradeshows that curved out HCS technologies with specialized sessions at SLAS and ISAC. But, it was Cambridge Healthtech Institute (CHI)'s "High-Content Analysis" meeting that capitalized on gathering international delegates of leading scientists to focus solely on HCS technologies. While these meetings helped bring together the High Content community as the field started to mature, a recognizable gap emerged between what a commercial conference and a professional society conference could do to support the demands of the attendees. A call to action was initiated after the CHI meeting in (2012) when Joe Trask and Paul Johnston debriefed in the Tonga Bar, in the basement of the iconic Fairmont SF hotel and one of the nation's renowned Tiki Bars. The result was the initiation and foundation of a professional, scientific society that provides unique benefits for its members in the following:

- **Cost.** SBI2 is almost completely volunteer-based and support has always been strongly channeled into the annual meeting to keep costs for attendees low and value high.
- **Volunteering.** The passion of the scientists and leaders of SBI2 have shaped the society by maintaining high-quality cutting-edge science while reducing costs for the greater community of young investigators, students, and professionals.
- **Community and networking.** A strength of SBI2 is building networking alliances to advance science with global leaders of HCS technologies. These relationships have helped foster partnerships between academia and the pharmaceutical industry, assist students and professionals in finding new positions or jobs, and align with agencies to participate in "standards" for the community.
- **Rigor and scientific content.** As a rapidly growing field with complexity of technologies (microscopy, cellular technologies, assay validation, information management and data sciences), establishing best practices is of critical importance to advance basic science and preclinical drug discovery. SBI2 has addressed this need through the educational programs and plenary sessions of the annual meetings, website content, and by contributions to the scientific literature.
- **Highlighting innovation.** SBI2 has been at the forefront of promoting cutting-edge imaging sciences that are known to expand in many directions. SBI2 members have embraced key areas of innovation, effectively funneling and disseminating information to the community through various communication channels, including annual conferences, scientific literature, and the SBI2 website.

From this nucleating event, the process of making this a reality played out on scales large (501(c)3 status, vendor support for the conference, etc.) and small (what would we name ourselves and how would the name shape what the society would evolve into). The latter were, in many ways, the thornier. Most societies focus on broad definitions: diseases, technologies, clinical/regulatory development. One of the things that made the High Content community so vibrant were the connections between:

- bench science and clinical relevance,
- wet lab work and computational biology,
- simple cell models and more complex translational biological systems,
- bench scientists and the vendors that enable the research, and
- between industrial drug discovery and basic science.

Trying to capture this breadth, The Society of Biomolecular Imaging and Informatics (SBI2) was chosen over names such as The Society of High Content Screening. While the latter had its advocates, and the branding was undeniable, SBI2 conveyed the growth potential of the fields under this banner.

On top of the broad spectrum of ways to define SBI2's scope, high emphasis has always been placed on serving scientists at all stages of expertise in imaging and informatics.

The best expression of SBI2's efforts to meet these goals has been embodied in the programs of the Annual Meetings. Significant work goes into the program for the Annual Meeting for each year, to highlight the process and challenges in developing image-based assays for screening, assays in novel biology, emerging biological models in health and disease, and the integration of imaging and informatics in algorithmically driven approaches to chemical biology, pathway biology and other bleeding-edge imaging science. A significant focus of our annual meetings has been to showcase innovation, whether it be different applications, new technologies, and/or novel informatics approaches.

As Founders, we are deeply thankful to the multitude of scientists who volunteered at SBI2. Their contributions have significantly advanced the society's growth while upholding its goals and principles.

We invite you to reach out and join the SBI2 family.

Consider becoming a member!

Register to become a member of the SBI2 community to access premium content.

https://sbi2.org/membership/register/

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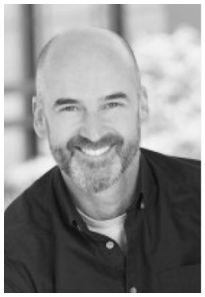

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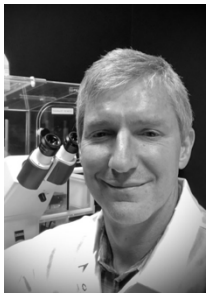

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Conference at-a-Glance

Wednesday, September 18

7:30 AM	**Check-in opens**
8:00 AM – 9:00 AM	**Breakfast**
9:00 AM – 12:00 PM	**Education Sessions & Hands-on Workshop:**

- **Track 1: Introduction to HCS**
  - *Introduction to HCS, Part 1: Fundamentals of HCS* – Steve Haney
  - *Best Practices for HCS Assay Development* – Paul A. Johnston (U Pittsburgh)
  - *Addressing the challenges of complex culture models to allow for high-throughput and high-content screening* – Joshua A Bauer (Vanderbuilt U)
- **Track 2: Large-Capacity Resources for HCI/HCS**
  - *A Toolbox for High-Content Screening in Complex Human Model Systems* - Ilya Lukonin (Roche)
  - *Strategies for performing image data analysis at scale* – Erin Diel (Glencoe Software)
  - *Transforming Digital Pathology through the convergence of Cloud and Generative AI* - Ujjwal Ratan & Pierre de Milliard (AWS)
- **Track 3: Advanced HCI/HCS Models and 3D Imaging Parameters**
  - *Tools & Techniques for Working with Spheroids and Organoids* - Hilary Sherman (Corning)
  - *Title: TBD* - Sylke Hoehnel-Ka (SunBiosciences)
  - *Imaging pitfalls: a practical guide to acquire the perfect image for restoration and quantitative analysis from 2D-5D* - Nicolaas van der Voort (Scientific Volume Imaging)
- **Hands-on workshop (9:30 AM start)** *Practical Training Guide to HCS Analysis & Tools* – Beth Cimini Lab (Broad Institute)

12:00 PM – 12:45 PM	**Lunch**
12:45 PM – 5:00 PM	**Colloquium: co-hosted with CytoData & Sponsored by Recursion**

- Colloquium Sponsor - Recursion
- John Hickey (Duke)
- Meghan Driscoll (U Minnesota)
- **Coffee Break sponsored by Calico Labs**
- Auguste Genovesio (IBENS, Paris)
- Proffered papers
- **Round Table Discussion:** *Future of image-based profiling (AI, bridges to other fields)*

5:00 PM – 6:30 PM	**Post-Colloquium Reception**

Thursday, September 19	
7:30 AM	**Check-in opens**
8:00 AM – 6:00 PM	**Exhibit Hall Opening**
8:00 AM – 8:50 AM	**Breakfast**
8:50 AM – 9:00 AM	**Opening Remarks:** Katherine Hales, SBI2
9:00 AM – 10:00 AM	**Keynote Speaker:** Daphne Koller (Insitro) *Transforming Drug Discovery using Digital Biology*
10:00 AM – 10: 15 AM	● Exhibitor Highlight - Revvity
10:15 AM – 10:45 AM	**Coffee Break & Exhibit Viewing & Poster Session**
10:45 AM – 1:00 PM	**Session 1: Advanced imaging platforms and technologies:** ● Laura Waller (UC Berkeley, co-chair) ● Anne Beghin (Mechanobiology Institute) ● Eric Lubeck (Genentech) ● Exhibitor Spotlight – Molecular Devices ● Proffered papers
1:00 PM – 2:00 PM	**Lunch & Learn Sponsored Sessions** ● CytoTronics ● Araceli
2:00 PM – 4:45 PM	**Session 2: Imaging of Next Generation Cellular Models** ● Evgeny Shlevkov (Lieber Institute for Brain Development, co-chair) ● Javier Frias Aldeguer (HUB Organoids) ● **Coffee Break & Exhibit Viewing & Poster Session** ● Josh Harrill (EPA) ● Exhibitor Spotlight - InSphero ● President's Innovation award
4:45 PM – 7:30 PM	**Poster Session, Exhibit Viewing, & Reception**

Friday, September 20	
7:30 AM	**Check-in opens**
8:00 AM – 5:00 PM	**Exhibit Hall Opening**
8:00 AM – 9:00 AM	**Breakfast**
9:00 AM – 10:00 AM	**Keynote Speaker:** Hongkui Zeng (Allen Institute for Brain Science) *Cell type diversity and organization in the mammalian brain*.
10:00 AM – 10:15 PM	● Exhibitor Highlight - Gubra
10:15 AM - 10:45 PM	**Coffee Break & Exhibit Viewing & Poster Session**
10:45 AM - 1:00 PM	**Session 3: Spatial biology: Creating cellular and molecular maps of tissues** ● Mingyao Li (UPenn, co-chair) ● Daniel KRENTZEL (Pasteur Institute, Paris)

	● Denis Wirtz (JHU) ● Exhibitor Spotlight – Genedata ● Proffered papers
1:00 PM- 2:00 PM	**Lunch & Learn Sponsored Sessions** ● Carl Zeiss Microscopy ● Thermo Fisher Scientific
2:00 PM - 4:30 PM	**Session 4: Advances in Informatics, Deep learning, and AI** ● Jean-Philippe Vert (Owkin) ● Juan Caicedo (U Wisconsin, co-chair) ● Exhibitor Spotlight – Glencoe Software ● Award Ceremony: Best Posters ● Caroline Uhler (MIT) ● Proffered papers
4:30 PM - 5:00 PM	**Coffee Break**
5:00 PM - 6:00 PM	**SBI2 Annual General Meeting (AGM)**
6:00 PM	**End of Conference**

Program Agenda: Day 1, Sept. 18

Education Sessions, Hands-on Workshop, & Colloquium

EDUCATION SESSIONS **9:00 AM – 10:00 AM**	
Track I	**Introduction to HCS**
Room: St George C&D 3rd Floor	*Introduction to HCS, Part 1: Fundamentals of HCS* **Steve Haney,** Independent Consultant

Abstract

This discussion will present the landscape of topics one encounters as they get started in HCS and imaging assays. General topics that are relevant to biology and drug discovery, such as assay design, will be covered in passing to allow more time for topics unique to imaging studies. These include the types of imaging assays that can be considered, the mechanics of capturing images for quantification and the quantification process itself. Image generation topics will include introducing development of multi-channel fluorescent assays for cell signaling and health endpoints as well as general phenotypic assays. Specialized assays including FRET-based biosensors for unique cellular events and live cells assays for immune cell function will be discussed. Image analysis, taking a set of images and extracting data can occur on several levels. The most common method for data analysis is to leverage an image analysis application, either proprietary for the instrument used or open source. Feature selection and statistical analyses to generate results will be discussed. Complex analytical methods, including profiling of multiple features, deep learning quantification and emerging AI methods will be covered as well.

Track II	Large-Capacity Resources for HCS
Room: Empire 7th floor	*A Toolbox for High-Content Screening in Complex Human Model Systems* **Ilya Lukonin,** Roche

Abstract

The use of high-content screening (HCS) in organoids offers a robust method for phenotypic discovery. This approach necessitates the integration of assay development, automation, microscopy, image analysis, and data mining. While individual components can be employed independently for smaller-scale experiments, the successful execution of a screening project demands the seamless integration of all these building blocks. Given the substantial time investment required for initial screening endeavors, it is of key importance to developing modular and transferable protocols and infrastructure to operationalize the use of advanced image processing methods and streamline subsequent projects. To illustrate the practical application of this framework, I will present a trailblazing case study focusing on patient-derived organoids (PDOs) in colorectal cancer liver metastasis (CRCLM). This study underscores the role of cell-to-cell variability in disease progression and highlights the necessity of understanding donor variability in compound response. Through the multivariate phenotypic characterization of PDOs, we effectively captured diverse cellular states and quantified the effects of compounds at both the organoid and single-cell levels. Our ongoing work centers on refining screen analysis by measuring single cells, describing organoids, identifying cellular states, and performing phenotypic clustering to elucidate donor-specific perturbation landscapes. Overall, my presentation will showcase the power of HCS as a phenotypic discovery method in complex model systems and underscores the potential of this approach to accelerate phenotypic discovery and facilitate the development of targeted therapeutic interventions. I will focus on the technical aspects of the screening experimental paradigm and how cutting-edge machine-learning tools can be employed in this context.

Track III	Advanced HCI/HCS Models and 3D Imaging Parameters
Room: Great Republic 7th floor	*Tools & Techniques for Working with Spheroids and Organoids* **Hilary Sherman,** Corning

Abstract

Spheroids and organoids have significant advantages over traditional two-dimensional (2D) cell cultures, in large part because of their ability to better mimic the architecture of tissue and organs and the in vivo microenvironment. The realistic cellular arrangement makes it possible to study biological behaviors as cell-cell interactions and cell migration in a physiologically meaningful context. Access to this information has important implications for developing personalized medicines and targeted therapies for a wide range of diseases.In this presentation, Hilary Sherman will discuss the advantages of spheroid and organoid models over traditional 2D models and highlight why they are the best option for biomedical research and drug development. Through this presentation, you'll learn about the variety of tools available for working with 3D culture and helpful tips for selecting the right tools for different applications.

EDUCATION SESSIONS
10:00 AM – 11:00 AM

Track I	Introduction to HCS
Room: St George C&D 3rd Floor	*Best Practices for HCS Assay Development* **Paul A. Johnston,** Univ. of Pittsburgh

Abstract

An introduction to High Content Screening (HCS/HCI/HCA) will be provided including a brief discussion of the typical requirements and components necessary to establish an HCS laboratory. The four major components of HCS assay development will be discussed; sample preparation, image acquisition, image analysis, and data analysis. Some case histories will be presented to illustrate the process.

Track II	Large-Capacity Resources for HCS
Room: Empire 7th floor	*Strategies for performing image data analysis at scale* **Erin Diel,** Glencoe Software

Abstract

As high-throughput imaging technology has advanced, researchers have been able to acquire increasingly large and multi-dimensional image datasets, which yield even more complex and high-volume derived analytical results. This poses a challenge for data management, image analysis, and data science workflows. The open source platform OMERO, and its commercial counterpart OMERO Plus, offer enterprise-level data management for bioimaging data and associated metadata, including rich image analysis results. The utility of any such system is enhanced by closer integration with existing data science tools for processing stored data and optimized performance of remote data retrieval. In this session, we detail considerations for the structure of imaging and analysis data which impact downstream workflows, in particular for TB-scale, remote datasets. We then demonstrate the impact of such data structures on interactive data analysis and visualization tools for an enterprise environment.

Track III	Advanced HCS Models and 3D Imaging Parameters
Room: Great Republic 7th floor	*Standardizing automated organoid workflows using the SUN bioscience Gri3D microwell plate* **Sylke Hoehnel-Ka,** SunBiosciences

Abstract

Gri3D® by SUN bioscience is a groundbreaking hydrogel 96-well plate that enables the culture of 10'000 organoids on a single focal plane. Featuring dense U-shaped hydrogel microwells, it supports in situ organoid formation and analysis including high-resolution imaging, thanks to the hydrogel's water-like refractive index. The Gri3D® plate design is automation-compatible, allows effortless medium changes without loss of 3D structures and is compatible with all major brands of imaging and analysis systems. In this talk we will highlight several applications for 3D image-based screenings including immune cell - tumoroid co-cultures.

EDUCATION SESSIONS
11:00 AM – 12:00 PM

Track I	Introduction to HCS
Room: St George C&D 3rd Floor	*Addressing the challenges of complex culture models to allow for high-throughput and high-content screening* **Joshua A. Bauer,** Vanderbilt University

Abstract

There remains an ongoing demand for more complex cell culture models that better mimic in vivo physiology and disease states compared to traditional monolayer cells. The need to better understand how these complex 3D models function in response to different perturbagens (chemicals, drugs, siRNAs, CRISPRs, growth factors, etc.) is a great need and would allow us to identify the usefulness and ultimate translatability of these culture models. However, because of their complexity, scaling down and doing high-throughput screening (HTS) and high-content screening (HCS) of these models is challenging. These challenges include: the development and maintenance of cultures of uniform size, the formation of viable 3D cultures from a small number of cells, cell plasticity (eg, iPSCs), the specific ratios of different cell types in co-culture, reproducibility of assays, genetic and phenotypic stability, the rigidity and content of matrices and scaffolds necessary for these cultures, media and growth factors for formation of cultures, and overall the lack of reliable, simple, standardized, automated high-throughput compatible assays for HTS or functional genomics screening. Additional challenges with imaging complex 3D cultures include: capturing high-quality images from large, dense cultures, long imaging times and z-stacks to capture large cultures, huge volumes of data (images) to store and process, necessary software for image analysis and quantification of the features and objects within three dimensions, identifying and classifying phenotypes, and interpreting the data to model

physiological relevance. These challenges will be discussed, along with examples of how the HTS core has collaborated to develop HCS assays for disease-specific culture models. In this manner, the HTS core has bridged the gap between the development of 3D culture models in individual labs with the ability to automate and screen in high-throughput. Establishing HCS assays and screening methods in the HTS core has the potential to identify novel drug targets, learn disease biology, identify drug response mechanisms and mechanisms of drug resistance at the single cell level, identify mode of action/drug target of small molecules, identify target engagement, learn important pharmacology, have the ability to miniaturize limited sample numbers to maximize the breadth of drug screening, standardize imaging and screening methods, and importantly, develop and screen translational models of disease using patient-derived material to strategize clinical treatment.

Track II	**Large-Capacity Resources for HCS**
Room: Empire 7th floor	*Transforming Digital Pathology through the convergence of Cloud and Generative AI* **Ujjwal Ratan & Pierre de Milliard,** Amazon Web Services

Abstract

The field of digital pathology is witnessing a profound transformation, driven by the convergence of cloud computing and the advent of powerful generative AI models. The integration of these enabling technologies holds immense promise for enhancing diagnostic accuracy, accelerating research discoveries, and improving patient outcomes. In this presentation, we will explore how Amazon Web Services (AWS) - as the leading cloud platform - is uniquely positioned to empower the future of digital pathology through its robust infrastructure, scalable services, and cutting-edge AI/ML capabilities. Building upon the foundation of cloud infrastructure, we will examine how the virtually limitless storage, seamless data management and elastic compute capabilities of the cloud allowed researchers to seamlessly handle the exponential growth of high-resolution digital slide data. Furthermore, we will examine the transformative potential of generative AI models in the field of pathology. By presenting specific use cases, we will demonstrate how AWS's comprehensive suite of services can empower pathologists, researchers and healthcare organizations to push the frontiers in digital pathology

Track III	**Advanced HCI/HCS Models and 3D Imaging Parameters**
Room: Great Republic 7th floor	*Imaging pitfalls: a practical guide to acquire the perfect image for restoration and quantitative analysis from 2D-5D* **Nicolaas van der Voort,** Scientific Volume Imaging

Abstract

Image analysis is a key bottleneck in obtaining relevant conclusions from fluorescent-based high throughput assays necessary for drug discovery. Existing for over 28 years, the Huygens software is known for powerful deconvolution and image restoration, allowing for higher throughput by means of shorter acquisition times and higher image quality overall. Further, Huygens comes with powerful image analysis tools that can be adapted and automated to suit your assay. Accelerate your screening experiments with Huygens by: 1. True deconvolution. Huygens true deconvolution efficiently increases the resolution and contrast while removing the noise. This even works on extremely noisy data. 2. Crosstalk Corrector. Record your channels simultaneously without channel crosstalk. Efficiently estimate and remove crosstalk up to 32 channels with the Crosstalk Corrector. 3. Workflow Processor. Combine the image restoration with the Huygens Object and Colocalization analyzers in the Workflow Processor to streamline the complete analysis pipeline from acquisition to quantitative results with one click of a button. Deconvolution and image restoration can also be integrated in the existing image analysis pipeline, for example with the Batch Processor. Specify the folder in which the images are acquired and get the images deconvolved instantaneously. For a more thorough

integration, we offer the powerful compute engine of the Huygens Core where you can fully integrate Huygens in your existing image analysis pipeline using the Huygens Command Line Interface. Run the Huygens images processing with a job scheduler like SLURM, or integrate it in an existing Python image analysis pipeline. Organoid & Cell Analysis Empower your research with the Object Analyzer tool, simplifying the segmentation and analysis of a multitude of morphological and statistical parameters, even in 3D and 5D (multichannel, time series). Whether quantifying organoid growth or counting individual cells, the Object Analyzer streamlines the process with just a few clicks. Dive deeper into your studies by exploring protein colocalization with the Colocalization Analyzer, or delve into the cellular dynamics using the AI-based Object Tracker. To conclude, with the advanced image restoration and analysis options of the Huygens software, you have an all-in-one solution for fast, robust, and reliable screening experiments.

HANDS-ON WORKSHOP
9:30 AM – 12:00 PM

Room: Staffordshire 3rd Floor	*Practical Training Guide to HCS Analysis & Tools* **Led by Beth Cimini Lab,** Broad Institute

Abstract

A major bottleneck for many scientists hoping to start High Content Screening (HCS) is uncertainty about how, computationally, to do so. In this workshop, we will give users a practical introduction to CellProfiler, a free open-source tool designed to facilitate high content, high throughput analysis. We will also explore Morpheus, a free open-source tool for exploring data from such experiments. Finally, we will point attendees at resources for learning more, including how to include deep learning in their HCS workflows.

12:00 PM – 12:45 PM	**Lunch**

COLLOQUIUM **Co-hosted with CytoData & Sponsored by Recursion**

12:45 PM – 5:00 PM
Room: Staffordshire

Title: Image-based profiling of biological systems across scales and modalities
Chairs: Loan Vulliard (DKFZ), Brian Feng and Zhenghao Chen (Calico Labs)

12:45 - 1:00 Recursion	**Colloquium Sponsor: Recursion**
1:00 - 1:10	**CytoData Society welcome**
1:10 - 1:30	**CytoData Hackathon 2024 highlights**
1:30 - 2:00	**John Hickey,** Duke University **Title:** *From Molecules to Multicell Modules: Transforming Pixels to Pathways*

Abstract

Advancements in single-cell multiplexed imaging coupled with sophisticated computational algorithms have greatly augmented our views into complex tissue microenvironments. In this seminar, I will present the approaches we have developed to deconstruct intricate tissue datasets and connect them across scales from molecular to multicell modules. Particularly, I will share a vignette of cell organizational rules we found within melanomas treated with effective and ineffective T cell therapies.

2:00 - 2:30	**Meghan Driscoll,** University of Minnesota **Title:** *Image analysis from the perspective of a moving cell*

Abstract

Cells shape and reshape themselves as they accomplish diverse functions in vivo. Numerous algorithms have been developed to locally track the cell edge in 2D microscopy movies, enabling discoveries ranging from cellular search strategies to the intracellular signaling hierarchies coupled to cell morphology. However, robust 3D surface tracking algorithms have yet to be developed. To track detailed 3D cell surfaces across large movements, we developed a computational framework based on functional maps, which were originally invented in computer graphics to solve shape correspondence problems between pairs of deformable 3D surfaces. To enhance interpretability, we framed the tracking parameters as physical conservation laws, enabling physical modeling or extraction of physically inspired quantities. We demonstrate the capabilities of our framework by tracking the surfaces of cells with diverse morphologies and imaged via multiple microscopy modalities. We also apply our framework to track morphological motifs, including blebs and filopodia, and compare surface velocities to local rates of change in underlying signaling activity.

2:30 - 3:00	**Coffee Break Sponsored by Calico Labs**
3:00 - 3:30	*Selected poster flash talk 1 and 2*
3:30 - 4:00	**Auguste Genovesio,** Ecole Normale Supérieure (IBENS) **Title:** *Deep Generative Models Reveal Invisible Phenotypes*

Abstract

For the last 25 years, automated cell image analysis has gradually transitioned from quantifying morphological features of interest to systematic morphological profiling, and then to deep learning representations. While this process has enabled us to shift toward more sensitive ways to discriminate or associate conditions effectively, interpreting these subtle phenotypic variations remains difficult. We have also learned that most cellular phenotypic changes of interest are subtle and thus hidden from us by natural cell variability: two cells in the same condition, prior to any treatment, already look different. In this talk, we will show how generative models can be leveraged to transform an image of cells from one condition to another, thereby canceling cell variability. We will then illustrate its effectiveness in displaying otherwise invisible cell phenotypes triggered by blood cells under parasite infection, by the presence of a disease-causing pathological mutation in differentiated neurons derived from iPSCs, or by low concentration drug treatments. We will then delve into recent methodological improvements that will make this type of approach possible with a very small quantity of images. Generative models open the door to more accessible discovery of biological and disease biomarkers.

4:00 - 5:00	**Round table:** *Future of image-based profiling (AI, bridges to other fields)* **Panel leads: Brian Feng** and **Zhenghao Chen** (Calico Labs) **Panelists: Meghan Driscoll** (Univ. of Minnesota), **William Godinez Godinez Navarro** (Novartis), **Juan Caicedo** (Univ. Wisconsin), **Oren Kraus** (Recursion), **John Hickey** (Duke Univ.), **Auguste Genovesio** (Institute of Biology of the École Normale Supérieure Paris (IBENS)
5:30 - 7:00	**Post-Colloquium Reception [Staffordshire & Foyer]**

Program Agenda: Day 2, Sept. 19

MAIN SESSION
Room: Staffordshire

KEYNOTE
9:00 - 10:00

Daphne Koller, Insitro
Title: *Transforming Drug Discovery using Digital Biology*

Abstract
Modern medicine has given us effective tools to treat some of the most significant and burdensome diseases. At the same time, it is becoming consistently more challenging and more expensive to develop new therapeutics. A key factor in this trend is that we simply don't understand the underlying biology of disease, and which interventions might meaningfully modulate clinical outcomes and in which patients. To achieve this goal, we are bringing together large amounts of high content data, taken both from humans and from human-derived cellular systems generated in our own lab. Those are then used to learn a meaningful representation of biological states via cutting edge machine learning methods, which enable us to make predictions about novel targets, coherent patient segments, and the clinical effect of molecules. Our ultimate goal is to develop a new approach to drug development that uses high-quality data and ML models to design novel, safe, and effective therapies that help more people, faster, and at a lower cost.

Daphne Koller
CEO and Found of Insitro

Keynote Bio
Daphne Koller is CEO and Founder of Insitro, a machine learning-driven drug discovery and development company. Daphne is also co-founder of Engageli, was the Rajeev Motwani Professor of Computer Science at Stanford University, where she served on the faculty for 18 years, the co-CEO and President of Coursera, and the Chief Computing Officer of Calico Labs. She is the author of over 300 refereed publications with an h-index of over 150. Daphne was recognized as one of TIME Magazine's 100 most influential people in 2012. She received the MacArthur Foundation Fellowship in 2004, the ACM Prize in Computing in 2008, the ACM AAAI Allen Newell Award in 2019, and the AnitaB.org Technical Leadership Abie Award Winner in 2022. Daphne was inducted into the National Academy of Science in 2023, into the National Academy of Engineering in 2011 and elected a fellow of the American Association for Artificial Intelligence in 2004, the American Academy of Arts and Sciences in 2014, and the International Society of Computational Biology in 2017.

10:00 - 10:15

revvity

Exhibitor Spotlight – Revvity
Joe Trask
Title: *Empowering Discovery Research Through Innovative Workflows*

Abstract
In this presentation, we will delve into innovative workflows designed to enhance the scientific discovery process. Leveraging cutting-edge tools, software, and methodologies, researchers can streamline their work. Our collaborative and interdisciplinary approaches prioritize data integrity and in-depth analytical process

10:15 - 10:45 **Coffee Break & Exhibit Viewing & Poster Session**

Session 1 10:45 - 1:00	**Advanced imaging platforms and technologies** **Chairs:** Stephen Walker (Abbvie) and Laura Waller (UC Berkeley)
10:45 - 11:15	**Laura Waller:** UC Berkeley **Title:** *Computational super-resolution microscopy with dynamic samples*

Abstract

Computational imaging involves the joint design of imaging system hardware and software, optimizing across the entire pipeline from acquisition to reconstruction. This talk will describe new microscopes and space-time algorithms that enable 3D or super-resolution fluorescence microscopy and phase measurement with high resolution on dynamic samples. Traditional model-based image reconstruction algorithms work together with neural networks to optimize the inverse problem solver and the data capture strategy in order to account for sample motion during the capture time of a multi-shot computational imaging method.

11:15 -11:45	**Anne Beghin:** Mechanobiology Institute, National University of Singapore **Title:** *AI, Imaging, and Organoids: Pushing the Boundaries Towards Space Exploration*

Abstract

Analysing the tissue morphogenesis and function is crucial for unravelling the underlying mechanisms of tissue development and disease. Organoids, 3D in vitro models that mimic the architecture and function of human tissues, offer a unique opportunity to study effects of external perturbators that are difficult to replicate in vivo. However, large-scale screening procedures for studying the effects of different 'stress' on cellular morphology and topology of these 3D tissue-like systems face significant challenges, including limitations in high-resolution 3D imaging, and accessible 3D analysis platforms. These limitations impede the scale and throughput necessary to accurately quantify the effects of mechanical and chemical cues. We present a novel, fine-tuned pipeline for screening morphology and topology modifications in 3D cell culture using multilevel segmentations and cellular topology, based on confocal microscopy and validated across different image qualities. Our technology incorporates advanced image analysis algorithms and artificial intelligence (AI) for multiscale 3D segmentation, enabling quantification of morphology changes at both the nuclear and cytoplasmic levels, as well as at the organoid scale. Additionally, we investigate cell relative position and employ neighbouring topology analysis to identify tissue patterning and their correlations with organoid microniches. Eventually, we have organized all the extracted features, 3D segmented masks and raw images into a single database to allow statistical and data mining approaches to facilitate data analysis, in a biologist-friendly way. We validate our approach through proof-of-concept experiments, including well-characterized conditions and poorly explored mechanical stressors such as microgravity, showcasing the versatility of this type of pipeline. By providing a powerful tool for discovery-like assays in screening 3D organoid models, such a holistic approach has wide-ranging interests from biomedical applications and tissue engineering to Space biology.

11:45 - 12:15	**Eric Lubeck,** Genentech **Title:** *Highly multiplexed, image-based pooled screens in primary cells and tissues with PerturbViews*
12:15 - 12:30 MOLECULAR DEVICES	**Exhibitor Spotlight – Molecular Devices** **Angeline Lim** **Title:** *Scaling Innovations: Overcoming Barriers to 3D cell culture adoption*

Abstract
The use of 2d and 3d cell models at scale— especially in high throughput cell- based assays— has become an important part of the drug discovery and development pipeline. Because cells grown in 3D can better mimic cell-cell interactions and the tissue microenvironment, there is an increased demand for use of 3D models such as PDOs in drug discovery. However, scaling up the processes involved in cell culture remains a significant challenge for most labs. One way to address these challenges is to provide researchers with large numbers of high quality, low-variability assay-ready organoids or a solution to grow their own cell lines. The newly launched CellXpress.ai™ Automated Cell Culture System- a fully automated cell culture system automates the entire cell culture process with an integrated incubator, liquid handler, and AI-powered, image-based decision-making. This hands-off system manages demanding feeding and passaging schedules 24/7 by monitoring the development of cell cultures with periodic imaging and analysis, and leverages machine learning to initiate passaging, endpoint assay, or troubleshooting steps.

12:30 - 12:45	**Selected Abstract talk 1** **Gennady Shvets** **Title:** *Metasurface-enabled Inverted Reflected-light Infrared Microscopy: a new label-free imaging platform*

Abstract
Fluorescent imaging of cells in culture with an inverted microscope is a “work horse” of high-content imaging (HCI) in a multi-well format that can be conveniently integrated with automated pipetting. An important limitation of fluorescence-based microscopy is the need for potentially photo-toxic labels. While several label-free modalities, such as quantitative phase imaging (QPI) and its derivatives, have recently emerged, these HCI techniques have their own limitations related to their transmission-based optical setup. In this presentation, I will introduce a new HCI approach to mid-infrared (MIR) vibrational imaging that utilizes the vibrational fingerprints of various molecular groups as endogenous in a label-free and non-destructive manner. The adoption of vibrational imaging to live-cell analysis has been limited so far because of the strong attenuation of MIR light in water, often necessitating awkward sample geometries (e.g., ten-micron deep cuvettes) incompatible with long-term (multi-day) studies of viable cells. I will describe a novel chemical imaging platform – Metasurface-enabled Inverted Reflected-light Infrared Microscopy (MIRIAM) – where cells are cultured atop of plasmonic metasurfaces [1] (arrays of metallic nanoantennas attached to the microwell bottoms) and imaged using a rapidly-tunable quantum cascade laser (QCL) for MIR illumination. Cells are imaged through their near-field interaction with the metasurface. Chemical contrast in the MIR band is used by us to image the proteins, lipids, and nucleic acids in the cells, obtaining images with sub-cellular resolution. Continuous time-lapse imaging of living fibroblast cells demonstrates that their behaviors, including motility, viability, differentiation, and liquid droplet formation, are not affected by the low-power MIR light. Our earlier results using well-integrated kinetic imaging of cellular responses to various compounds (GPCR-activating peptides, enzymes, and chemotherapeutics) will also be briefly outlined [2]. The MIRIAM approach provides a method for HCI-MIR imaging of living cells, which is well-suited for integration with modern high-throughput screening technologies for the label-free, high-content chemical imaging of living cells in culture. Our reflected-light imaging approach – with all the optics placed below the microplate – makes MIRIAM fully compatible with automated liquid dispensing. This is important for kinetic assays involving serial additions of multiple compounds. I will demonstrate our validation of our imaging approach by standard endpoint fluorescent imaging, and discuss the advantages of not having to fix (i.e. kill) the cell or to use any fluorescent stains. Further applications to label-free high-content drug screening will be discussed.
We acknowledge the support by the National Cancer Institute (R21 CA251052) and the National Institute of General Medical Sciences (R21 GM138947) of the NIH. The nanofabrication work was performed at the NSF-supported Cornell NanoScale Facility (Grant NNCI-2025233).
[1] Wu, C. et al. Fano-resonant asymmetric metamaterials for ultrasensitive spectroscopy and identification of molecular monolayers. Nat. Mater. 11, 69–75 (2012).

[2] Huang, S. H. et al. Metasurface-enhanced infrared spectroscopy in multiwell format for real-time assaying of live cells. Lab. Chip 23, 2228–2240 (2023).

12:45 – 1:00	**Selected Abstract talk 2** **Martina Zowada** ***Title:*** *ACHILLEUS – Next-generation drug discovery for targeting cancer stem cell pathways*

Abstract

Stem cell activity is one of the main drivers of metastasis, treatment resistance, and relapse in colorectal cancer (CRC) and contributes to its high mortality. Thus, there is an unmet medical need to identify and develop novel anti-cancer therapies explicitly targeting the stemness pathways of CRC cells. As a toolkit to study stem cell activity, we have established a large biobank of patient-derived CRC organoid cultures, a collection of three-dimensional in vitro models retaining patient characteristics regarding mutations, gene expression, and drug response. DNA sequencing and gene expression profiling have confirmed the heterogeneity of this biobank and the representation of different CRC subtypes. In the ACHILLEUS project, we use this unique biobank of CRC organoid cultures for high-throughput, phenotypic drug profiling, and high-content screening. Our screening approach treats representative CRC organoid cultures reproducibly with hundreds of drugs per assay. The phenotypic changes induced by the drug treatments are then assessed by imaging the fixed and stained organoids. Z-stacks are acquired to capture the three-dimensionality of the organoids.

In our high-performance, cloud-based image analysis pipeline, acquired images are preprocessed, and segmentation and feature extraction are performed. The resulting phenotypic profiles, in combination with the organoid metadata, are then incorporated into the knowledge base. Overall, the unique combination of our high-throughput, three-dimensional organoid screening platform and machine learning-based profiling pipeline constitutes a novel drug discovery platform with the potential to identify stem cell-targeting drugs against colorectal cancer.

1:00 - 2:00	**Lunch & Learn Sponsored Sessions**
Room: St George A/B CytoTronics	**CytoTronics** **Shalaka Chitale** **Title:** *Multiplexed electrical imaging as a tool to study live cell phenotypes in high throughput*

Abstract

CytoTronics Pixel electrical imaging platform boasts a state-of-the-art semiconductor 96-well microplate platform designed for high-resolution, real-time, multi-parametric electrical “imaging” of cells. Each well in the microplate boasts an array of >100,000 electrochemical electrodes spaced at 12.5 µm pitch, enabling single-cell resolution. The platform uniquely offers three live-cell modalities –impedance, electrochemical and electrophysiological, all utilizing the same electrode array. The measurements are label-free, non-invasive, and non-destructive, facilitating continuous cell monitoring through growth, pharmacological modulation, and cell death over days or weeks. Combining the modalities into a single microplate generates high-dimensional, live cell datasets, capturing >30 functional and morphological parameters, including tissue barrier, cell-surface attachment, cell flatness, and motility through unique field-based impedance measurements. Electrophysiological techniques enable functional assessments of electrogenic cells like cardiomyocytes and neurons. All modalities harness the 12.5 µm spatial resolution and allow measurements at intervals ranging from minutes to hours, creating electrical “heat-map” images and time-lapsed videos revealing the end-to-end journey of the experiment. Further insights are derived from spatial image and time-domain analyses. This high-dimensional data provides unique signatures for cell types, capable of resolving even subtle differences in cell function or phenotype. Thus, electrical imaging can quantitatively distinguish

cell-types based on their unique morphological and functional phenotype, eliminating the need for labels, and greatly expanding the applications of live cell imaging. These capabilities are integrated into a standard-sized microplate, serving as a self-contained measurement device, capable of measuring over 30 types of cells, ranging from epithelial and mesenchymal cancer cells to suspension cell lines, primary rodent cells, and human induced pluripotent stem cells (iPSCs). During experiments, each semiconductor microplate seamlessly interfaces with readers, with slots for 1 to 8 plates at a time – with the potential to scale and integrate with high throughput screening automation. In conclusion, the Pixel's multiplexed readouts enable a new approach in cell-based assays.

Room: St George C/D

Araceli

Claudia McCown: The Herbert Wertheim UF Scripps Institute for Biomedical Innovation and Technology, Dept of Molecular Medicine

Title: *Combining HCA Imaging with Binary AI to Identify Modulators of Neurite Outgrowth*

Abstract

With increasing life expectancy and the rising prevalence of neurodegenerative diseases, innovative approaches to neuronal drug discovery are urgently needed. Human induced pluripotent stem cell (hiPSC)-derived neurons, also known as induced neurons (iNs), show significant promise for elucidating the mechanisms of brain disorders and propelling drug discovery efforts. iNs are excellent candidates for high-throughput screening because they are scalable and demonstrate unique morphological features. High-Content Analysis (HCA) is often used to identify potential drug candidates by quantifying neurite outgrowth from neurons as a measure of neuronal health. Here, we expand upon this well-established methodology by utilizing the high-resolution imaging capabilities of the Araceli Endeavor® alongside a series of binary AI models from ViQi's AutoHCS analysis toolkit. Using these tools, we train a machine learning model to phenotypically separate images of iNs treated with control compounds known for their positive and negative effects on neurite outgrowth. The high-resolution images captured on the Endeavor are a crucial aspect of the machine learning image analysis, enabling the detection of minute morphological differences between treated cells and the categorization of these cells into distinct clusters. This advanced clustering allows us to determine the degree of similarity between control compounds and those with unknown effects. For example, we demonstrate the impact of this technology by showing that a novel test compound groups closely with negative outgrowth controls, suggesting that this compound negatively impacts neurite outgrowth in our iNs. These methodologies enable the rapid assessment of novel compounds on neuronal morphology. Such screening technologies represent a significant advancement in identifying neuronal drug candidates through unbiased AI-driven data analysis. Overall, our iN technologies hold substantial potential to enhance compound screening throughput for human neurons, thereby advancing drug discovery in neurological disorders.

Session 2 2:00 - 4:45	**Imaging of Next Generation Translational Cellular Models** **Chairs:** Ahmet Coskun (Ga Tech and Emory Univ) and Chris Bakal (Institute of Cancer Research UK)
2:00 - 2:30	**Evgeny Shlevkov:** Assistant Director, Drug Discovery Lieber Institute for Brain Development Assistant Professor Department of Pharmacology and Molecular Sciences Johns Hopkins University School of Medicine **Title:** *Morphological Profiling of Trophoblast Stem Cells Derived From Patients with Schizophrenia*

Abstract

Genomic risk for schizophrenia converges with early life complications, associated with placenta pathophysiology, in affecting risk for the disorder and sex-biased neurodevelopmental trajectories. The candidate molecular mechanisms highlight nutrient-sensing capabilities of placenta and trophoblast invasiveness. Trophoblast stem cells (TSCs) are in vitro precursors of the differentiated cells of the placenta and represent a powerful model for the study of placental development and function. TSCs can be generated through differentiation of fibroblast-derived induced pluripotent stem cells (iPSCs) followed by resetting to naïve-like state. Morphological profiling represents a promising avenue to map diagnosis and genotype-driven pathways in iPSC-derived cells. We have leveraged the Cell Painting assay to profile 23 genotypically distinct TSC lines derived from human patient iPSCs from SCZ (13 cell lines) and non-SCZ donors (10 cell lines). TSC lines were randomly seeded in 96 well plates and were amenable to standard Cell Painting procedures, passing all quality control metrics. A machine learning-based approach developed by Spring Science coupled with more traditional feature extraction and analysis through Cell Profiler and Pycytominer revealed that TSC lines display unique phenotypic signatures, with each line occupying their own phenotypic space. At the individual cell line level, AI-powered unbiased embeddings demonstrated that, while all Cell Painting stains achieved some degree of cell line clustering, nuclear staining was the most significant driving force of line-to-line separation. Furthermore, line-to-line clustering was independent of cell density, allowing for the comparison of cell lines that grow at drastically different rates. At the diagnosis level, traditional feature extraction revealed that SCZ patient-derived TSC lines displayed significant deviations from control lines. When stratified by sex, male and female SCZ lines had unique profiles relative to their respective control groups, suggesting that certain morphological changes in TSCs are influenced by sex. Our work demonstrates the utility of morphological profiling in iPSC-derived TSC cell lines and paves the way for future mechanistic studies.

2:30 - 3:00	**Javier Frias Aldeguer:** HUB Organoids **Title:** *Patient-Derived Organoids: A New Frontier in Drug Discovery and Bioimaging*

Abstract

Compared to traditional in vitro methods, patient-derived organoids (PDOs) represent a cellular model that better recapitulates the complexity observed in vivo in exchange for the many challenges linked to 3D biology research. Indeed, an assay co-developed by HUB Organoids using PDOs is currently used to steer patient treatment in the Netherlands. However, the increase in biological complexity associated with the move from 2D to 3D models is accompanied by increased complexity in assay execution. As we overcome some of those challenges with standardization and automation, we can use our biobank to develop more complex in vitro assays that allow us to identify new phenotypic readouts related to relevant disease hallmarks, paving the way for future advancements in medical research. Imaging readouts are increasingly represented in our research, often being the primary readout in assays designed to be involved in different steps of the drug discovery pipeline and diagnostics. In this presentation, we will cover some of the image-based readouts applied in the assays that we have developed and are developing for fields such as cystic fibrosis, oncology, immuno-oncology, inflammatory bowel disease, and toxicology.

3:00 - 3:30	**Coffee Break & Exhibit Viewing & Poster Session**
3:30 - 4:00	**Joshua A Harrill:** US Environmental Protection Agency **Title**: *Determination of Human Health Protective In Vitro Points-of-Departure With the Cell Painting Assay*

Abstract

Researchers at the US EPA's Center for Computational Toxicology and Exposure (CCTE) are using high-throughput profiling (HTP) assays conducted in human-derived in vitro models as the first tier in chemical hazard evaluation. High-throughput phenotypic profiling (HTPP) with the Cell Painting assay has been identified as a molecular profiling assay that can be deployed across a broad array of human-derived in vitro models in order to evaluate different aspects of human biology. The Cell Painting assay can be used to identify benchmark concentrations for biological activity and inform putative mechanism-of-action predictions based on changes in cell morphology. Benchmark concentrations (in μM) can be converted to administered equivalent doses (AEDs in mg/kg-day) using in vitro to in vivo extrapolation and used as in vitro points-of-departure (POD) for chemical risk assessment. An envisioned goal of in vitro hazard evaluation is generation of PODs that are protective of human health. However, human biology is complex and the breadth of this complexity cannot be captured in any one in vitro cell model. Therefore, US EPA has performed several large-scale chemical screening studies involving hundreds of chemicals using the Cell Painting assay. The studies were conducted in a variety of biologically diverse human-derived cell lines originating from different tissues (e.g., breast, bone, liver, kidney, lung, vascular). These cell lines express different combinations of proteins and receptors that are potential molecular targets that mediate chemical bioactivity and toxicity. This presentation will evaluate the impact of cell line choice as well as the combinatorial use of multiple cell lines in determining in vitro PODs from the Cell Painting assay that are human health protective. In addition, chemotype enrichment analysis will be used to identify groups of chemicals where in vitro PODs are underpredicting or overpredicting hazard. Participants in this session will gain a broader understanding of how information from molecular profiling assays can be used to inform chemical risk assessment. This abstract does not reflect US EPA policy.

4:00 - 4:15 insphero	**Exhibitor Spotlight – InSphero** **Özlem Yavas-Grining** **Title:** *Resolving compound mechanism through phenotypic analysis of morphologic features in a 3D liver steatosis model*

Abstract

Lipid droplets are ubiquitous organelles which play an important role in the production of metabolic energy and the resolution of cellular stress in healthy tissue. However, excessive accumulation of intracellular neutral lipid droplets is associated with several disease conditions, including atherosclerosis, obesity, and non-alcoholic fatty liver disease (NAFLD), alcoholic liver disease (ALD), as well as certain drug induced liver injury (DILI) conditions. Lipid storage related diseases (e.g. NAFLD) often involve multiple cell and tissue types and as a result they are notoriously difficult to treat and challenging to model in vitro. Therefore, the successful discovery and development of novel therapeutic treatments for such diseases may depend on the implementation of drug discovery approaches that utilize a combination of physiologically relevant in vitro models, clinically relevant endpoints, and more holistic lead identification approaches such as phenotypic drug discovery (PPD). Here we describe the development of a liver steatosis model and assay to evaluate compounds for the treatment of NAFLD/NASH. To maximize the translational potential of the assay we utilized a physiologically relevant 3D model of NAFLD comprised of multiple cell types. To accurately quantify and characterize steatosis associated intracellular lipid droplets in the 3D model we employed a combination of Deep-Learning assisted image analysis and multiparametric data analysis.

4:15 - 4:45	**President's Innovation Award Sponsored by Spring Science**
SPRING	**Jiacheng Gu**, Columbia University **Title**: *Mapping multi-modal phenotypes to perturbations in cells and tissue with CRISPRmap*

Abstract
Unlike sequencing-based methods, which require cell lysis, optical pooled genetic screens enable investigation of spatial phenotypes, including cell morphology, protein subcellular localization, cell-cell interactions and tissue organization, in response to targeted CRISPR perturbations. Here we report a multi-modal optical pooled CRISPR screening method. CRISPRmap combines in situ CRISPR guide-identifying barcode readout with multiplexed immunofluorescence and RNA detection. Barcodes are detected and read out through combinatorial hybridization of DNA oligos, enhancing barcode detection efficiency. CRISPRmap enables in situ barcode readout in cell types and contexts that were elusive to conventional optical pooled screening, including cultured primary cells, embryonic stem cells, induced pluripotent stem cells, derived neurons, and in-vivo cells in a tissue context. We conducted a screen in a breast cancer cell line of the effects of DNA damage repair gene variants on cellular responses to commonly used cancer therapies and show that optical phenotyping pinpoints likely pathogenic patient-derived mutations that were previously classified as variants of unknown clinical significance.

4:45 - 7:30	**Poster Sessions, Exhibit Viewing, & Reception**

Program Agenda: Day 3, Sept. 20

MAIN SESSION
Room: Staffordshire

KEYNOTE 9:00 - 10:00	**Hongkui Zeng:** Allen Institute for Brain Science **Title:** *Cell type diversity and organization in the mammalian brain*.

Abstract
To understand the function of the brain and how its dysfunction leads to brain diseases, it is essential to uncover the cell type composition of the brain, how the cell types are connected with each other and what their roles are in circuit function. At the Allen Institute, we have built multiple technology platforms, including single-cell transcriptomics, spatial transcriptomics, single and multi-patching electrophysiology, 3D reconstruction of neuronal morphology, and brain-wide connectivity mapping, to characterize the molecular, anatomical, physiological, and connectional properties of brain cell types in a systematic manner, towards the creation of multi-modal cell atlases for the mouse and human brains. We have now generated a comprehensive and high-resolution transcriptomic and spatial cell type atlas for the whole adult mouse brain, based on the combination of two single-cell-level, whole-brain-scale datasets by scRNA-seq and MERFISH. We systematically analyzed the neuronal, non-neuronal, and immature neuronal cell types across the brain and identified a high degree of correspondence between transcriptomic identity and spatial specificity for each cell type. We also found that transcription factors are major determinants of cell type classification in the adult mouse brain and identified a combinatorial transcription factor code that defines cell types across all parts of the brain. This study reveals extraordinary cellular diversity and underlying rules of brain organization. It establishes a benchmark reference atlas and a foundational resource for deep and integrative investigations of cellular and circuit function, development, and evolution of the mammalian brain.

Hongkui Zeng, Executive Vice President and Director of Allen Institute for Brain Science

Keynote Bio

Hongkui Zeng is Executive Vice President and Director of Allen Institute for Brain Science. She studies neuronal diversity and connectivity in the mouse brain-wide circuits in the context of development, function and disease. Through her leadership of multidisciplinary teams, she has built research programs using transcriptomic, connectomic and multimodal approaches to characterize and classify the wide variety of cell types that constitute the mammalian brain, laying the foundation for unraveling the cell type basis of brain function. Her work has led to widely adopted community resources and standards, including transgenic mouse lines, Allen Mouse Brain Connectivity Atlas, the Common Coordinate Framework (CCF), and the brain-wide transcriptomic cell type taxonomy and atlas. Zeng received her Ph.D. in molecular and cell biology from Brandeis University and postdoctoral training in neuroscience at Massachusetts Institute of Technology. She has received many honors, including the 2023 Pradel Research Award from the National Academy of Sciences. She is an elected member of the National Academy of Sciences and the National Academy of Medicine.

10:00 - 10:15 gubra	**Exhibitor Spotlight – Gubra** **Casper Graversen Salinas** **Title:** *Using advanced image analysis to quantify 3D histology endpoints in the mouse brain*

Abstract

Using light sheet microscopy, it is possible to image intact mouse brains with single cell resolution. Visualising the brain in 3D is already revolutionizing the field of neuroscience but in combination with advanced image analysis it is possible to quantify diverse endpoint ranging from cell counts to biodistribution. This will likely transform the way we study CNS disorders and treatment effects in the future.

10:15 – 10:45	**Coffee Break & Exhibit Viewing & Poster Session**
Session 3 10:45 - 1:00	**Spatial biology: Creating cellular and molecular maps of tissues** **Chairs:** Evgeny Shlevkov (Johns Hopkins University) and Mingyao Li (University of Pennsylvania)
10:45 - 11:15	**Mingyao Li,** University of Pennsylvania **Title***: Unlocking the power of spatial omics with AI*

Abstract

Spatial omics technologies have revolutionized biomedical research by providing detailed, spatially resolved molecular profiles that enhance our understanding of tissue structure and function at unprecedented levels. Histopathology is considered the clinical gold standard for disease diagnosis. However, the integration of histological information in spatial omics data analysis has been limited due to a lack of computational pathology expertise among computational biologists. In this talk, I will present several tools that we have recently developed to leverage pathology image information, thereby enhancing spatial omics data analysis.

11:15 -11:45	**Daniel KRENTZEL,** Pasteur Institute, Paris **Title:** *Deep learning approaches for antibiotic target identification from high-throughput images*

Abstract

Bacterial cytological profiling is a powerful image-based technique to identify the mode of action of antibiotics directly from microscopy images. Deep learning promises to further boost cytological profiling thanks to its ability to learn powerful discriminative features from raw images end to end. However, most deep learning methods implicitly assume homogeneous cell morphologies. This assumption can mask perturbation effects on sub-populations of cells, thereby precluding the identification of subtle hits in phenotypic drug screens. Here, we move away from aggregated measures of bacterial phenotypes to consider phenotype distributions of entire cell populations instead. In brief, we developed a rotation-invariant variational autoencoder (RI-VAE) and trained it in an unsupervised manner on single-cell crops of genetically and chemically perturbed bacteria. The latent feature vectors result in high-dimensional phenotype distributions that capture cellular sub-populations. We show that the Wasserstein distance can be used to quantify the similarity between these phenotype distributions and to link mutants to drug-treated bacteria. Specifically, we trained a VAE to become rotation-invariant by repeatedly encoding rotated versions of the same image crop and performing maximum pooling over all but one of the feature dimensions before reconstructing the input image (see Fig. 1A). This forces rotational information to be stored in the last dimension of the latent feature vector. We trained our RI-VAE model on a dataset of single-cell crops of perturbed C. glutamicum (Cglu) bacteria, a non-pathogenic surrogate model of M. tuberculosis. After training, phenotype distributions for each condition were obtained by t-SNE maps of the VAE latent representations of single-cell crops (see Fig. 1B). Interestingly, we could observe similar phenotype distributions for mutants disrupting similar cellular processes (see Fig. 1C). We quantified these phenotypic similarities with the Wasserstein distance (see Fig. 1D). In an attempt to relate drug-induced phenotypes to mutant phenotypes, we collected images of Moxifloxacin-treated wild-type Cglu bacteria. Moxifloxacin is a well-known antibiotic that inhibits the DNA gyrase complex. Comparing the phenotype distribution of a GyrA (GA) mutant, a subunit of the gyrase complex, to Moxifloxacin-treated bacteria revealed high similarity (see Fig. 2A). Moreover, with increasing Moxifloxacin concentrations, phenotype distributions became more similar to those of the GyrA mutant (see Fig. 2B). Interestingly, we were able to identify a latent feature that correlated strongly with Moxifloxacin concentration (see Fig. 2C). Using the RI-VAE decoder to generate synthetic images showed that increasing the value of this dimension resulted in images with higher DNA segregation, a phenotype consistent with impeding DNA replication as a result of gyrase inhibition (see Fig. 2D). We propose that our RI-VAE approach, by fully capturing cellular heterogeneity, will allow the identification of subtle shifts in bacterial phenotype distributions and hence benefit bacterial cytological profiling. Moreover, the ability to link drug-induced phenotypes to mutants is poised to accelerate the identification of novel modes of action in antibiotic drug screens.

11:45 - 12:15	**Denis Wirtz,** Johns Hopkins University **Title:** *3D multi-omic mapping of tissues, tumors and organisms*

Abstract

I will present two technological platforms recently developed in my lab: (1) CODA: An AI-based workflow to image whole human organs and tumors at single-cell resolution. Using CODA, we determined the number, morphology, and mutational profile of precursor lesions of pancreatic cancer, PanINs, in the human pancreas. We have also used CODA to map the complex micro-anatomy of whole fallopian tubes in pre- and post-menopausal women.

12:15 – 12:30 Genedata	**Exhibitor Spotlight – Genedata** **Cameron Scott** **Title:** *Efficiency in Image-Based Screening: Hands-Off Data Analysis from Raw Images to Selection of Hits*

Abstract
Image-based assays offer profound insights about candidate molecules, but their analyses can create a bottleneck at the high throughput required for the Drug Discovery process. In this spotlight presentation, we will show how to tackle such multiparametric analyses end-to-end using Genedata Screener, an enterprise platform for assay data analysis and management. Using a deep learning-based analysis platform fully integrated with plate and sample-centric analytics, Genedata Screener automates the entire high-content screening workflow, from instrument-agnostic image loading to automated reporting of hits with the desired pharmacological profile. This dramatically shortens the analysis time of high-content screens.

12:30 – 12:45	**Selected Abstract Talk 1** **Loan Vulliard** **Title:** *Multiplexed representation learning to profile the tumor microenvironment*

Abstract
In recent years, spatial proteomics technologies such as IMC, CODEX and MIBI were developed to quantify the abundance and location of tens of proteins at once in their original tissue context. Such approaches can be used for many applications, ranging from basic to clinical research. However, this flexibility comes at cost, as many parameters differ between experiments, making it hard to streamline and standardize analysis pipelines. Each experiment requires an antibody panel targeting biological markers relevant to the studied disease and tissue. Because of the use of different markers, aggregating and comparing data to study cellular organization across multiple experiments is a challenge. We observed that descriptors of pathway activity as well as of heterogeneity and spatial organization provide complementary information about the content of multiplexed images. Accordingly, we devised an approach for spatial cellular representation with explainable and adaptive models ("scream"), to integrate and contextualize data from multiplexed imaging experiments. Using explainable deep learning models, we infer the activity of broad molecular programs from the markers available and use this cell-level information to represent and compare samples. We validate our approach by comparing representations of the same tissues based on different sets of markers in MIBI data. Overall, the "scream" profiles offer a convenient way to compare conditions across multiplexed imaging datasets and could further serve as the basis for imputation of markers, integration of spatial data across modalities, disease stratification and prediction of drug response.

12:45 – 1:00	**Selected Abstract Talk 2** **Alexandr Kalinin** **Title:** *Foreground-aware virtual staining for accurate representation of 3D nuclear morphology*

Abstract
Changes in cell nuclear morphology are associated with reorganization of chromatin architecture related to altered functional properties such as gene regulation and expression. Fluorescence (FL) imaging is the primary method for studying nuclear morphology. It provides a high-resolution readout of cellular state, but is complex, costly, time-consuming, and hard to use for live-cell imaging. Moreover, the limited availability of fluorescence spectra restricts its utility for multiplexing. These challenges motivated the development of deep learning-based techniques collectively termed “virtual staining”, which predict FL signals from transmitted-light (TL) images, a cheaper and simpler imaging modality. However, one drawback of existing approaches to virtual staining is that they are trained to predict all pixels of the target image, including those in background areas with no cells. In 3D, such models learn to predict axial aberrations, making downstream tasks such as segmentation of individual nuclei and measuring their size and shape characteristics more challenging.

In this work, we addressed these issues by binarizing target FL images into informative (foreground) and uninformative (background) regions using histogram thresholding and computing a novel loss function that consists of two components. The first component includes the mean squared error (MSE) loss typically used

in virtual staining, but we masked it to focus on foreground pixels. In the second component, we directed the model to learn accurate representations of nuclear shapes by soft-thresholding model outputs and computing Dice loss with binary target masks. The combined loss function balances accurate pixel-wise foreground intensity predictions with learning representative morphologies. As a baseline, we re-trained the popular F-net model with the standard MSE loss on the 3D Allen Cell imaging dataset. We reported Pearson correlation coefficient (PCC), peak signal-to-noise ratio (PSNR), structural similarity index (SSIM) to evaluate predictions at the pixel level. We segmented nuclei using two approaches: thresholding-and-watershed and Cellpose. Segmentation quality is reported as recall at different intersection over union (IoU) thresholds against the curated ground truth segmentation masks provided within the dataset. Finally, we also extract morphological features from 3D segmented nuclei and calculate morphological distance with the features extracted from the ground truth images. Our results demonstrate that addition of foreground-aware loss function improves prediction of virtually stained nuclei by reducing artifacts such as axial elongation (Figure 2A), which is supported by reduced metrics when calculated on the whole image and improved scores on just the foreground. This also improves segmentation performance independently of a method used and morphological feature representation.

These findings show that learning from informative foreground regions and ignoring background noise in virtual staining can improve its utility for 3D nuclear morphometry, especially when combined with a robust evaluation framework. We are currently working on two more exciting applications of these models: to cells perturbed by small molecules and to larger 3D organoid structures. The ability to use less invasive, cost-effective computational imaging that does not compromise on morphological detail will be useful for a wide range of applications in biomedicine.

1:00 - 2:00	**Lunch & Learn Sponsored Sessions**

Room: St George A/B

Carl Zeiss Microscopy
Brennan McFarland
Title: *From Data Complexity to Research Confidence: Streamline Your Workflows and Ensure Reproducibility with ZEISS arivis Solutions*

Abstract

The FDA's approval of organoids in preclinical research has led to a significant shift toward using complex in vitro models (CIVM) for drug testing and disease research. Today, modern microscopes are capable of capturing detailed 3D and 4D images of such CIVM, providing unprecedented insights. However, classical 2D high-content analysis (HCA) approaches struggle with analyzing these complex images effectively. To address this challenge, ZEISS offers the arivis software platform that leverages AI for advanced 3D/4D HCA. This platform assists researchers in creating automated, robust, and reproducible assays to accelerate the drug discovery process when using CIVM.

Room: St George C/D

Thermo Fisher Scientific
Leticia Montoya
Title: *Advancements in multiplexed spatial phenotyping: Applications using the EVOS S1000 Spatial Imaging System*

Abstract

Spatial omics is an expanding research area focused on integrating spatial knowledge of tissue with transcriptomics (RNA) and proteomics (protein). Understanding the complexity of the biological structure(s) is an important aspect of cancer immunotherapy research which requires accurate target classification. Simultaneous translational profiling of 4+ targets on a single sample presents various challenges that include panel design, staining protocols, and data analysis. Furthermore, designing a reliable multi-target biomarker

panel introduces additional complexities and considerations such as protein abundance and localization, fluorophore compatibility, diverse tissue types, and data characterization. To address the needs of high target multiplexibility, labeling methods have advanced in cyclic detection enabling iterative labeling of primary antibody conjugates. To enable broader adoption of spatial biology, we have developed the Invitrogen™ EVOS™ S1000 Spatial Imaging System, a high throughput spectral microscope for single step detection of 8-12 targets. The EVOS S1000 platform is a highly flexible optical system with exceptional spatial resolution and scan speed, which when paired with our broad assortment of IHC-validated reagents, antibodies and labeling technologies, enables highly accurate and robust assessments for IHC cellular phenotyping.

Session 4 2:00 - 4:30	**Advances in Informatics, Deep learning, and AI** **Chairs:** Christophe Zimmer (Univ. of Würzburg, Institut Pasteur Paris) and Juan Caicedo (Univ. Wisconsin–Madison)
2:00 - 2:30	**Jean-Philippe Vert:** Owkin **Title**: *Foundation models, from pathology to genomics*

Abstract

Large self-supervised foundation models have boosted the capabilities of AI models in natural language processing and computer vision. In this talk I will present our efforts to train foundation models for digital pathology, and to connect visual observations to the underlying genomics.

2:30 - 3:00	**Juan Caicedo,** Univ. Wisconsin **Title:** *Towards foundation models of cellular morphology*

Abstract

Deep learning models have advanced the potential to analyze microscopy images and to quantify cellular phenotypes for many types of biological applications. However, for every new experiment, a new deep learning model needs to be designed to meet the image analysis requirements of the study. In this talk, we will discuss the technical limitations of reusing models across experiments and current efforts to design and train foundation models for microscopy image analysis.

3:00 - 3:15 Glencoe SOFTWARE	**Exhibitor Spotlight – Glencoe Software** **David Stirling** **Title:** *Integrating high content data management and analysis: End-to-end Cell Painting workflows in OMERO Plus*

Abstract

OMERO Plus is an image data management platform designed for storage and analysis of bioimaging data and metadata, including complex image analysis results. Analytical workflows such as “Cell Painting” involve performing measurements and analysis on large high content imaging datasets. The size of these datasets and the downstream results poses a challenge for researchers who need to maintain traceability and usability in technical workflows. Herein we utilize the metadata management and high-performance computing integration capabilities of OMERO Plus to produce a comprehensive pipeline for the Cell Painting assay within a unified web interface.

3:15 – 3:30 SPRING	**Award Ceremony: Best Posters** Awards Sponsored by Spring Science
3:30 - 4:00	**Caroline Uhler,** MIT **Title:** *Causal Representation Learning in the Context of Cell State Transitions*

Abstract
The development of CRISPR-based assays and small molecule screens holds the promise of engineering precise cell state transitions to move cells from one cell type to another or from a diseased state to a healthy state. The main bottleneck is the huge space of possible perturbations/interventions, where even with the breathtaking technological advances in single-cell biology it will never be possible to experimentally perturb all combinations of thousands of genes or compounds. This important biological problem calls for a framework that can integrate data from different modalities to identify causal representations, predict the effect of unseen interventions, and identify the optimal interventions to induce precise cell state transition. Traditional representation learning methods, although often highly successful in predictive tasks, do not generally elucidate causal relationships. In this talk, we will present a statistical and computational framework for causal representation learning and its application towards optimal intervention design.

4:00 - 4:15	**Selected Abstract Talk 1** **Kian Kenyon-Dean,** Recursion **Title:** *Generative Phenomic Foundation Models for High Content Microscopy*

Abstract
A fundamental challenge in biological research is quantifying cellular responses to genetic and chemical perturbations and relating them to each other. Recent public releases of High Content Screening (HCS) image sets, like RxRx3 and JUMP-CP's cpg0016, consist of millions of cellular images across 100,000s of unique perturbations. The scale of such experiments presents a unique opportunity for extracting meaningful biological representations of microscopy data. Many SOTA approaches for featurizing HCS images use weakly supervised learning (WSL) to train models that predict the perturbation used to treat the cells in an image.

In this work, we propose an alternative perturbation-agnostic generative AI framework for self-supervised representation learning on HCS datasets with masked-autoencoders (MAEs). We trained MAEs [1] with convolutional and vision transformer (ViT) backbones of different sizes, as well as baseline WSL models to predict the perturbation applied to the cells in a well. We leveraged the unique architecture of ViTs to also develop a novel channel-agnostic model that can process different numbers and orders of channels at inference time, overcoming a major limitation associated with sharing deep learning models across different imaging protocols. This model has been released to the public as Phenom-Beta on NVIDIA's BioNemo platform.We evaluate each model's ability to recall known gene-gene relationships by using the multivariate metrics described in Celik et al. [2]. We correct for batch effects using typical variation normalization, and also correct for possible chromosome arm biases known to exist in CRISPR-Cas9 HCS data. To predict biological relationships, we aggregate embeddings to perturbation-level over their experimental replicates, and use the cosine similarity between a pair of perturbation representations as the relationship metric, setting the origin of the space to the mean of negative controls. We compare these similarities with the relationships found in the following public databases: CORUM, hu.MAP, Reactome, and StringDB. We report the recall of known relationships amongst the top and bottom 5% of all cosine similarities between CRISPR knockout representations in RxRx3 and cpg0016. Our most scaled MAE, Phenom-1, achieves better downstream results than smaller MAEs and WSL models on both HCS datasets. For example, Phenom-1 achieves an 11.5% relative improvement improvement in hu.MAP relationship recall over our best scaled WSL baseline [1] on RxRx3, and a 12.4% relative improvement in StringDB recall over CellProfiler features on cpg0016.

Our results demonstrate that performance on biological relationship recall continues to improve as we scale the model and dataset size. Our findings motivate continued research into scaling generative AI on microscopy data to create powerful foundation models of cellular biology with the potential to catalyze advancements in drug discovery and beyond.
[1] Kraus, Oren, et al. "Masked Autoencoders for Microscopy are Scalable Learners of Cellular Biology." Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition. 2024.
[2] Celik, S. et al. "Biological Cartography: Building and Benchmarking Representations of Life." bioRxiv 2022.12.09.519400 doi:10.1101/2022.12.09.519400.

4:15 - 4:30	**Selected Abstract Talk 2** **Jenna Tomkinson,** University of Colorado Anschutz Medical Campus **Title:** *High-content imaging and machine learning predicts fibrosis in cardiac fibroblasts*

Abstract

Cardiovascular disease remains the leading cause of mortality worldwide, accounting for nearly 18 million deaths each year. Most cardiovascular disease etiologies involve the development of cardiac fibrosis, or pathological expansion of the extracellular matrix, mediated by the proliferation and activation of resident cardiac fibroblasts into a myofibroblast state. There are currently no FDA-approved drugs specifically targeting the cardiac fibroblast or its role in fibrotic remodeling, and standard-of-care medications for heart failure (including angiotensin II receptor blockers and SGLT2 inhibitors) have generally demonstrated only a modest benefit in reducing fibrotic burden. Given the impact of cardiac fibrosis on cardiovascular disease worldwide and the lack of effective therapies, more innovative strategies to discover new treatments are in great need.

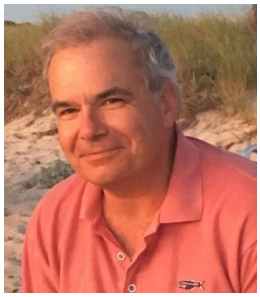
The Cell Painting assay has become a critical tool in cellular phenotype analysis and drug discovery by providing unbiased readouts of cell morphology. Our primary in vitro model system for studying cardiac fibrosis and evaluating potentially novel anti-fibrotic agents utilizes primary cardiac fibroblasts isolated from myocardial biopsies from human heart failure patients. Therefore, we combined Cell Painting with machine learning to gain insights into the biological mechanisms regulating cardiac fibroblast activation in failed hearts. We modified the Cell Painting assay by swapping the cytoplasmic RNA stain with F-actin, a key component upregulated in activated myofibroblasts. We applied the assay to cardiac fibroblasts that we isolated from four heart failure patients with idiopathic dilated cardiomyopathy and two hearts we acquired from healthy donors who passed from unrelated events. We acquired the five-channel fluorescence microscopy images, and filtered images and cells that failed quality control. We segmented 16,887 single cells and applied an image-based profiling pipeline to process 638 high-content morphology features. Next, we optimized and trained a binary logistic regression model to predict healthy or failing single cells.

Our model demonstrates high performance in predicting healthy versus failing cells, with weighted F1 scores of 0.91 in the training and 0.89 in the testing sets. We saw high accuracy across each individual heart in the test set, averaging approximately 0.88. We also saw high performance when applying the model to the held-out datasets, with accuracy ranging from 0.79-0.92. These held-out datasets included single cells from wells the model had never seen before. We further applied the model to a second plate containing cardiac fibroblasts treated with DMSO and TGFRi (TGF-β inhibitor), which are negative and positive controls. We expected TGFRi to cause a failing heart to be predicted as healthy. Indeed, applying our model to these cells showed higher healthy probabilities in cells from failing hearts when treated with the TGFRi positive control, indicating that our model can accurately distinguish between cell conditions. Our results provide a proof of concept that we can use this approach to identify new therapeutic strategies that make failing single-cell cardiac fibroblasts healthy. We plan to evaluate our model further in a large drug screen to discover novel therapeutic strategies to reverse cardiac fibrosis.

4:30 - 5:00	**Coffee Break**
5:00 - 6:00	**SBI2 Annual General Meeting**
6:00	**End of Conference**

Speaker Bios

Education Sessions & Hands-On Workshop



Steven Haney,
Independent Consultant

Steven Haney has been involved broadly involved in drug discovery, from target identification to clinical development. Centrally focused on early drug discovery, Steven has led teams engaged in assay development, HTS and hit advancement, including extensive development of cellular assays for drug discovery and translational biology, working in HTS through Candidate Selection at Eli Lilly and translational biology in Oncology, Diabetes, Neurodegeneration and Cardiovascular Diseases at Eli Lilly, Pfizer and Valo Health.Steven has made several contributions to the Lilly/NIH Assay Guidance Manual on imaging assays, machine learning in morphological profiling and in fluorescent artifacts. He also held early roles at SBI2, including Secretary and President as well as Co-Organizer for the educational and plenary sessions for the first Annual Meetings of SBI2.

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

Dr Johnston has >33 years of drug discovery experience in the Pharmaceutical, Biotechnology and academic sectors. An innovator of cell-based lead generation/optimization, he pioneered the application of high content imaging in drug discovery. In 2005, he designed/built the University of Pittsburgh Molecular Library Screening Center where he led 21 HTS campaigns and reconfigured the NCI 60 cell line assays for drug combination HTS. In 2011, he established independent chemical biology laboratories to apply novel drug discovery strategies to find new and effective drugs or combinations for prostate, melanoma, head and neck, and hepatocellular carcinoma. He provides expertise in HTS/HCS assay development and implementation for drug discovery collaborations in other therapeutic areas. He's been a member of SBS/SLAS since 1998 and was a founding member of the Society for Biomolecular Imaging and Informatics in 2012. Dr. Johnston teaches biochemistry and drug discovery courses in the Pharm.D. and Ph.D. programs.

Erin Diel
Head of Product,
Glencoe Software

Erin Diel is the Head of Product for Glencoe Software. She has worked with imaging data directly and in the context of educating and supporting users of imaging data for over 10 years. She received her PhD from Harvard University, where she studied the neuroanatomical and functional basis of topographic maps in the auditory cortex using various microscopy techniques. She then worked in the Harvard Center for Biological Imaging, advising on image acquisition and analysis for scientists from both within Harvard and local biotech companies. She has worked with Glencoe Software for four years, in particular supporting large academic institutions and pharmaceutical companies in their management of imaging data in computational pathology use cases, including image segmentation and data mining in the context of varied spatial biology techniques.

Sylke Hoehnel-Ka
CEO, SUN bioscience

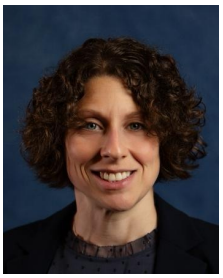
Sylke was trained at ETH Zurich and holds a PhD degree in Stem Cell Bioengineering from EPFL. She co-invented multiple organoid technologies that she spun-out successfully over the past five years including SUN bioscience. She was named to Forbes' 30 Under 30 Europe list in 2016 and is a fellow of the Cartier Woman's Initiative.

Joshua A Bauer
Research Associate Professor of Biochemistry
Vanderbuilt University

Joshua A. Bauer, Ph.D. is the director of the Vanderbilt High-throughput Screening (VHTS) facility and director of functional genomics screening and high-content imaging, within the Vanderbilt Institute of Chemical Biology. He has a broad background in pharmacology, cancer biology and biochemistry, with specific experience in oncology-related functional genomics screening (FGS), high-content screening (HCS), and chemical/drug library screening. Dr. Bauer currently leads the HTS team to facilitate the development of biological assays and screens to enable the discovery of chemical and genetic modulators of a variety of molecular targets and pathways in cell biology for therapeutic implications. His research interests are focused on bioinformatics and chemical genomic approaches, including FGS and HCI, to identify novel drug targets and to better understand the molecular and genetic mechanisms that underlie how cells and patient-derived samples (eg, organoids) respond to therapeutics. A main goal is to identify novel strategies to overcome therapy resistance or new indications that will have clinical application.

Illya Lukonin
Senior Scientist,
Roche Institute of Human Biology

Ilya Lukonin, Roche
Ilya works on establishing phenotypic screening assays in organoid systems. He combines cell culture and assay automation, high-content imaging and data analysis. Currently, Ilya leads the Organoid Phenotyping team at the Roche Institute of Human Biology with a mandate to develop robust and high-throughput organoid screening assays and accompanying computational tools for data-driven characterisation of various organoid models. With a strong interest in cell-to-cell variability, the group assesses complex human models at various biological scales, gaining single-cell-level insight into complex biology in thousands of arrayed conditions.s



Hilary Anne Sherman
Senior Applications Scientist Corning Life Sciences

Hilary Sherman is a Senior Scientist in the Corning Life Sciences Applications Lab located in Kennebunk, ME. Hilary has been with Corning Incorporated since 2005 and has worked with a wide variety of cell types including mammalian, insect, primary, stem cells and organoids in a vast array of applications. Her key roles at Corning involve creating technical documents such as protocols and whitepapers as well as providing technical support and training for both the Corning sales force and customers. In the last several years, Hilary has worked extensively with 3D cell culture applications including human organoid culture.

Pierre de Malliard,
Sr. AI Solutions Architect,
Global HCLS, AWS

Pierre de Malliard is a Senior AI/ML Solutions Architect within the Global Healthcare & Life Sciences division at Amazon Web Services (AWS). With a diversified background spanning data engineering, data science and machine learning operations, Mr. de Malliard has a track record of delivering transformative AI-powered solutions in the healthcare and pharmaceutical sectors.

Ujjwal Ratan
Leader for Data Science & ML, Healthcare & Life Sciences, AWS

Ujjwal Ratan is the leader for AI/ML and Data Science team in the Amazon Web Services (AWS) Healthcare and Life Science business unit and is also a Principal AI/ML Solutions Architect. Over the years, Ujjwal has been a thought leader in the healthcare and life sciences industry, helping multiple Global Fortune 500 organizations achieve their innovation goals by adopting machine learning. His work involving the analysis of medical imaging, unstructured clinical text and genomics has helped AWS build products and services that provide highly personalized and precisely targeted diagnostics and therapeutics. Ujjwal's work has also been featured in multiple global conferences, peer-reviewed publications or technical and scientific blogs.

Nicolaas van der Voort
Director scientific affairs,

Nicolaas van der Voort has a solid background in fluorescence microscopy and its application in biology. In his current position as director scientific affairs, he bridges the gap between Scientific Volume Imaging (SVI)'s powerful image analysis tools and the biological impacts that it has by utilizing his technical knowledge together with his sales experience.SVI's flagship product, the Huygens software, provides an all-in-one solution for restoration and analysis of Fluorescence microscopy data. Ranging from super-resolution methods like STED, to tissue-oriented methods like Lightsheet and Multi-photon, Huygens is best known for its deconvolution options, which can dramatically improve the image quality. Its analysis module can do object analysis, colocalization and track objects in time. All of which can be automated, making it ideal for high-throughput application. Lastly, SVI can provide consultancy services for the best image quality and quantitative output.Nicolaas studied Physics at the University of Utrecht. Afterwards he worked at an optics company in Amsterdam working directly with international customers. For his PhD he moved to Düsseldorf, Germany to work in the group of Claus Seidel. There he developed novel methods using super-resolution STED in combination with FRET and fluorescence spectroscopy.

Colloquium

John W Hickey
Assistant Professor of Biomedical Engineering, Duke University

John Hickey is an Assistant Professor of Biomedical Engineering at Duke University with secondary appointments in the Cell Biology and Biostatistics & Bioinformatics Departments of the School of Medicine. His lab is composed of a diverse set of engineers and scientists solving health problems by using and developing systems biology tools and technologies to describe and control spatial relationships between cells in tissues. John completed his postdoctoral training in Garry Nolan's lab at Stanford University, where he used and developed systems biology tools to analyze spatial relationships among cells in tissues. He obtained his PhD in Biomedical Engineering from Johns Hopkins University with Dr. Jonathan Schneck and Hai-Quan Mao, where he developed magnetic nanoparticles for rare antigen-specific T cells and designed hydrogels for adoptive T cell therapy. John has been recognized by a number of organizations for his work including receiving: American Cancer Society Postdoctoral Fellowship, NCI Postdoctoral Fellowship, ARCS Scholar, Siebel Scholar, and NSF Graduate Research Fellowship.

Meghan Driscoll
Assistant Professor,
Dept. of Pharmacology,
University of Minnesota

Meghan Driscoll is an Assistant Professor at the University of Minnesota Medical School in the Department of Pharmacology. The Driscoll Lab investigates how cell morphology, dynamics, and signaling couple to govern cell function, particularly in cancer and immune cells. To do so, they combine image analysis methods development with careful experimentation. Dr. Driscoll earned her PhD from the University of Maryland, working under the mentorship of Dr. Wolfgang Losert. Moving to the University of Texas Southwestern Medical Center, she joined the lab of Dr. Gaudenz Danuser as a Postdoctoral Fellow and later Instructor. Dr. Driscoll joined the University of Minnesota in 2022.

Auguste Genovesio
Lab head, Professor,
Institute of Biology of the École Normale Supérieure Paris

Auguste Genovesio graduated in applied mathematics, computer science, and artificial intelligence from Paris VI University (now Sorbonne University), France, in 2001. After completing a Ph.D. in computer vision in 2005 at Institut Pasteur, he has led research efforts in large biological image and experimental data analysis for the last 19 years at Institut Pasteur in Korea, the Broad Institute of MIT and Harvard in the USA, and at École Normale Supérieure in France. His lab develops deep learning methods to study and mine the morphology and dynamics of cells at a large scale in various contexts. His research has led to the identification of host factors involved in HIV infection and novel antibiotics against tuberculosis, as well as discoveries in various fields such as developmental biology, neuroscience, and drug discovery. A complete list of publications and patents is available here:
https://www.ibens.bio.ens.psl.eu/spip.php?article243.

Main Session Day 1

Joe Trask
Life Sciences Segment Manager, Revvity

Joe Trask is the Life Sciences Segment Manager for North America at Revvity. Joe is instrumental in collaborating with customers, providing educational content, teaching, and awareness to the scientific community. Joe brings over 25 years of experience in drug discovery programs with emphasis on cell-based assay including high content screening and flow cytometry technologies from academia, pharmaceutical, and biotechnology studying cancer, immunology, neurodegeneration, and toxicology. Joe is an associated editor for the NIH/NCATS Assay Guidance Manual and co-founder and first President of Society for Biomolecular Imaging and Informatics (SBI2).

Laura Waller
Charles A Desoer Professor,
Division of Electrical Engineering, UC Berkeley

Laura Waller is the Charles A. Desoer Professor of Electrical Engineering and Computer Sciences at UC Berkeley. She received B.S., M.Eng. and Ph.D. degrees from the Massachusetts Institute of Technology in 2004, 2005 and 2010. After that, she was a Postdoctoral Researcher and Lecturer of Physics at Princeton University from 2010-2012 before joining UC Berkeley. She is a Packard Fellow for Science & Engineering, Moore Foundation Data-driven Investigator, OSA Fellow, and Chan-Zuckerberg Biohub Investigator. She has received the Carol D. Soc Distinguished Graduate Mentoring Award, OSA Adolph Lomb Medal, NSF CAREER Award and the SPIE Early Career Achievement Award.

Anne Beghin
MechanoBiology Institute - MBI/NUS, National University of Singapore

Dr. Anne Beghin is a multidisciplinary scientist with more than fifteen years of research experience in industry, microscopy platforms, and academia. With a PhD focused on breast cancer and chemoresistance, she specializes in cellular and physiological biology, cutting-edge microscopy and image analysis, and High Content Screening (HCS) for pharmaceutical applications. Her publications are focused on imaging methods for biopharmaceutical applications. Anne has spearheaded the development of innovative approaches in Single Molecule Light Microscopy (SMLM), enabling the transfer of this advanced imaging technology to pharmaceutical companies (HCS-SMLM). As the Director of the Microscopy Platform at the Mechanobiology Institute of Singapore (MBI), she leads the development of new tools and software in the fields of 3D segmentation and High Content Screening (HCS) with applications to challenging models such as organoids and spheroids. Additionally, Anne heads a project that combines microfabrication technology and AI-based analysis, which has led to a patent and more recently to interests and applications in Space biology. She also serves as an expert consultant for the European Space Agency (ESA).

Angeline Lim
Senior Applications Scientist, Molecular Devices

Dr. Angeline Lim is a Sr. Applications Scientist at Molecular Devices where she specializes in high-content imaging and analysis. She works predominately in developing automated 3D biology workflows and leverages AI to derive actionable readouts from complex phenotypic assays. She provides scientific support for the company's portfolio of ImageXpress® High-Content Imaging Systems and their applications in high-throughput phenotypic profiling and 3D models in biology. Dr. Lim has a number of patents for her work in automated passaging and has been published in various scientific publication. In addition to her work at Molecular Devices, she is an active member and sits of the board of SBI2 and teaches educational courses for SLAS. Dr. Lim has over 10 years of research experience and holds a PhD in Molecular Cell and Developmental Biology from the University of California at Santa Cruz.

Gennady Shvets
Professor, Cornell University

Gennady Shvets is a J. Preston Levis Professor of Applied and Engineering Physics at Cornell University. He received his PhD in Physics from MIT in 1995. Before moving to Cornell in 2016, he was on the physics faculty of the University of Texas at Austin for 12 years. His research interests at the intersection of nanotechnologies and biophotonics include bio-spectroscopy, chemical imaging of live cells, and microfluidics. He is a Fellow of the American Physical Society (APS), Optical Society of America (OSA), and SPIE.His most recent work deals with the applications of metamaterials and plasmonics to biosensing and molecular fingerprinting of proteins and live cells using metamaterial arrays. He is particularly interested in the integration of plasmonic metasurfaces with various applications-specific platforms such as microfluidics and optical fibers. His group is exploring the nano-bio interface between plasmonic structures and living cells, tissues, and bacterial colonies. Recently, he demonstrated the first metasurface-based tool for studying the effects of pharmaceutical stimuli on living cells in real time, including intra-cellular protein transport, cell membrane modifications, and the mode-of-action of different therapeutics.

Shalaka Chitale
Director of Biology,
CytoTronics, Inc

Dr. Chitale, Director of Biology at CytoTronics, is at the forefront of pioneering efforts to harness and showcase the distinctive capabilities of CytoTronics' measurement platform across diverse biological applications. Leveraging extensive expertise in phenotypic screening and cell biology, Dr. Chitale is instrumental in driving innovation and demonstrating the transformative potential of CytoTronics' cutting-edge tools.

Martina K. Zowada
Postdoctoral Researcher
German Cancer
Research Center (DKFZ)
Heidelberg

Martina K. Zowada is a postdoctoral researcher from Heidelberg, Germany. Her research focus is the targeting of stem cell activity in colorectal cancer (CRC). She obtained her BSc and MSc in Molecular Biotechnology from the University of Heidelberg gaining research experience at the German Cancer Research Center (DKFZ) Heidelberg and the Dana-Farber Cancer Institute in Boston. In 2016, she joined the National Center for Tumor Diseases (NCT) Heidelberg, where she started working with patient-derived 3D models to gain understanding of stem cell activity in CRC. In 2021, she obtained her PhD in Biology from the University of Heidelberg and continued her work at NCT in an academia-industry collaboration. In 2023, she started as a postdoctoral researcher in the Division of Signaling and Functional Genomics at the DKFZ Heidelberg headed by Prof. Michael Boutros. In the EIC transition project ACHILLEUS, she is an experimental scientist establishing a high-throughput phenotypic screening platform for CRC organoids to identify stem cell-targeting drugs against CRC.

Claudia McCown
Dept. of Molecular
Medicine, UF Health

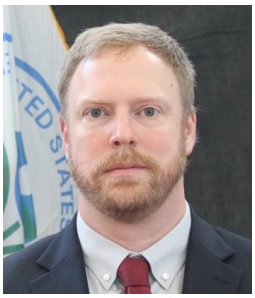
Claudia of the The Herbert Wertheim UF Scripps Institute for Biomedical Innovation and Technology, earned her Ph.D. in Integrated Biomedical Sciences from the University of Texas Health Science Center at San Antonio in December 2023. Her doctoral research delved into the biophysical and enzymatic properties of the innate immune protein SAMHD1. Currently, Claudia is a Post-Doctoral Fellow in the Spicer/Scampavia lab, where she has been advancing novel high-throughput screening (HTS) methodologies since early 2024. Her current focus is on leveraging induced neuron technologies to enhance neuronal drug discovery processes.

Chris Bakal
Professor of Cancer
Morphodynamics,
Institute of Cancer
Research, London

Chris is the Professor of Cancer Morphodynamics and Group Leader at the Institute of Cancer Research in London, UK. Chris' work combines artificial intelligence (AI), integrative omics, and single cell imaging to understand how changes in cell shape and size drive tumorigenesis and metastasis.
Chris is recognized as a world-leader in the fields of cancer cell biology, AI-based cell image analysis, data integration, and systems biology. While at Harvard Medical School he was the first scientist to show that machine learning can be used to analyse cell shape in ways that provide information regarding genes, proteins, and clinical outcomes.
His own lab has continued to use, develop and deploy new image analysis methods to understand the basis for cell morphogenesis in cancer cells. This work led to the discovery that phenotypic heterogeneity can be an evolvable process, and that cell shape regulates signalling processes involved in inflammation and immunity.
Outside of science Chris is a competitive track cyclist, a former national-level runner, and a former world-ranked downhill ski racer. Chris has run a mile in just over 4 min, and aims to compete in the Ironman World Championships.

Javier Frias Aldeguer
Senior Scientist, HUB organoids

Javier Frias Aldeguer received his BSc and MSc in biochemistry at the Universidad Autonoma de Madrid and his PhD in embryo modelling at the Maastricht university, conducted at the Hubrecht Institute. Currently working as a senior scientist at HUB organoids, where I lead commercial projects, often related to assay development or screening. Exposure to a large number of projects with very different scopes spanning across disease areas and assay formats, has made me very familiar with some of the challenges we face when developing complex assays and get them to work for multiple biobank samples. I have developed an interest in imaging-related readouts and the expansion of our phenotypic screen expertise. 2 notable publications: PMID: 29720634 and PMID: 35803228. Just filed a patent for an organoid-fibroblast co-culture assay.



Joshua A Harrill
Toxicologist, US Environmental Protection Agency

Dr. Harrill is a toxicologist with the US EPA's Center for Computational Toxicology and Exposure (CCTE). Dr. Harrill's expertise is in vitro toxicology, specifically transcriptomics, high content imaging (HCI) and other complementary technologies for high-throughput chemical hazard screening and risk assessment. Dr. Harrill is a lead investigator for CCTE's high-throughput toxicology research area. He uses molecular profiling assays such as targeted RNA-Seq and Cell Painting to characterize the bioactivity of environmental chemicals in human and animal-derived in vitro models. Dr. Harrill received his B.S. in Biochemistry from North Carolina State University and a Ph.D. in Toxicology for the University of North Carolina at Chapel Hill. His post-doctoral training focused on the use HCI-based methods for in vitro developmental neurotoxicity screening. Dr. Harrill then served as an investigator at a non-profit research institute researching the role of ligand-activated nuclear receptors in tissue development and liver carcinogenesis as well as developing novel in vitro models for assessing chemical effects on hepatic stem/progenitor cells. Dr. Harrill also has experience in conducting human health risk assessments using USEPA and state-level guidance as well as devising and managing rapid-phase environmental sampling, analysis and data interpretation programs during events involving the release of potentially hazardous chemicals.

Özlem Yavas-Grining
InSphero AG

Ozlem is an engineer with a keen interest in developing automation, imaging and image analysis pipelines for advancing 3D spheroid-based drug discovery applications. She joined InSphero in 2020 as an engineer in the T&P team, focusing on automation of lab protocols and development of new high-content-imaging endpoints.Ozlem received her Bachelors degree in Physics from Middle East Technical University in Turkey. In 2019, she completed her PhD in Photonics based on her work on lab-on-chip platform development for plasmonic biosensing applications at the Institute of Photonic Sciences (ICFO), Barcelona.She has co-authored 8 papers in the leading journals in her field and contributed in >15 conferences.

Jiacheng Gu
Ph.D. candidate,
Columbia University

Jiacheng Gu is from Shanghai, China. He graduated from the University of Hong Kong in 2019 with a B.S. in Molecular Biology & Biotechnology. During his senior year, Jiacheng studied long non-coding RNAs in Hepatocellular Carcinoma in the Zhang Lab and received the University Research Fellowship.
Jiacheng studied at Columbia University under the Ph.D. program of Biological Sciences since 2019. He joined the Gaublomme Lab in 2020 where he started the development of a novel optical pooled CRISPR screen method CRISPRmap and its application in DNA damage repair base-editing screening and pooled barcode readout on xenograft tumor sections.
Jiacheng has a particular interest in genome editing, high-throughput optical screens and cancer immunology. He wishes to further his current research after graduation from his Ph.D. program.

Main Session Day 2

Casper Salinas
Sr. Department Manager,
Gubra A/S

Casper Salinas is an experienced scientist having worked with different aspects of quantitative 3D imaging since 2014. During his PhD project he worked with image registration and the construction of a digital mouse brain atlas optimized for cleared brain samples. Later, he focused on using AI for segmentation of signals in the brain relevant for pharmaceutical discovery. Today, Casper works as department manager with responsibility for advancing software and AI at Gubra.

Evan Macosko
Principal Investigator,
The Broad Institute of MIT and Harvard

Dr. Macosko is a neuroscientist and psychiatrist focused on developing new genomics technologies to study brain diseases. Technological innovations he has led include Drop-seq, the first high-throughput single cell analysis method, and Slide-seq, a method for localizing gene expression within intact tissue sections. His lab works to extend these technologies to measure connections amongst neurons in the brain, and to uncover molecular mechanisms of schizophrenia and Parkinson's disease. He is the co-director of the newly established Center for Human Brain Cell Variation at the Broad, funded by the NIH Brain Initiative. Macosko is an attending psychiatrist at Massachusetts General Hospital, an institute member of the Broad Institute, and an associate professor of psychiatry and neurobiology at Harvard Medical School.

Cameron Scott
Product Manager,
Genedata

Cameron became interested in high content screening during his PhD studies at the Hospital for Sick Children in Toronto before moving to continue work at the University of Geneva and the EPFL in Lausanne. Here he continued using high content screening approaches to address questions of cell trafficking before joining Genedata in 2019. At Genedata has worked to support customers using Genedata Screener and Imagence for high content screening applications and now works as a Product Manager.

Denis Wirtz
TH Smoot Professor and VP for Research. Johns Hopkins University

Denis Wirtz
Through research at the interface of physics, biology, and oncology, Wirtz has made seminal contributions in cancer cell migration, cytoskeleton biophysics, mechanobiology, 3D imaging, and immuno-oncology. He has also pioneered research in cell migration in 3D settings, bacterial cell division, high-throughput cell phenotyping, and more recently in CAR T cell engineering. Recently, he has developed CODA, a, AI-based method to image large volumes of tissues and tumors in 3D dimensions. Wirtz has founded the Johns Hopkins Institute for NanoBioTechnology (INBT). He is the Director of the NCI-funded Physical Sciences-Oncology Center (PS-OC) and the Johns Hopkins Cellular Cancer Biology Imaging Cancer (CCBIR) Center. Wirtz was named Theophilius H. Smoot Professor of Engineering and Science in 2009, fellow of the Institute for Medical and Biological Engineering (AIMBE) in 2007, fellow of the American Association for the Advancement of Science (AAAS) in 2009, and fellow of the American Physical Society (APS) in 2010, and member of the Royal Academy of Medicine of Belgium. Wirtz received a physics engineering degree from the Free University of Brussels in 1988, and MSc and PhD in Chemical Engineering from Stanford University in 1993. Wirtz has been the Vice Provost for Research of Johns Hopkins University since 2014.

Brian Feng, Calico Labs

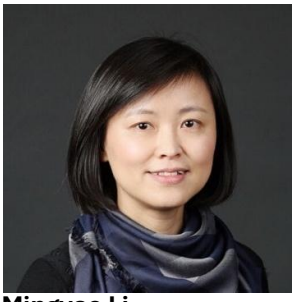
Brian Feng joined the CytoData board in 2024. He is currently a Principal Investigator at Calico Labs, a aging-focused biotechnology company. Brian's lab uses scalable, information-rich methods such as high-content imaging to study cellular phenotypes associated with aging and age-related diseases. His group collaborates extensively with data scientists to tease out unexpected observations from complex, multidimensional data. Prior to joining Calico, Brian spent many years working at Novartis, applying phenotypic screening to the discovery of new antibiotics. He has also worked at Google[x], an Alphabet-backed company specializing in "moonshot" research projects.

Loan Vulliard
Postdoctoral Fellow, German Cancer Research Center

Loan Vulliard is currently serving as president of the CytoData society and has been on the board since 2021. He is an AIH Postdoctoral Fellow at the DKFZ in Heidelberg, Germany, where he works together with Felix Hartmann and Julio Saez-Rodriguez to reveal the quantitative principles underlying molecular biology and to better understand human health and diseases. For this, he uses data analysis methods and collaborate with experimentalists and experts in the fields of immunology and cell biology. In particular, he is developing machine learning approaches to identify and contextualize spatial patterns in multiplexed ion beam imaging (MIBI) data.

Brennan W McFarland
Software Applications, Carl Zeiss Microscopy, LLC

Brennan obtained his PhD from Drexel University at the School of Biomedical Engineering and Health Sciences in the Neural Circuit Engineering lab. During his PhD, he investigated the development neural circuits in the animal Drosophila melanogaster by using a variety of imaging techniques, worked with fixed tissue and live samples, and wrote scripts in Python and MATLAB to automate 2D and 3D image analysis workflows. Brennan brings over 10 years of microscopy and image analysis experience to ZEISS, and resides in Philadelphia, PA.



Mingyao Li
Professor of Biostatistics and Digital Pathology, University of Pennsylvania

Dr. Mingyao Li received her PhD in Biostatistics from the University of Michigan in 2005. She was trained as a statistical geneticist, but since she joined the faculty at the University of Pennsylvania in 2006, she has gradually transitioned her research from traditional statistical genetics to statistical genomics with the goal of having a deeper understanding of the molecular mechanism of human disease. The central theme of her current research is to use statistical and machine learning methods to understand cellular heterogeneity in human-disease-relevant tissues, to characterize gene expression diversity across cell types, to study the patterns of cell state transition and crosstalk of various cells using data generated from single-cell and spatial omics studies, and to translate these findings into clinics. More recently, she expanded her expertise into computational pathology, which is critical when processing and analyzing spatial transcriptomics data. At UPenn, she serves as the Director of the Statistical Center for Single-Cell and Spatial Genomics. She also chairs the Graduate Program in Biostatistics. She is an elected member of the International Statistical Institute, a Fellow of the American Statistical Association, and a Fellow of the American Association for the Advancement of Science.

Caroline Uhler
Andrew (1956) and Erna Viterbi Professor of Engineering in the Dept. of Electrical Engineering and Computer Science and the Institute for Data, Systems, and Society at MIT.

Caroline Uhler is a core institute member of the Broad Institute of MIT and Harvard, where she directs the Eric and Wendy Schmidt Center, and she is a Full Professor in the Department of Electrical Engineering and Computer Science and the Institute for Data, Systems, and Society at MIT. She holds an MSc in mathematics, a BSc in biology, and an MEd all from the University of Zurich. She obtained her PhD in statistics from UC Berkeley in 2011 and then spent three years as an assistant professor at IST Austria before joining MIT in 2015. She is a SIAM Fellow, a Sloan Research Fellow, and an elected member of the International Statistical Institute. And she received various awards including an NIH New Innovator Award, a Simons Investigator Award, and an NSF Career Award. Her research lies at the intersection of machine learning, statistics, and genomics, with a particular focus on causal inference, representation learning, and gene regulation.

Leticia Montoya Ph.D
Staff Scientist, R&D, Thermo Fisher Scientific

Leticia Montoya is a chemical biologist, with a Doctorate in Chemistry from University of Oregon. She has been at Thermo Fisher Scientific since 2018 as a Staff Scientist in R&D focusing on protein and cell analysis. Dr. Montoya has experience in chemical approaches towards analyte detection in biological systems and development of immunoassay kits against metabolic and signaling targets. She now develops technology and solutions for detection of cellular targets and functions using flow cytometry, microplate readers, and imaging tissue and cell-based assay platforms. She serves as a technical lead for product development workflows and collaborates amongst several biologists and chemists on cross-functional teams.

Kian Kenyon-Dean,
Staff Machine Learning Engineer, Recursion

Kian is a Staff Machine Learning Engineer at Recursion working on creating powerful foundation models of biology. Prior to Recursion, he pursued his undergraduate and Master's at McGill University with a strong focus in deep learning, computational linguistics, and natural language processing. As part of the first cohort of students at the newly formed Mila Quebec AI Institute, Kian finished his Master's in Computer Science with a focus in word embedding algorithms. Since then, Kian has worked in industry in a variety of roles. After joining Recursion, Kian quickly expanded his knowledge of biological data and developed an understanding of how deep learning technology can be applied to it. At Recursion, Kian has played a critical role in writing and using distributed deep learning code to train the largest-scale deep learning models ever made for Phenomics (to our knowledge). These generative AI models, such as Phenom-Beta and Phenom-1, have become a core part of the Recursion OS and play a significant role in the drug discovery workflows at Recursion. Outside of work, Kian enjoys rock climbing, camping, and listening to live music.

Jenna M Tomkinson
Quantitative Cell Biologist, University of Colorado Anschutz Medical Campus

Jenna Tomkinson is a Quantitative Cell Biologist in the Gregory Way Lab at the University of Colorado Anschutz Medical Campus. She earned her Bachelor of Science in Biology with a minor in Behavioral Cognitive Neuroscience from the University of Colorado Denver in 2022. During her undergraduate studies, Jenna conducted research on the impact of temperature stress on gene expression across developmental stages in Drosophila melanogaster (common fruit fly).
Jenna facilitates image analysis and image-based profiling for multiple projects in her current role, including studies on Neurofibromatosis Type 1 and pyroptotic cell death. She is also actively developing her skills in machine learning models to support various research initiatives at the lab, including studies on cardiac fibrosis and nuclear speckles. Jenna is committed to advancing the field of computational biology/bioinformatics and contributing to the development of innovative workflows and pipelines.

Juan C Caicedo
Assistant Professor, Univ. of Wisconsin–Madison

Juan Caicedo is a Morgridge Investigator and Assistant Professor at the University of Wisconsin–Madison. His research work is focused on the use of deep learning and machine learning to advance the understanding of cellular phenotypes and tissue organization in images. He started his independent research group as a Schmidt Fellow at the Broad Institute. Prior to this, we held postdoctoral positions in the Imaging Platform at the Broad, and in the Computer Vision group at the University of Illinois in Urbana-Champaign. He obtained his PhD from the National University of Colombia, and as a grad student he was a research intern at Google and Microsoft Research.

David Stirling
Glencoe Software

David Stirling is a data scientist at Glencoe Software. He specialises in producing image analysis workflows and tooling to assist researchers in quantifying and exploring image-based data. He is also interested in integrating popular open source tools with the OMERO ecosystem to provide user-friendly connectivity between packages. David previously worked in the Cimini Lab within the Broad Institute of MIT and Harvard, where he contributed to the CellProfiler image analysis software package. He also produced popular plugins which allow users to make use of powerful AI packages such as Cellpose and StarDist from within this software.

Jean-Philippe Vert
Chief R&D Officer, Owkin

Jean-Philippe Vert is Chief R&D Officer at Owkin, an AI Biotech company that uses AI to discover and develop treatments for unmet medical needs, co-founder and CEO at Bioptimus, a start-up building AI foundation models in biology, and professor (on leave) at PSL University Mines Paris. Before joining Owkin in 2022, he was a research scientist at Google Brain (2018-2022), where I led a research team working on core machine learning and computational biology; a research professor at ENS Paris' mathematics Department (2016-2018); a Fullbright and Miller visiting professor at UC Berkeley's Department of Statistics (2015-2016); a research team leader at the Curie Institute's research center (2008-2018); a research professor and founding director of Mines ParisTech's Centre for Computational Biology (2002-2018); and a research associate at Kyoto University's Bioinformatics Center (2001-2002). He graduated in applied mathematics from Ecole Polytechnique (1995) and received his PhD in mathematics from Paris University (2001). His research interest concerns the theory and practice of statistical machine learning and artificial intelligence to model complex, high-dimensional and structured data, and their applications in computational biology and medicine.

Poster Abstract Titles

Poster Titles, Abstracts, and Placement Numbers accessible below. Poster placement in Exhibit hall and Essex Foyer area.	
SBI2 Conference Website: https://sbi2.org/conference/2024-posters/	

SBI2 Wi-Fi

Wi-Fi Network: SBI22024
Wi-Fi Password: SBI2CONF24

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 2025

Exhibit Hall Map

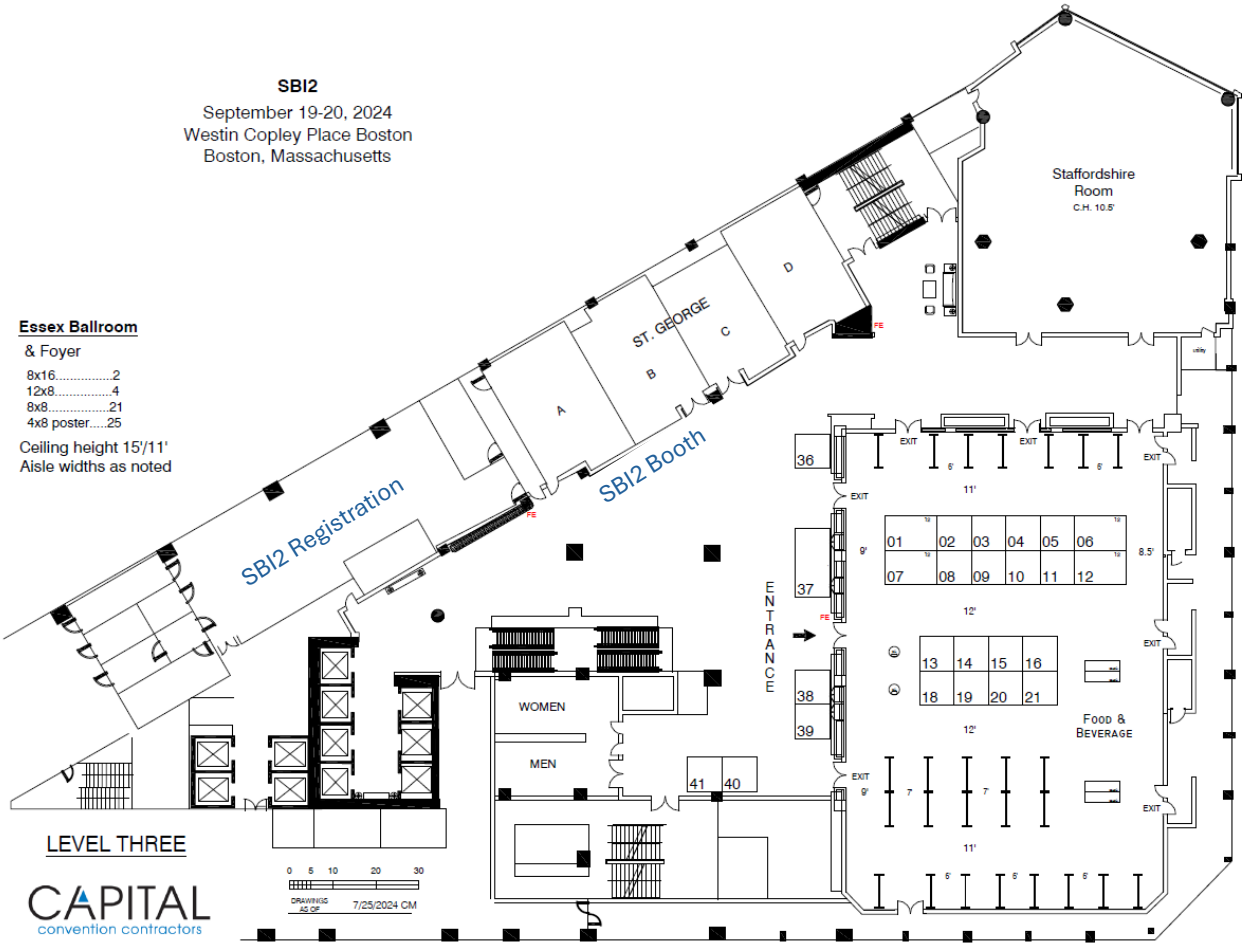


Exhibit Hall and Foyer
• Posters
• Exhibit booths
• High tops + EH map
• Food/Beverage stations
• SBI2 Registration Desk

Exhibitor Booths			
Revvity	1	Ardigen	11
BluecatBio	2	Yokogawa	12
Saguaro	3	Nikon	13
Etaluma	4	CytoTronics	14
Agilent	5	Glencoe	15
Miltenyi	6	Thrive	16
Araceli	7	Thermo	18
syGlass	8	Curia	19
Genedata	9	Molecular Devices	21
Aurora	10	BioMedTech	36
		Cephla	38