High Content 2021

SBI²'s 8th Annual Conference

October 4 – 6, 2021

A virtual event
hosted by LabRoots

Program and event guide

SBI² SOCIETY OF BIOMOLECULAR IMAGING AND INFORMATICS

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PRESIDENT'S WELCOME

On behalf of the SBI² Board of Directors, I would like to welcome you to High Content 2021. This year, we are pleased to be able to bring you four Scientific Sessions, each with a terrific line up of invited speakers. To kick off each day, we excited to have two highly topical Keynote talks by renowned scientists, Dr. Aydogan Ozcan and Dr. Yinyin Yuan. The Keynotes and Scientific Sessions will take place on October 5 and 6 and will be held in the Auditorium.

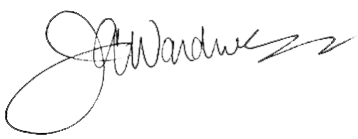
The Poster Hall is also going to be an exciting place to visit during this year's event. We have approximately 35 posters, many with an accompanying 5 min video presentation. The poster presenters will be on hand during the designated poster hall hours to walk you through their posters and to answer your questions. We really hope you will use the live chat features to help make the virtual poster hall a better experience for both you and the presenters. On the final day of the conference, the Poster Hall will also host the Poster and President's Award Ceremony and the Conference closing remarks.

SBI² also strives to bring meaningful educational content and scientific discourse to the biomolecular imaging community. This year we are offering eight Education Courses ranging from introductory to advanced level imaging and analysis. Six of these will take place on October 4, officially known as Education Day, and two the afternoon of October 5 and 6. We will also hold four, exhibitor-sponsored Roundtables which will cover a variety of provocative topics. The Education Courses and Roundtables are accessible from the Education and Roundtable Room.

I would also like to encourage you to visit the Exhibitor Hall where you can live-chat with booth representatives about their latest imaging products including the newest instruments, software, reagents, and consumables. SBI² is extremely grateful to our 2021 exhibitors and sponsors and hope you will support them by stopping by their booths or by attending the exhibitor-sponsored events (Educational Courses, Roundtables, and Poster Hall).

And finally, we invite you to stop by the SBI² Lounge where you can find out more about the Society, become a member, search the job board, volunteer for a committee, fill out our feedback form, or just stop in for a chat with a member of the SBI² Board of Directors.

Enjoy the conference. We hope it meets your expectations!



A brief history of SBI²

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

SBI² was conceived by a groundswell emerging from scientists working in image analysis and screening that realized the enormous potential of image-based assays in academic basic biological investigation, drug discovery and development, but lacked the kind of interactive environment necessary to establish best practices and transparency. Two of us (Joe and Paul) took matters into their own hands at the end of a commercial meeting to define what such a society would look like, and to take the steps necessary to establish such a society [1]. This effort was built from the very positive interactions developed from this and previous versions of such commercial conferences, but needed transparency to support growth of the technical basis of imaging sciences to fully realize their contributions into toxicology, neuroscience, oncology, immunology, diabetes and other disease-driven research. On this point, several impactful elements of the key imaging technologies (e.g. file and image formats) were locked down by proprietary analytical streams that prevented direct comparisons across systems (SF HCI conference session led by Ann, Paul and others). The need for transparency in imaging sciences emerged in parallel with initiatives from NCATS, the 'minimal information' initiatives, and the eventual 'STAR methods' documentation.

After identifying a critical gap in the professional society landscape, the next step was to build this society with representation from some of the key constituencies. With Joe as a member of an independent research organization (the Hamner Institute) and Paul as an academic investigator (UPitt), for this society to function harmoniously, they sought to engage representation from platform developers and pharma. They did so through bringing in Mark from Thermo Scientific and Steve from Wyeth to work together to build a small leadership team. The four of us worked through a similarly spare legal team (Bud Nelson) to incorporate the society as a 501(c)3 professional society. While we brought in a very strong team of board members the commitment we made was made clear when we contracted with Harvard Medical School in 2014 to host our first annual conference and the four of us were held to a pre-payment that none of us could readily absorb and we had only 3 registered attendees. The 2014 conference was ultimately endorsed by several corporate partners including Thermo Scientific and Janssen of the Pharmaceutical Companies of Johnson and Johnson at the founding level, GE Healthcare at the Executive level, and Chroma, Genedata, and Perkin Elmer at the supporting level. We bet the house and have never looked back. This first conference was as successful as we could have hoped and each of the following ones have been better [2]. Through the continued support of our corporate partners, exhibitors, and the active participation of our membership SBI2 continues to evolve with an upward trajectory!

How does engaging with SBI² help you?

Success with launching scientific conferences, establishing a set of online resources and active discussions on setting standards and transparency are key accomplishments. However, as we begin our first virtual conference to a much broader group of researchers, it is important to discuss how your participation in SBI² can be helpful to you.

Let's start with the activities that SBI² engages with.

- **Education**. All activities within SBI² are tied to education platforms to define and teach the current and emerging approaches. Reduction to practice is the definition of promoting a new approach. New investigators are particularly important to SBI², and current approaches are consistently discussed in our educational platforms.
  We are focused on providing guidance to those new to the principles and nuances of imaging approaches.
- **Standards**. One critical role of a scientific society is to define data standards that are foundational to all derivative steps. This is a data integrity phase of building an analytics process. SBI² aggressively pursues the use of open image analysis standards.
- **Transparency, rigor and reproducibility**. Imaging sciences only contribute to basic biology and drug discovery if the image and data processing phases are open to reanalysis, from image capture to numerical results. Methods along each of these steps are expected to be made available to the research community. In most cases, image analysis standards do not exist, so to address this gap, transparency is essential, and fundamental concepts of assay reproducibility are irreplaceable elements of scientific studies.
- **Leading edge approaches, such as informatics and machine learning**. Imaging is highly sensitive to morphological changes as well as heterogeneous responses. The ability to leverage these changes to help understand the effects of genetic and pharmacological perturbations can be differentiated by sophisticated informatic methods. SBI² promotes such approaches in ways that conform to the transparency and reproducibility guidelines discussed above.
- **Approaches that leverage imaging methods, such as imaging mass spectrometry and tissue histology informatics**. Complex analytical methods developed for microscopic imaging approaches are being applied to non-microscopy based or large-scale methods such as tissue histology using multiple markers. Imaging sciences already have a sophisticated set of analytical methods for characterizing morphology, correlation and other comparisons across channels.

From all of these areas of emphasis, it is clear that imaging sciences are expanding broadly into both root level scientific rigor as well as novel technical territory. Engaging with SBI² to learn and contribute to these areas benefits individual scientists through staying abreast of best practices in current applications of imaging sciences as well as how leading-edge methods will change what the definition of imaging sciences is. Therefore, the mission of SBI² is to engage every scientist who steps forward with an interest in understanding their work better or to proffer their study as one that can extend the definition of imaging sciences.

Again, all are welcome!

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High Content 2021 takes place in six rooms within the virtual conference center.

In the **Lobby**, you will find the reception area, the welcome video, the help desk, and a posting of the conference agenda. Click on exhibitor logos to be taken to their websites and promotions.

Keynote Presentations and Scientific Sessions take place in the **Auditorium**.

In the **Exhibit Hall**, you will find exhibitor booths (and a live-chat function), product demos, videos, and brochures.

Education Courses and Roundtables take place in the **Education and Roundtable Room**.

In the **Poster Hall**, you will find posters and be able to chat with the presenters. The Award Ceremony, Closing Remarks, and the SBI² Annual General Meeting take place here as well.

In the **SBI² Lounge**, you can meet SBI² board members, scan the Job Boards, and provide feedback.

PROGRAM FACULTY

Keynote speakers

Aydogan Ozcan, PhD

Aydogan is the Chancellor's Professor and the Volgenau Chair for Engineering Innovation at UCLA and an HHMI Professor with the Howard Hughes Medical Institute, leading the Bio- and Nano-Photonics Laboratory at UCLA School of Engineering and is also the Associate Director of the California NanoSystems Institute. Dr. Ozcan is elected Fellow of the National Academy of Inventors (NAI) and holds > 45 issued/granted patents and > 20 pending patent applications and is also the author of one book and the co-author of > 700 peer-reviewed publications in major scientific journals and conferences. Dr. Ozcan is the founder and a member of the Board of Directors of Lucendi Inc., Hana Diagnostics, Pictor Labs, as well as Holomic/Cellmic LLC, which was named a Technology Pioneer by The World Economic Forum in 2015. Dr. Ozcan is also a Fellow of the American Association for the Advancement of Science (AAAS), the International Photonics Society (SPIE), the Optical Society of America (OSA), the American Institute for Medical and Biological Engineering (AIMBE), the Institute of Electrical and Electronics Engineers (IEEE), the Royal Society of Chemistry (RSC), the American Physical Society (APS) and the Guggenheim Foundation, and has received major awards including the Presidential Early Career Award for Scientists and Engineers, International Commission for Optics Prize, Biophotonics Technology Innovator Award, Rahmi M. Koc Science Medal, SPIE Early Career Achievement Award, Army Young Investigator Award, NSF CAREER Award, NIH Director's New Innovator Award, Navy Young Investigator Award, IEEE Photonics Society Young Investigator Award and Distinguished Lecturer Award, National Geographic Emerging Explorer Award, National Academy of Engineering The Grainger Foundation Frontiers of Engineering Award and MIT's TR35 Award for his seminal contributions to computational imaging, sensing and diagnostics. Dr. Ozcan is also listed as a Highly Cited Researcher by Web of Science.

Yinyin Yuan, PhD

Yinyin leads the Computational Pathology and Integrative Genomics team in the Centre for Evolution and Cancer and the Division of Molecular Pathology at ICR. She brings over a decade of experience in machine learning and digital pathology to cancer research to develop innovative clinical tests and cancer therapies. At the new Centre for Cancer Drug Discovery at ICR, her team focuses on building the interface between artificial intelligence, cancer biology, and clinical science to decipher and target cancer evolution and immune escape.

PROGRAM FACULTY

Scientific session chairs

Karen Dowell, PhD
A business software marketer turned scientist turned biotech product marketer, Karen is senior partnership marketing manager at Akoya Biosciences. She works closely with biotechnology companies and consortia that are collaborating with Akoya to advance single-cell imaging and spatial analysis solutions that enable researchers to visualize how cells organize and interact to influence disease progression and treatment response. Prior to joining Akoya, Karen was a product marketing manager at CrownBio, overseeing a portfolio that spanned in vitro and in vivo oncology models and services, including high-content imaging and analysis using tumor organoids. She also spent several years with InSphero, helping to raise awareness of the utility of multicellular spheroid models for drug discovery and development. Karen earned her PhD in Biomedical Sciences from the University of Maine at the Jackson Laboratory, where she applied machine learning and big data visualization techniques to explore molecular foundations of mouse and human stem cell self renewal programs. She did her postdoctoral studies in computational immunology at Dartmouth College.

Heba Sailem, PhD
Heba is interested in developing innovative quantitative imaging methods for facilitating knowledge discovery from large biomedical datasets. Her work combines techniques from Computer Vision, Bioinformatics and Systems Biology and she created several new tools for analysing and quantifying microscopy data. In 2017, She was awarded a four-year Sir Henry Wellcome Research Fellowship to develop knowledge-driven machine learning for functionalising cancer genes from genetic perturbation screens. She did her doctoral studies at the Institute of Cancer Research in London. While at the ICR she developed methods for integrating phenotypic data with gene expression, modelling the relationship between cell signalling and its context, and modelling the dynamics of cell morphogenesis. In these studies, she discovered new links between cell shape and breast cancer progression. Dr. Sailem is also interested in data visualisation and science communication. She devised several bespoke tools for visualising phenotypic data including PhenoPlot and Shapography. These methods facilitate the interpretation of high-dimensional data by generating pictorial representations of cells based on hundreds to thousands of measurements.

Scientific session chairs

Spencer Shorte, PhD
Spencer graduated (1988) in Biochemistry from the University of Kent at Canterbury (UK) and received his PhD (1992) in the same subject from Bristol University (UK). His interests in development of dynamic cell and tissue imaging techniques in living systems provided focus for his studies during several post-doctoral fellowships in Europe and a visiting professorship in the USA before being appointed group leader at the Institut Pasteur Paris (2001). Founding the *Imagopole* comprising some fifty scientists with expertise in optical microscopy, ultrastructural and cytometry-based imaging technologies his work has swathed fundamental and translational research studies using diverse infectious disease models and paradigms. Author of over one hundred research articles, learned reviews, and numerous patents, his work on “micro-rotation tomography” in collaboration with the French mathematician Professor Bernard Chalmond (ENS) earned him the French engineer of the year award in 2005. Recipient in 2015 of the *Prix Thérèse Lebrasseur* (Fondation de France), he is stalwart member of the Royal Microscopical Society, and in 2018 was named Scientific Director at the Institut Pasteur Korea where he continues his work.

Greg Way, PhD
Greg is a senior postdoc in Anne Carpenter’s lab in the Imaging Platform at the Broad Institute of Harvard and MIT, where the Cell Painting assay was developed. Greg is a biomedical data scientist using image-based profiling for biological discovery. He is also the lead software engineer for the “cytominer ecosystem,” which is a Python package for reproducibly processing and evaluating image-based profiling readouts. He serves on the Board of the CytoData society whose mission is to advance the field of image-based profiling. Having also trained in genomics, he is interested in methods that integrate morphological and molecular readouts.

PROGRAM FACULTY

Scientific session presenters

Ella Atlas, PhD
Ella received her bachelor's and master's degrees from Tel Aviv University, Israel, and her PhD from Queen's University, Canada. She subsequently underwent postdoctoral training at the Lawrence Berkeley National Lab, University of California at Berkeley and was later appointed as a research scientist at that institution. After serving as a research assistant professor, Northwestern University, Illinois, she joined Health Canada, serving as adjunct professor at the University of Ottawa. Her laboratory's main focus is to develop in vitro models to investigate toxicity of environmental pollutants and metabolic effects. Her research uses 3D- and 2D-cell models to investigate metabolic disruption of adipocytes and liver toxicity.

Nataliia Beztsinna, PhD
Nataliia joined OcellO (now Crown Bioscience Netherlands) in 2018 as a Senior Scientist on the Immuno-Oncology team. Since 2020, she has led work on the Near Vivo Drug Response Platform designed to evaluate preclinical drug candidates in ultrafresh patient tumor material. Her expertise is in assay development for oncology and immuno-oncology drug testing in ex vivo 3D tumor tissues with preservation of their native TME and with help of 3D high-content image analysis. Dr. Beztsinna received her PhD in Biochemistry from the University of Bordeaux and continued post-doctoral studies in Pharmaceutics at Utrecht and Leiden Universities. Her broad experience with 3D high-content imaging, organoids, in vitro and in vivo cancer models, and tumor-targeted drug delivery helps in expanding and developing drug testing in patient-derived microtumors on the Near Vivo Drug Response Platform.

Paul Blainey, PhD
After obtaining degrees in mathematics and chemistry from the University of Washington, Paul joined Professors Gregory L. Verdine and X. Sunney Xie in the Department of Chemistry and Chemical Biology at Harvard University. There, he elucidated the mechanics of proteins diffusing along DNA using single-molecule mechano-optical assays and earned a PhD in Physical Chemistry. He then transitioned to Professor Stephen R. Quake's group at Stanford University where he developed high-throughput microoptofluidic methods for whole-genome amplification of DNA from individual, uncultivated microbial cells. Paul has served as a faculty member in Biological Engineering at MIT and a Core Member of the Broad Institute since 2012, where his group integrates microfluidic, molecular, and imaging tools to prepare practical, robust, and scalable solutions to major challenges in next-generation sequencing sample preparation, single-cell analysis, genomic screening, and therapeutics development.

Jenna Bradley, PhD

Jenna is an Associate Principal Scientist in the Functional Genomics group in Discovery Sciences in AstraZeneca, Cambridge. Jenna received her PhD from the University of East Anglia in 2014 where she studied the regulation of gene expression during inflammation. Jenna joined AstraZeneca in 2014, where she generated oncology cell models using CRISPR/Cas9 and used CRISPR technologies to improve cell model development. In 2020, Jenna moved to the Functional Genomics team where she leads target identification and validation projects to identify new drug opportunities in oncology and respiratory diseases.

Philip Gribbon, PhD

Philip is Head of Discovery Research, Fraunhofer Institute for Translational Medicine and Pharmacology, Hamburg, Germany, which he joined in 2014 as Assistant Head of Department, Fraunhofer Institute of Molecular Biology and Applied Ecology (IME). Fraunhofer IME ScreeningPort (IME SP) acts as a translational platform between basic research and industrial development. From 2014 – 2018, he was Coordinator of EU-OPENSCREEN, a non-profit research infrastructure hosted by Germany and offering access to academic high-throughput screening facilities and medicinal chemistry groups in eight European countries. Philip's principal scientific interest is the development of technologies and methodologies for improving early-stage drug discovery, in particular using disease-relevant in vitro models and biophysical methods for evaluation of target engagement. He has considerable experience in drug discovery programs across a wide range of target classes, experience acquired while working at Pfizer and GSK. He received his undergraduate and PhD degrees (Biophysics) from Imperial College, London and pursued post-doctoral studies at the University of Manchester.

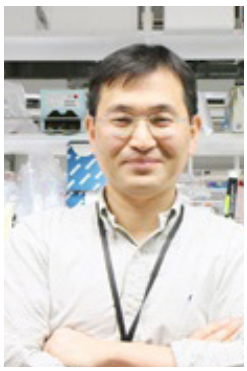
PROGRAM FACULTY

Scientific session presenters

Patrick Guye, PhD
Patrick looks back at more than 15 years of experience in engineering cells, tissues, and organoids as a scientist, executive, entrepreneur, and consultant. At Princeton and MIT, he developed synthetic biology-inspired tools and methods to genetically program human pluripotent stem cells to develop into complex tissues such as liver, pancreas, and the hematopoietic system. At Sanofi, he established a lab in cell therapy and drug discovery based on stem-cell-derived differentiation to 3D tissues and another lab in cell & biologics engineering. Later, Patrick joined InSphero as CSO, leading R&D, product management, and services, developing new 3D models, and offering drug discovery services on various platforms, including body-on-a-chip devices. As co-founder of Cephalion Technologies and Trilliome, he supports clients in developing organotypic, scalable, robust 3D models while applying machine learning, deep learning, and automation to these processes. On the commercial side, he is helping incubators, companies, and investors understand & assess the technology and commercialization potential and guide founders to set up their companies successfully.

Katie Heiser, PhD
Katie received her PhD in molecular and cellular biology, with a focus in virology, from the University of Colorado at Boulder. Additionally, she has worked in rare genetic disorder diagnostics and the optical imaging field as an advanced microscopy applications specialist. She is currently a senior scientist in the in vitro pharmacology department at Recursion Pharmaceuticals. She leads assay development and drug discovery efforts in multiple disease areas, including the COVID-19 and fibrosis associated diseases.

Peter Horvath, PhD
Peter is a director and group leader in the Biological Research Center in Szeged and holds a Finland Distinguished Professor (FiDiPro) Fellow position in the Institute for Molecular Medicine Finland (FIMM), Helsinki. He graduated as a software engineer and received his PhD from INRIA and University of Nice, Sophia Antipolis, France in satellite image analysis. Between 2007 and 2013 he was a senior scientist at the ETH Zurich in the Light Microscopy Centre. Peter is interested in solving computational cell biology problems related to light microscopy and is involved in four main research fields: 2/3D biological image segmentation and tracking; development of microscopic image correction techniques; machine learning methods applied in high-throughput microscopy; and the development of single-cell isolation methods. He is the co-founder of the European Cell-based Assays Interest Group and a former councilor of the Society of Biomolecular Imaging and Informatics.



Seungtaek Kim, PhD
Seungtaek studied biochemistry at Iowa State University for his PhD and did postdoctoral training with Dr. Paul Ahlquist at Howard Hughes Medical Institute and University of Wisconsin-Madison and with Dr. Stan Lemon at University of North Carolina at Chapel Hill. During his postdoctoral training, he studied hepatitis B and C viruses focusing on viral entry and virus assembly. In 2017, he joined Institut Pasteur Korea as a Head of Zoonotic Virus Laboratory and expanded his research into emerging virus infections including coronaviruses, flaviviruses, and bunyavirus. During the COVID-19 pandemic, his team was one of the first in the world to discover potential drug candidates against COVID-19 by drug repositioning, and some of these candidates are now in phase 2 and 3 clinical trials in multiple countries. His work has been recognized by the Korean government—he received the “Scientist of the Year” Award from the Ministry of Science and ICT–and he serves as a member of several government committees for COVID-19 and other infectious diseases.

PROGRAM FACULTY

Scientific session presenters

Madhu Lal-Nag, PhD
Madhu earned her PhD in Molecular and Cellular Oncology from The George Washington University and her Master's in Bioscience Business from The Keck Graduate Institute of Applied Biosciences, Claremont, CA. Prior to that she earned her Master's in Biochemistry from the University of Mumbai, India. Her main passion lies in being able to bridge the gap between the academic and the translational aspects of cutting-edge science in oncology, and in using the results of current chemotherapeutic response/regimens to creatively translate cutting edge research to immediately serve patient needs. Her research interests lie in the development of predictive alternative models for safety and efficacy in drug development and evaluation. Her work at the National Center for Advancing Translational Sciences (NCATS/NIH) focused on the development of single- and multi-cellular tumor spheroids and organoids for high-throughput small molecule and functional genomics screening. At NCATS, Dr. Lal-Nag served as the Director of the Trans NIH RNAi Facility that ran high-throughput functional genomics screens for the entire NIH intramural program serving 21 institutes. Her group established an arrayed functional genomics robotics platform to run high-throughput phenotypic screens for the NIH Intramural Program and built a high caliber multi-disciplinary team of scientists, postdoctoral fellows, and post-baccalaureate students to complement and broaden the TNRF scientific expertise. She also led the formation of the first 3D standards working group with Insphero Inc, which comprised of a group of scientists representing the breadth of academia, pharma, and government-run research institutions. The premise of this group is to develop a set of standards for "best fit" models that can be used to answer specific questions as they pertain to disease biology in more complex in vitro cellular systems.

Emma Lundberg, PhD

At the interface between bioimaging, proteomics, and artificial intelligence Emma's research aims to define the spatiotemporal organization of the human proteome at a cellular and subcellular level, with the goal of understanding how variations in protein expression patterns can contribute to cellular function and disease. She is Professor of Cell Biology Proteomics at KTH Royal Institute of Technology in Sweden and recently spent three years as a visiting professor at Stanford School of Medicine and the Chan–Zuckerberg Biohub. For the past 13 years she has been a Director of the Human Protein Atlas project, leading the effort to create the Cell Atlas part of this database. She is an advocate for open science and has a strong interest in science communication, both to scientific audiences and the general public through innovative media. She has been secretary general of the Human Proteome Organization, and am involved in advisory roles for many open access databases and cell mapping efforts such as the Human Cell Atlas consortium, UniProt db, Reactome db, Human Proteome Project, EMBL-EBI Bioimaging Ecosystem Steering Group and pharma companies. As a token of her leadership skills, she was twice recognized as top 10 under 40 future leaders in biopharma and omics.

Vilja Pietiäinen, PhD

Vilja (PhD in virology, Adj. Prof. in Cell and Molecular Biology) is a team leader and senior researcher at FIMM, with expertise in cell biology, precision medicine, patient-derived 2D-3D cell models, and high-content microscopy. She is also a co-director and co-founder of FIMM High Content Imaging and Analysis Core unit. She has led and managed several high-content imaging-related projects at FIMM (e.g., EU FP7 on Systems Microscopy, industrial collaborations, BusinessFinland 2014 – 2018, EraPERMED COMPASS project for standardized drug testing of pediatric solid tumors 2019 – 2023). During the COVID-19 pandemic, her team initiated collaborative research projects with virologists to establish assays for identifying antivirals as well as antigen responses in infected individuals.

PROGRAM FACULTY

Scientific session presenters

Roser Vento-Tormo, PhD
Roser's research interest is to understand the influence of cellular microenvironments on individual cellular identities and responses, in the context of immunity and development. Her team (https://ventolab.org/) employs single-cell and spatial transcriptomics methods to deconstruct the cell signals in human organs and tissues, and utilise this information to inform the reconstruction of novel in vitro models. Essential to this work are the novel computational tools her team develops to build cell–cell interaction networks from transcriptomics data. Her training in genomics and bioinformatics puts her in a unique position to lead multidisciplinary projects. In her predoctoral research, she studied the interplay between cell signalling and epigenetic machinery, key to regulating cellular fate decisions in myeloid cells. She pursued her postdoctoral studies in the Teichmann laboratory as an EMBO / HFSP fellow, where she developed CellPhoneDB.org, a computational tool to study cell–cell communication from single-cell transcriptomics data, and use it to disentangle the complex communication between maternal and fetal cells in the uterine–placental interface during early human pregnancy. Her work has been funded by many recognised international agencies (H2020, MRC, CZI, Wellcome–LEAP), and she has recently obtained the Early Career Research Award from the Biochemistry Society (2021).

Yuhan Wang, PhD
Yuhan is a postdoc associate in the multiFISH project team at the HHMI Janelia Research Campus. She and the team develop spatio-molecular methods for cell type profiling, especially in the brain. She received her PhD from Oregon Health & Science University with a focus on stem cell biology and gene/cell therapy.

Tae Yeon Yoon, PhD

Tae is a postdoctoral fellow in the group of Dr. Timothy Mitchison at Harvard Medical School. As a cell biophysicist, he seeks quantitative understanding of cellular processes to discover fundamental mechanisms and how their perturbation causes diseases using advanced light microscopy, molecular/cellular engineering, and computational analysis. His current research interests center on the machinery which transports macromolecules between the nucleus and cytoplasm in all eukaryotes. He established an optogenetic-based assay that quantitatively measures the nuclear transport kinetics in a large number of individual living cells. Using this tool, he studied the role of glycosylation of the nuclear pore complex and the inhibitory effect of a SARS/SARS-CoV-2 polypeptide on the efficiency of nuclear transport. He received his PhD in applied physics from Harvard University and his BA in physics and mathematics at the University of Chicago.

Paula Andrea Marin Zapata, PhD

Paula is a data scientist at Bayer AG in Berlin. She obtained a PhD in biology from the German Cancer Research Center DKFZ, an MSc in Applied Mathematics from Eindhoven University of Technology, and a BSc in Biological Engineering from the National University of Colombia in Medellin. In 2017, she joined Bayer as a postdoctoral fellow, where she developed deep-learning methods for phenotypic profiling in plant sciences and cellular images. Since 2019, she works at the Machine Learning Research group in Bayer R&D, where she focuses on image analysis applications to drug discovery.

CONFERENCE AT A GLANCE

Monday, October 4, 2021

11:00 a.m. – 2:00 p.m.	Exhibit Hall open
11:00 a.m. – 2:00 p.m.	Education Course Day

Tuesday, October 5, 2021

9:00 a.m. – 5:00 p.m.	Exhibit Hall open / Digital networking
9:00 – 11:00 a.m.	Poster session with live chat and video (1)
10:00 – 11:00 a.m.	Roundtable
11:00 a.m. – 12:00 p.m.	Keynote presentation Toward intelligent microscopes: deep learning's potential for biomedical imaging applications
12:15 – 2:15 p.m.	Session I How does high-content intersect with single-cell analysis and/or spatial omics?
2:30 – 4:30 p.m.	Session II 3D biology: instrument platforms, consumables, software, and models
4:30 – 5:30 p.m.	Roundtable & Education course
4:30 – 6:00 p.m.	Poster session with live chat and video (2)

Wednesday, October 6, 2021

9:00 a.m. – 5:00 p.m.	Exhibit Hall open / Digital networking
9:00 – 11:00 a.m.	Poster session with live chat and video (3)
10:00 – 11:00 a.m.	Roundtable
11:00 a.m. – 12:00 p.m.	Keynote presentation Co-evolving AI and pathology to target cancer evolution
12:15 – 2:15 p.m.	Session III Infectious disease: SARS-CoV-2 and beyond
2:30 – 4:30 p.m.	Session IV Functional genomics and imaging: genotype to phenotype
4:30 – 5:30 p.m.	Roundtable & Education course
4:30 – 6:00 p.m.	Poster session with live chat and video (4)
5:30 p.m.	Award Ceremony (Poster Hall) and Annual General Meeting

PROGRAM AGENDA

Monday, October 4, 2021
All times US Eastern

11:00 a.m. – 2:00 p.m. **Exhibit Hall open**

11:00 a.m. – 2:00 p.m. **Education Course Day**

Track 1	Track 2
11:00 a.m. – 12:00 p.m.	11:00 a.m. – 12:00 p.m.
Introduction to 3D assays: from experimental design to biological applications Özlem Yavas Grining, PhD (InSphero) and Alexandra Title, PhD (InSphero)	Overcoming challenges in HCS Kayla Hill, PhD (Molecular Devices)
Sponsored by inSphero	Sponsored by Molecular Devices
12:00 – 1:00 p.m.	12:00 – 1:00 p.m.
HCS assay development best practices & considerations – Cell models Joe Trask (PerkinElmer)	An introduction to deep learning Alice Lucas, PhD (Broad Institute)
Sponsored by PerkinElmer For the Better	Sponsored by Aracei Bioscienc
1:00 – 2:00 p.m.	1:00 – 2:00 p.m.
3D imaging for high-content screening: introduction and some best practices Jonny Sexton, PhD (University of Michigan)	Introduction to assay statistics Bartek Rajwa, PhD (Purdue University)
Sponsored by Yokogawa Co-innovating tomorrow	

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9:00 a.m. – 5:00 p.m. **Exhibit Hall open / Digital networking**

9:00 – 11:00 a.m. **Poster session with live chat and video (1)**

10:00 – 11:00 a.m. **Roundtable**

Cloud-optimized data management and analysis for high-content screening

Sponsored by Glencoe SOFTWARE

11:00 a.m. – 12:00 p.m. **Keynote presentation**

Toward intelligent microscopes: deep learning's potential for biomedical imaging applications

Aydogan Ozcan (University of California, Los Angeles)

Deep learning is a class of machine learning techniques that uses multi-layered artificial neural networks for automated analysis of signals or data. Beyond its main stream applications such as the recognition and labeling of specific features in images, deep learning holds numerous opportunities for revolutionizing image formation, microscopic reconstruction and sensing fields. In this presentation, I will provide an overview of some of our recent work on the use of deep neural networks in advancing computational microscopy and sensing systems, also covering their biomedical applications.

12:15 – 2:15 p.m. **Session I**

How does high-content intersect with single-cell analysis and/or spatial omics?

Chair: Greg Way (Broad Institute)

Spatial omics technologies use imaging methods to acquire localized molecular readouts. While powerful, these technologies pose many challenges. The field requires sophisticated computational infrastructure, novel analytical methods, and innovative approaches in order to realize its full potential. Combined with high-content screens, these applications will reveal the impact of perturbations on biological scales, such as tissues and organ systems, as never before possible. This session will highlight emerging solutions to increase information content of spatial omics data that will power the ultra-high-content screens of the future.

12:15 – 12:40 p.m.

Life beyond the pixels: single-cell analysis using deep learning and image analysis methods

Peter Horvath (FIMM, Szeged University)

In this talk I will give an overview of the computational steps in the analysis of a single cell-based large-scale microscopy experiments. First, I will present a novel microscopic image correction method designed to eliminate illumination and uneven background effects which, left uncorrected, corrupt intensity-based measurements. New single-cell image segmentation methods will be presented using differential geometry, energy minimization and deep learning methods (www.nucleAIzer.org). I will discuss the Advanced Cell Classifier (ACC) (www.cellclassifier.org), a machine learning software tool capable of identifying cellular phenotypes based on features extracted from the image. It provides an interface for a user to efficiently train machine learning methods to predict various phenotypes. For cases where discrete cell-based decisions are not suitable, we propose a method to use multi-parametric regression to analyze continuous biological phenomena. To improve the learning speed and accuracy, we propose an active learning scheme that selects the most informative cell samples.

Our recently developed single-cell isolation methods, based on laser-microcapturing and patch clamping, utilize the selection and extraction of specific cell(s) using the above machine learning models. I will show that we successfully performed DNA and RNA sequencing, proteomics, lipidomics and targeted electrophysiology measurements on the selected cells.

12:40 – 1:05 p.m.

Expansion-assisted iterative FISH (EASI–FISH): spatio-molecular profiling in thick tissue

Yuhan Wang (Janelia Research Campus)

Recent emergence of low-cost, high-throughput single-cell RNA-Sequencing technology (scRNA-Seq) has enabled systematic identification of new cell types. Molecular definition of cell types provides a way to classify cells and survey cellular heterogeneity. Establishing the spatial organization of cell types identified by scRNA-Seq analysis is essential and requires mapping of these cell types in three-dimensional (3D) tissue volumes. Here, we developed Expansion-Assisted Iterative Fluorescence In Situ Hybridization (EASI–FISH) to survey gene expression and molecular cell types in thick tissue. We also developed a turnkey,

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open-source computational pipeline that allows for rapid and automated data processing, facilitating adoption of high-plex FISH in thick tissue as a routine laboratory method.

1:05 – 1:30 p.m.

Spatiotemporal dissection of the human proteome

Emma Lundberg (KTH Royal Institute of Technology)

Biological systems are functionally defined by the nature, amount and spatial location of the totality of their proteins. Resolving the spatiotemporal distribution of the human proteome at a subcellular level increases our understanding of human biology and disease. In the Human Protein Atlas project, we are systematically mapping the human proteome in a multitude of human cells and organs using microscopy. We have generated a high-resolution map of the subcellular distribution of the human proteome and have shown that as much as half of all proteins localize to multiple compartments. Such proteins may have context specific functions and 'moonlight' in different parts of the cell, thus increasing the functionality of the proteome and the complexity of the cell from a systems perspective.
Recently, we performed a single cell spatiotemporal dissection of the transcriptome and proteome over the cell cycle. We could identify 20% of the human proteome to display cell-to-cell variability, and present the first evidence of cell cycle association for 301 proteins. Our results show that cell cycle progression explains less than half of all cell-to-cell variability, and that most cycling proteins are regulated post-translationally, rather than by transcriptomic cycling.

All this work is critically dependent on computational image analysis, and I will discuss machine learning approaches for classification and embedding of spatial subcellular patterns, including the results from two recent Kaggle competitions.

In summary, I will demonstrate the importance of spatial proteomics data for improved single cell biology and present how the freely available Human Protein Atlas database (www.proteinatlas.org) can be used as a resource for life science.

1:30 – 1:55 p.m.

Mapping the temporal and spatial dynamics of the human endometrium in vivo and in vitro

Roser Vento-Tormo (Wellcome Sanger Institute)

The endometrium, the mucosal lining of the uterus, undergoes dynamic changes throughout the menstrual cycle in response to ovarian hormones. We have generated single-cell and spatial reference maps of the human uterus and 3D endometrial organoid cultures. We dissect the signalling pathways that determine cell fate of the epithelial lineages in the lumenal and glandular microenvironments. Our benchmark of the endometrial organoids highlights common pathways regulating the differentiation of secretory and ciliated lineage in vivo and in vitro. We show in vitro that downregulation of WNT or NOTCH pathways increases the differentiation efficiency along the secretory and ciliated lineages, respectively. These mechanistic insights provide a platform for future development of treatments for a range of common endometrial disorders including endometriosis and carcinoma.

1:55 – 2:15 p.m.

Q & A

2:30 – 4:30 p.m.

Session II
3D biology: instrument platforms, consumables, software, and models

Chair: Karen Dowell (Akoya Biosciences)

Over the past 10 years, we've seen tremendous advances in 3D cell technologies, such as 3D in vitro models that more closely reflect morphological characteristics, cellular complexity, and physiology of tissues and organ systems in the human body. In this session, our speakers will discuss how the era of 3D biology is transforming preclinical research today. They will share how they are applying 3D liver models to investigate the toxic response to exposure to forever chemicals (per- and polyfluoroalkyl substances), introduce novel approaches for developing immune-competent 3D tumor models from fresh patient tumor tissue to better predict patient response to immunotherapies, identify synergies between translational and regulatory science in the context of microphysiological systems that mirror interactions between multiple tissue types, and provide expert advice on how to successfully implement these types of new 3D cell technologies in your workflow.

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2:30 – 2:55 p.m.

Primary human liver cell spheroids as a platform for evaluating liver toxicity and potency of per- and polyfluoroalkyl substances (PFAS)

Ella Atlas (HealthCanada)

Human exposure to Per- and polyfluoroalkyl substances (PFAS) is ubiquitous and these compounds are some of the most prominent contaminants in humans. The toxicity of perfluorooctane sulfonate (PFOS) and perfluorooctanoate (PFOA) is somewhat known, however data on lesser-understood PFAS are limited. Studies in rodents showed that exposure to PFAS resulted in liver toxicity and liver carcinogenesis. Whether this is also the case in humans it is less clear. Thus we used primary human liver cell spheroids to identify toxic liver effects. New approach methodologies (NAMs) that apply bioinformatic tools to high-throughput data are being increasingly considered to inform risk assessment for data-poor chemicals. In this study we identified biological response potencies (i.e., benchmark concentrations: BMCs) following PFAS exposures to inform read-across for risk assessment of data-poor PFAS. Gene expression changes were measured in the primary human liver cell microtissues (i.e., 3D spheroids) after 1-day and 10-day exposures to increasing concentrations of 23 PFAS. The cells were treated with subgroups of PFAS: carboxylates (PFCAs), sulfonates (PFSAs), fluorotelomers, and sulfonamides. We identified differentially expressed genes and transcriptomic BMCs. Further, we examined phenotypic changes by microscopic imaging. The combined high-throughput transcriptomic and bioinformatic analyses and microscopy support the capability of NAMs to efficiently assess the effects of PFAS in liver microtissues.

2:55 – 3:20 p.m.

The development and utility of physiologically relevant models in drug discovery

Madhu Lal-Nag (Research Governance Council, FDA)

There is a great need to understand the synergy between the areas of translational and regulatory science research as they pertain to microphysiological systems and their application in evaluating safety and efficacy for therapeutic indications for different disease areas. There has been much progress towards the experimental development of robust, scalable, and reproducible 3D cellular models, including spheroids, organoids, biofabricated tissues and microphysiological on chip systems, as assay platforms for preclinical drug testing. However, there is a need for systematic physiological and pharmacological validation and benchmarking of the different 3D cellular models to establish their true clinical predictability and use for decision making in the drug discovery and development pipeline. This talk will focus on identifying these areas of synergy and focus on the development of microphysiological systems that are a best fit for different applications.

3:20 – 3:45 p.m.

Redefining patient-relevant 3D in vitro models

Nataliia Beztsinna (Crown Bioscience)

Patient-derived organoids, are aiming to bridge the gap between tissue culture systems and patients in the clinic. However, even in these advanced models, the endogenous cells of the tumor microenvironment (TME), such as tumor infiltrating lymphocytes (TILs), fibroblasts, macrophages and other immune cells, are absent. These TME components have been shown to express important drug targets and play a critical role in both tumor progression and modulation of the response to drugs. Here we present a novel Near Vivo Drug Response platform that combines a short-term 3D ex vivo tumor culture system with high content image-based analysis. Patient tumor tissues from pleural fluid, ascites, surgical resections or biopsy were tested ex vivo to preserve tumor heterogeneity and resident immune cells, removing the need for artificial co-culture systems. This study entailed a detailed quantification of tumor sensitivity to targeted therapies, standard of care, and novel immune drugs and drug combinations, tested on different cancer types.

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3:45 – 4:10 p.m.

From works of art to a scalable industry

Patrick Guye (Trilliome)

The field of 3D tissues and organoids has seen massive growth, with applications ranging from disease modeling, drug discovery, cell therapy, personalized medicine, and cosmetics to food & cultured meat. While there is lots of excitement about the possibilities of 3D models, many academic labs and commercial entities experience similar bottlenecks for successful development, application & translation, scaling up, and finally, commercialization of these models. In this presentation, Patrick will review bottlenecks, solutions, and new opportunities in the field, covering science, data & automation, as well as commercialization challenges.

4:10 – 4:30 p.m.

Q & A

4:30 – 5:30 p.m.

Roundtable

The current landscape of oncological testing using high-content technology

Sponsored by ThermoFisher SCIENTIFIC The world leader in serving science

Education course

Imaging the transcriptome with MERFISH

Jeffrey Moffit, PhD
(Boston Children's Hospital / Harvard Medical School)

4:30 – 6:00 p.m.

Poster session with live chat and video (2)

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9:00 – 11:00 a.m. **Poster session with live chat and video (3)**

10:00 – 11:00 a.m. **Roundtable**

AI and automation of high-content screening analysis

Sponsored by Genedata

11:00 a.m. – 12:00 p.m. **Keynote presentation**

Co-evolving AI and pathology to target cancer evolution

Yinyin Yuan (The Institute of Cancer Research, London)

A fundamental question in cancer biology is how cancers evolve heterogeneity and treatment resistance. The evolution trajectory of cancer is dictated by selective pressures from treatments and the tumour ecosystem. Artificial intelligence (AI) allows us to measure geographical patterns of the microenvironment in pathological samples, to study cancer habitats and niches. Current challenges are establishing multidisciplinary platforms and developing reproducible AI tools by leveraging pathology, genetic, molecular, cellular, and clinical data to improve personalized oncology.

Charles Darwin described how the intimate coexistence between flowering plants and insects leads to reciprocal evolutionary changes; this is now known as coevolution. Today, through the demolition of disciplinary barriers, AI and pathology can coevolve to create evolutionary changes and new paradigms. I will discuss our latest progress on combining AI and experimental technologies for spatial histology and omics data analysis. We aim to understand how cancer evolves within diverse environmental conditions. Our work has revealed a high level of geospatial variation in the tumour microenvironment, with profound implications for early diagnosis, biomarker development, and cancer therapeutics.

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12:15 – 2:15 p.m.

Session III
Infectious disease: SARS-CoV-2 and beyond

Chair: Spencer Shorte (Institut Pasteur / Institut Pasteur Korea)

The COVID-19 pandemic catalyzed an unprecedented effort to establish vaccine, diagnostic and therapeutic tools to fight SARS-CoV-2. Remarkable successes underlie todays' deployment of high-efficacy vaccines, and fast, affordable diagnostics. However, the area of therapeutic drug discovery lagged behind, and as yet there are just a handful of clinically proven drugs showing promise to treat COVID-19. It is clear that in the future new technologies and strategies for high-content screening for early drug discovery could hold the key to rethinking how we go about drug-discovery, and our preparedness for future emergent infectious disease outbreaks. This session invites keynote research scientists to share with us their views on how existing technologies for early drug discovery might be better deployed against infectious disease targets like SARS-CoV-2, and what new technologies and strategies look promising for the future.

12:15 – 12:40 p.m.

SARS-CoV-2 biology and drug development

Seungtaek Kim (Institut Pasteur Korea)

COVID-19 is an ongoing emerging infectious disease and the causative agent of COVID-19 was identified as SARS-CoV-2. Although this virus is very similar to SARS-CoV based on the viral genome sequence, the transmission, pathogenesis and case fatality are substantially different from those caused by other coronaviruses such as SARS-CoV and MERS-CoV. The unprecedented socioeconomic burden by COVID-19 has prompted very fast development of diagnostic tools, vaccines, and therapeutics. Remarkably, within ten months after the release of the viral genome sequence, a couple of vaccines were successfully developed and after emergency use authorization, several of them are now being used for vaccination of people in many countries. Compared to the vaccine development, drug development has been partially successful so far, and the most potent antiviral drugs were developed as therapeutic antibodies which would inhibit interaction between viral spike protein and host receptor ACE2, thereby blocking viral entry. In this presentation, the COVID-19 drug development efforts will be discussed focusing on drug repositioning and the recent SARS-CoV-2 variants of concern.

12:40 – 1:05 p.m.

Deep-learning enabled phenomics applied to COVID-19 drug discovery

Katie Heiser (Recursion Pharmaceuticals)

We applied deep-learning-driven analysis of cellular morphology to develop a scalable “phenomics” platform and here we demonstrate its ability to rapidly identify potential therapeutic stop-gaps for the COVID-19 pandemic. High-throughput screening on this platform demonstrates rapid identification and triage of hits for COVID-19. We deploy the platform to develop phenotypic models of active SARS-CoV-2 infection and of COVID-19-associated cytokine storm, surfacing compounds with demonstrated clinical benefit, such as Remdesivir, and deprioritizing compounds that had no benefit such as hydroxychloroquine. The associated library of images, deep learning features, and compound screening data from COVID-19 screens are available at rxrx.ai and serve as a resource for immune biology and cellular-model drug discovery with potential impact on the COVID-19 pandemic

1:05 – 1:30 p.m.

Compound repurposing by target based and phenotypic approaches to identify in vitro inhibitors of SARS-CoV-2 viral entry and replication

Philip Gribbon (European ScreeningPort, Fraunhofer ITMP)

SARS-CoV-2 is a novel coronavirus responsible for the COVID-19 pandemic, in which acute respiratory infections are associated with high socio-economic burden. We applied target based and high-content screening approach to a well-defined collection of 5632 compounds including 3488 that have undergone previous clinical investigations across 600 indications. In phenotypic assays, compounds were screened by microscopy for their ability to inhibit SARS-CoV-2 cytopathicity in the human epithelial colorectal adenocarcinoma cell line, Caco-2. The primary screen identified 258 hits that inhibited cytopathicity by more than 75%, most of which were not previously known to be active against SARS-CoV-2 in vitro. The high-content screening data are suitable for reanalysis across numerous drug classes and indications and may yield additional insights into SARS-CoV-2 mechanisms and potential therapeutic strategies. Target based screens were run against key viral targets including the main (M) and papain like (PL) proteases and structural biology approches used to conform the MoA

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1:30 – 1:55 p.m.

High-content screening for the serology and treatment of SARS-CoV-2 infection

Vilja Pietiäinen (FIMM, University of Helsinki)

The COVID-19 pandemic, caused by SARS-CoV-2, has presented a global need for research efforts enabling the interventions, as well as to discover the disease biology and pathology. Here, we described our two high-content, cell-based assays to 1) identify antivirals and, 2) understand the development of antigen responses/immunity against the virus in the infected individuals.

The drug sensitivity and resistance testing (DSRT) technology, established earlier by us to repurpose targeted therapies for cancer patients, was used to develop a high throughput platform for drug testing of > 1000 compounds against the SARS-CoV-2 infection using different cell lines with cell viability -based readout, with further validation with image-based assays. The top hits are currently being tested in rodent infection models.

We have also set up a rapid and accurate high-capacity serological method to measure the antibodies against SARS-CoV-2. The assay is a next-generation miniaturized version of the indirect immunofluorescence assay (IFA) commonly applied in viral serodiagnostics. Here we show how the assay enables machine-learning -guided detection of up to three immunoglobulin (Ig) classes from a single sample in a high throughput manner with high sensitivity and specificity, enabling quantitative data interpretation and visualization.

1:55 – 2:15 p.m. Q & A

2:30 – 4:30 p.m.

Session IV
Functional genomics and imaging: genotype to phenotype

Chair: Heba Sailem (University of Oxford)

Microscopy has been instrumental to our understanding of gene functions at different system-levels. Recent convergence of technological advances in automated microscopy, image analysis and genome editing, such as CRISPR, open new avenues for studying how gene perturbations at the molecular level contribute to cellular processes and tissue phenotypes. Tremendous progress has been made towards systematic

mapping of gene functions; from genome-wide CRISPR screens, target-annotated small molecule and functional protein screens at the cell and organism level utilizing automated data analysis. This session invites speakers who developed innovative image-based screening approaches for profiling gene and protein function. They will discuss how these approaches can be used to discover new therapeutic targets and disease genes as well as challenges and opportunities ahead.

2:30 – 2:55 p.m.

Genome-wide optical pooled screens and analysis of high-content genomic screening data

Paul Blainey (MIT / Broad Institute)

Genetic screens are critical for the systematic identification of genes underlying cellular phenotypes. While pooling gene perturbations can greatly increase screening throughput, this approach was not previously compatible with the high-content imaging of complex and dynamic cellular phenotypes. We set out to develop optical pooled screening, a method to link pooled perturbations with their associated visual phenotypic outcomes in mammalian cells. In this approach, libraries of genetic perturbations are demultiplexed following image-based phenotyping using targeted in situ sequencing. By applying improved sample preparation, in situ sequencing by synthesis, and microscopy protocols, we have established this approach at a genome-wide scale and report here the results of our first genome-wide optical pooled screen.

Intracellular responses to viral infection are mediated by a key innate immune signaling pathway detecting cytosolic dsRNA that results in phosphorylation and nuclear translocation of IRF3 upon detection of cytosolic dsRNA. In a screen of 80,000 sgRNA across >10 million HeLa cells infected with Sendai virus, we identified direct regulators of IRF3 translocation which modulate responses to RNA stimuli. In this project and others entailing high-content imaging of cell lines and primary cells, we apply machine learning to identify biological phenotypes associated with genomic perturbations in large pooled experiments.

Moving forward, we continue to improve optical pooled screening throughput to ease adoption of this approach by the research community and support large screening projects in a range of biological models. We also aim to integrate additional types of phenotypic readouts to further enrich cellular characterization and provide useful flexibility in screen design.

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2:55 – 3:20 p.m.

Arrayed functional genomics screens for identification and validation of drug targets

Jenna Bradley (AstraZeneca)

Identification of novel drug targets is a key part of the drug discovery process required to address clinical unmet need in many disease areas. The functional genomics group at AstraZeneca have developed a platform capable of screening the entire genome in an arrayed format. This high-throughput multi-parametric confocal imaging platform, enables complex phenotypic assays and Cas9 genome editing at whole genome scale, for the identification of novel drug targets. This imaging platform has enabled identification of novel targets across several disease areas. This talk will focus on the application of arrayed CRISPR screening for the identification of novel targets for Idiopathic Pulmonary Fibrosis. We will describe the complex assay development required for arrayed CRISPR screening in primary human lung fibroblasts and how this multiparametric imaging platform has enabled us to identify and validate hits with high confidence from primary screening to bespoke target validation.

3:20 – 3:45 p.m.

An update on the JUMP–CP Consortium: insights from pilot experiments and outlook

Paula Andrea Marin Zapata (Bayer AG)

The JUMP-CP consortium (Joint Undertaking for Morphological Profiling-Cell Painting) has committed to create a public Cell Painting dataset of over 140,000 genetic and chemical perturbations and establish experimental and computational best practices for image-based profiling. We believe this unprecedented public resource will catalyze drug discovery by enabling the prediction of compounds' mode of action and toxicity, characterizing disease phenotypes, uncovering new biology, and more. During its first year, the consortium conducted pilot experiments which set down experimental guidelines and explored various computational approaches for profile generation and downstream applications. In this talk, we will present the latest results, discussing the applicability of Cell Painting to link genetic and chemical perturbations among other findings.

3:45 – 4:10 p.m.

President's Innovation Award Presentation: Live-cell dose-response characterization of nuclear transport inhibition by SARS-CoV-2 ORF6

Tae Yeon Yoon (Harvard Medical School)

Macromolecular transport between the nucleus and the cytoplasm is central to a myriad of eukaryotic cellular processes. This process depends on facilitated diffusion through nuclear pore complexes (NPCs) which selectively allow permeation of cargoes bound to nuclear transport receptors while blocking most other large cargoes. The nucleocytoplasmic transport machinery is subject to various physiological and pathological regulation. For example, several types of viruses, including SARS-CoV-2, manipulate the nucleocytoplasmic transport machinery to nullify the innate anti-viral defense of the host cells. However, there has been no quantitative assay that measures the nucleocytoplasmic transport kinetics in live cells in a high-throughput manner, limiting a deeper mechanistic understanding of such regulations and translational research. To overcome this obstacle, we developed high-throughput assays based on optogenetic probes to quantify the kinetics of nuclear import and export in living human cells. In our recent publication, we validated these assays and studied the role of O-linked N-acetylglucosamine (O-GlcNAc) modification of NPCs in modulating the kinetics of nuclear import and export. We further expanded the use of these assays for quantitative assessment of pathological proteins that compromise the nucleocytoplasmic transport by combining the assays with a novel technique for measuring intracellular level of exogenously expressed protein. Using this combined assay, we simultaneous measured the intracellular level of SARS-CoV-2 ORF6 protein in transiently transfected cells and the resulting reduction in the nuclear transport kinetics. This enabled a dose-response characterization of the nuclear transport inhibition by ORF6 protein. Using this approach, we quantitatively compared various ORF6 variants, including those of SARS-CoV and SARS-CoV-2, providing a mechanistic insight into how ORF6 inhibits the nuclear transport.

4:10 – 4:30 p.m.

Q & A

PROGRAM AGENDA

	Roundtable	Education course
4:30 – 5:30 p.m.	How to choose and insert the right reporter protein for your project Sponsored by ExpressCells	Deep learning-based point-scanning super-resolution microscopy Uri Manor, PhD (Salk Institute for Biological Studies)
4:30 – 6:00 p.m.	**Poster session with live chat and video (4)**	
5:30 p.m.	**Award Ceremony (Poster Hall) and Annual General Meeting**	

POSTER PRESENTATIONS

Category: High Content Screening 2D/3D and Phenotypic Screening

1. A single cell, multi-parametric high content assay to quantify and classify endocrine disrupting chemicals in environmental contaminants that affect Erβ functions—Derek Abbott

2. Iterative data mining of a Cell Painting multiparametric dataset allows identification of 'pre-toxic' phenotypes—Victor Wong

3. Phenotypic lipid droplet assay models foamy macrophages formation after SCI—Christine Ryan

4. Improve the robustness of Cell Painting with a near-infrared label —Angeline Lim

5. Spatiotemporal image analysis of CRC organoids within an organ-on-chip platform—Kimya Ghaffarian

6. Automated high-throughput assessment of calcium signals in micropatterned cells—Choon Leng So

7. 3D HCI islet assay performed in a spheroid plate with minimal optical aberration—Judi Wardwell-Swanson

8. HCS/A with affordable dyes: revealing cells and silver nanoparticles interaction—Fernanda Garcia-Fossa

9. Painting in 3D: High throughput phenotypic screening in printed 3D cell cultures—Martin Engel

10. High content quantitative confocal imaging of 3D InSight™ human liver spheroids—Katia Fiaschetti-Egli

11. A phenotypic platform to screen for non-hormonal male contraceptive —Franz Gruber

12. MetaXpress analysis – Ca^{2+}, transcription factors and using IF after live imaging—Francisco Sadras

13. Organoids for in vitro drug screening: automated culture, imaging and analysis—Oksana Sirenko

POSTER PRESENTATIONS

14. High-content screening reveals CLL patient cohorts with distinct drug responses—Mark Li
15. Phenotypic and transcriptional profiling to identify chemical mechanisms —Johanna Nyffeler
16. iScreen – a comprehensive, high-content imaging platform for genetic toxicology—Wen Sun
17. Image-based in vitro assay for muscle differentiation—Natalie Prigozhina
18. Objective “Brain”: Using internalization assays to identify new potential brain—Viviana Gatta
19. Application of spatial genomics for high-throughput and high-plex profiling —David Corney
20. Optical projection tomography of zebrafish embryos using the VAST BioImager—Rock Pulak

Category: Machine Learning/Artificial Intelligence/Image and Data Analysis

21. Building scalable resources for FAIR biological imaging data —Petr Walczysko
22. Label-free image analysis of colorectal cancer organoids using neural networks—Brandon Choi
23. Deep learning-based image analysis for label-free monitoring of organoids —Angeline Lim
24. Integration of tools for quantitative image analysis—Lakshmi Balasubramanian
25. ShapoGraphy: a visualisation approach for microscopy data—Heba Sailem
26. Network optimization with limited bioimage data for robust semantic segmentation—Jihyeon Je

Category: Therapeutic Drug Discovery/Infectious Disease

27. Developing a small molecule therapeutic to treat diabetic kidney disease—Hassan Al-Ali

28. Accelerating high-throughput screening using FirePlex®-384 multiplexing particle—Daniel Schwartz

29. Phenomics-guided antiviral drug discovery—Jonne Rietdijk

Category: New and Novel

30. High-content *C. elegans* toxicology assays as an alternative to animal testing—Adam Laing

31. A quantitative activity probe of proteasomal protein degradation in live cell—Dang Nguyen

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Genedata transforms data into intelligence with innovative software solutions that incorporate extensive biopharma R&D domain knowledge. Multinational biopharmaceutical organizations and cutting-edge biotechs around the globe rely on Genedata to digitalize and automate data-rich and complex R&D processes. From early discovery all the way to the clinic, Genedata solutions help maximize the ROI in R&D expenditure. Founded in 1997, Genedata is headquartered in Basel, Switzerland with additional offices in Boston, London, Munich, San Francisco, Singapore, and Tokyo

SPONSORING COMPANY DESCRIPTIONS

Glencoe Software builds and delivers innovative, scalable, easy-to-use scientific imaging solutions for its clients and partners. Our proven image database technology, OMERO Plus, makes the viewing, sharing, analysis and management of large sets of images and metadata easy and accessible to everyone in a group, team, project or organization. Glencoe's products are deployed on premises or in the cloud and used in several world-leading academic labs, biotechs, pharmas and publishers, solving mission-critical problems in high-content screening, digital pathology, and many other modalities. Through our OEM licensing programme, our software tools are embedded in some of the world's most powerful and market-leading software data products. We combine world-beating technology and expertise with dedicated, reliable customer support.

InSphero is a Swiss-based biotech that has been perfecting 3D cell-based drug discovery platforms and scaffold-free 3D OoC technologies for more than 10 years. InSphero deploys its patent-pending technologies for highly scalable drug discovery programs against liver diseases, T1 and T2 diabetes, and solid cancers, as well as for Safety testing with the market leading 3D InSight™ Liver Toxicology platform. In August 2021 InSphero announced the launch of the Online R&D Solutions Store and made their proprietary, patented Akura™ 96- and 384-microwell plates available to researchers – a pivotal part of the company's mission to enable the access to industry-leading products for 3D cell culture for physiologically relevant models for disease research and drug discovery

At **Luminex**, our mission is to empower labs to obtain reliable, timely, and actionable answers, ultimately advancing health. We offer a wide range of solutions applicable in diverse markets including clinical diagnostics, pharmaceutical drug discovery, biomedical research, genomic and proteomic research, and food safety. We accelerate reliable answers while simplifying complexity and deliver certainty wih a seamless experience.

Molecular Devices is one of the world's leading providers of high-performance bioanalytical measurement systems, software and consumables for life science research, pharmaceutical and biotherapeutic development. Included within a broad product portfolio are platforms for high-throughput screening, genomic and cellular analysis, colony selection and microplate detection. These leading-edge products enable scientists to improve productivity and effectiveness, ultimately accelerating research and the discovery of new therapeutics. Molecular Devices is committed to the continual development of innovative solutions for life science applications. The company is headquartered in Silicon Valley, California with offices around the globe.

PerkinElmer enables scientists, researchers and clinicians to address their most critical challenges across science and healthcare. With a mission focused on innovating for a healthier world, we deliver unique solutions to serve the diagnostics, life sciences, food and applied markets. We strategically partner with customers to enable earlier and more accurate insights supported by deep market knowledge and technical expertise. Our dedicated team of about 14,000 employees worldwide is passionate about helping customers work to create healthier families, improve the quality of life, and sustain the well-being and longevity of people globally.

Pfizer Inc. is a research-based global biopharmaceutical company engaged in the discovery, development, manufacture, marketing, sales, and distribution of biopharmaceutical products.

SPONSORING COMPANY DESCRIPTIONS

Thermo Fisher Scientific is the world leader in serving science. Our mission is to enable our customer to make the world healthier, cleaner and safer. High-content screening/analysis (HCS) was invented by and registered as a trademark of Cellomics, which is now part of Thermo Fisher Scientific. Our high-content screening portfolio consists of Thermo Scientific CellInsight CX5, CX7 LED, and CX7 LZR HCS platforms and HCS Studio software designed to provide you cutting-edge images and data in no time. Explore our high-content screening platforms that are designed to provide exceptional resolution for subcellular detection, automated detection, and phenotyping with intact, fixed, or live cells. Thermo Fisher Scientific is the world leader in serving science. Our mission is to enable our customer to make the world healthier, cleaner and safer. High-content screening/analysis (HCS) was invented by and registered as a trademark of Cellomics, which is now part of Thermo Fisher Scientific. Our high-content screening portfolio consists of Thermo Scientific CellInsight CX5, CX7 LED, and CX7 LZR HCS platforms and HCS Studio software designed to provide you cutting-edge images and data in no time. Explore our high-content screening platforms that are designed to provide exceptional resolution for subcellular detection, automated detection, and phenotyping with intact, fixed, or live cells.

Tools for High Content Zebrafish Screening. **The VAST BioImager™** platform automatically loads and rotationally orients 2-7 day-post-fertilization zebrafish larvae for organ-level imaging. Mounts on many upright microscopes for cellular-level fluorescence imaging. **Union Biometrica COPAS FP™** and **BioSorter® Large Particle Flow Cytometers** automate the analysis and sorting of objects too big (5-1500µm) or too fragile for traditional cytometers. Examples include zebrafish eggs & larvae as well as other small model organisms and large cells / cell clusters. The **COPAS VISION™** cytometer adds brightfield image capture on the fly for convenient identification of objects.

Yokogawa formally launched its life innovation business in FY2018 with the aim of contributing to the achievement of well-being for all, which is one of Yokogawa's "Three goals" for sustainability. In this business, the company provides platforms for the effective utilization of human intelligence in research related to life sciences, biotech, and pharmaceutical and foodstuff production processes through high-level linking with information from observation and measurement, and autonomous control utilizing the results of analysis of this information. Along with its customers, the business aims to enable a world of Bio Industrial Autonomy.