32nd Annual Meeting

Great Lakes International Imaging and Flow Cytometry Association

Madison Marriott West
Friday, September 8 – Sunday, September 10, 2023
Madison, Wisconsin
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The Great Lakes International Imaging and Flow Cytometry Association (GLIIFCA) was started in 1992 by Carleton and Sigrid Stewart and Alex Nakeff, and fosters the interaction of professionals from Great Lakes region (U.S. states of Illinois, Indiana, Michigan, Minnesota, New York, Ohio, Pennsylvania and Wisconsin as well as the Canadian province of Ontario) with interests in flow and image cytometry. GLIIFCA organizes affordable annual meetings allowing the Great Lakes region cytometrists to learn about the latest developments in cytometry and related fields, network with colleagues, and share the excitement about their research.

THE HISTORY OF GLIIFCA - WRITTEN BY CARLETON C. STEWART

In 1992 GLIIFCA began as... GLIFCA (the Great Lakes International Flow Cytometry Association - the word Imaging was added in 1993) and was first part of an outreach program for a Clinical Cancer Resource Grant that I was writing at Roswell Park Cancer Institute in Buffalo, NY. I had been thinking and discussing forming an organization that would primarily focus on young investigators and technologists doing research in cancer using imaging and flow cytometry. The established leaders in each of these fields were invited to form the first Steering Committee. Carleton C. Stewart was elected first President, Alexander Nakeff first Vice President, Sigrid Stewart, first Secretary/Treasurer and James Jacobberger first Educational Officer. Alan Landay and Maurice O’Gorman were to be the Scientific Chairs for the next meeting which was held October 1 - 3, 1993 at the Hotel St. Regis in Detroit, MI. Other members of the Steering Committee were Paul Robinson, Waclaw Jaszcz, David Hedley, Betsy Ohlsson-Wilhelm and James Leary. This Steering Committee was established to help determine the policies of the organization, maintain a budget, and create the program for the annual meeting. In addition to funding for this organization by the grant, I envisioned participation by the vendors as equal members of GLIIFCA. The reps from each company were instrumental in passing the word to their customers throughout the capture area. And you know the rest of the story...

Our first meeting of the Great Lakes International Flow Cytometry Association was held September 25 - 27, 1992 at the Hotel St. Regis in Detroit, MI: The meeting was an overwhelming success. The scientific agenda included sessions on Immunophenotyping, tumor biology and instrumentation. Over 130 charter members, some of which had never attended a flow meeting before, were able to attend because the total cost per person amounted to under $150 including registration and accommodations. Because of the central location of Detroit to the Great Lakes Region most people were able to carpool. The meeting started with a well-attended reception on Friday evening with food and an open bar sponsored by Becton Dickinson Immunocytometry Systems. On Saturday the Flowdown, sponsored by Coulter Cytometry, was thoroughly enjoyed by all. Most participants stayed until the very end. The greatest single state/province represented was Ontario, Canada. US charter members were from Michigan, Indiana, Minnesota, Illinois, Ohio, New York, Pennsylvania, Wisconsin and New Jersey. We even had two guests from Russia, which truly made this an international event. While our main region of emphasis is the Great Lakes, we welcome our colleagues from across the land to participate.
The GLIIFCA 32 meeting is kindly supported by:

- **Gold Sponsors**
  - BD Biosciences
  - BioLegend
  - Slingshot Biosciences

- **Silver Sponsors**
  - Agilent Technologies
  - Beckman Coulter Life Sciences
  - Bio-Rad Laboratories
  - Cytek Biosciences, Inc.
  - Deepcell
  - Miltenyi Biotec
  - Nexcelom
  - Particle Metrix
  - Sony Biotechnology Inc
  - Thermo Fisher Scientific

- **Bronze Sponsors**
  - Bangs Laboratories, Inc.
  - Canopy Biosciences
  - Cytek Biosciences, Inc
  - Deepcell
  - Immudex
  - Miltenyi Biotec
  - Proteintech
  - Slingshot Biosciences
  - Thermo Fisher Scientific

First Time Attendee gift items sponsored by:

- Bangs Laboratories, Inc.
- BioLegend
- Canopy Biosciences
- Cytek Biosciences, Inc
- Deepcell
- Immudex
- Miltenyi Biotec
- Proteintech
- Slingshot Biosciences
- Thermo Fisher Scientific

Banquet Raffle Prizes Sponsored by:

- Cytek Biosciences, Inc
- Immudex
- Leinco Technologies
- Nodexus Inc
- Sony Biotechnology Inc
- Spherotech Inc
FRIDAY

GLIIFCA 32 Core Facility Managers’ Workshop (LaCrosse/Milwaukee/Green Bay)
12:00 PM – 5:00 PM
This workshop offers perspectives on developing marketing strategies for core facilities as well as addressing public relations and conflict resolution. Core managers and staff can network with colleagues facing similar challenges marketing and running flow core facilities. We will have a discussion regarding the challenges of educating our users on Current Best Practices in flow cytometry to build rigor and reproducibility into research. In addition, attendees are encouraged to bring their own issues for a general networking session. Come prepared to actively participate in this workshop. We look forward to learning from everyone’s experiences.

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<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>12:00 PM – 12:30 PM</td>
<td>Opening Networking Luncheon: Welcome and Introductions, Matt Cochran, Dagna Sheerar, Vicki Smith, Ann Marie DesLauriers-Cox, Celine Silva-Lages</td>
</tr>
<tr>
<td>12:30 PM – 1:30 PM</td>
<td>Implementing novel core facility technologies, the BD S8 Discover, Joel Martin Sederstrom, Baylor College of Medicine</td>
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<tr>
<td>1:30 PM – 2:30 PM</td>
<td>Small Group Discussions – Technical</td>
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<tr>
<td>2:30 PM – 3 PM</td>
<td>Refreshment Break</td>
</tr>
<tr>
<td>3:00 PM – 4 PM</td>
<td>Unlocking the Potential of Your Shared Resource: Forecasting, Rates, and Change, A. Nicole White, Ph. D, MBA, Cincinnati Children’s Hospital Medical Center</td>
</tr>
<tr>
<td>4 PM – 4:45 PM</td>
<td>Small Group Discussions – Management</td>
</tr>
<tr>
<td>4:45 PM - 5:00 PM</td>
<td>Closing Thoughts and Ideas</td>
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Thank you to GLIIFCA for generous sponsorship of this workshop
Organizing Committee: Matthew Cochran, Vicki Smith, Sally Quataert, Dagna Sheerar, Ann Marie DesLauriers-Cox, Celine Silva-Lages

OPENING RECEPTION (SALONS A-E)

The Opening Reception will take place in the Salons A-E from 6:00 PM to 9:00 PM. Come and interact with the Vendors and fellow GLIIFCA conference participants!

MEET-AND-GREET (SALONS A-E)

Come meet other attendees!

EXHIBITOR TECH TALKS PART 1 (SALONS H-F)
**Session Chair: Christiane Hassel (Indiana University)**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>7:00 PM - 7:10 PM</td>
<td>Exhibitor Tech Talk Introduction</td>
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<tr>
<td>7:10 PM - 7:17 PM</td>
<td>Beckman Coulter Life Sciences - Jake Norley</td>
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<tr>
<td>7:17 PM - 7:24 PM</td>
<td>Particle Metrix - Sven Kreutel</td>
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<tr>
<td>7:24 PM - 7:31 PM</td>
<td>Deepcell - Matthew Nakaki</td>
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<tr>
<td>7:31 PM - 7:38 PM</td>
<td>Miltenyi Biotec - Allie Guiang</td>
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<td>7:38 PM - 7:45 PM</td>
<td>Bio-Rad Laboratories - Alice Valentin-Torres</td>
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<tr>
<td>7:45 PM - 7:52 PM</td>
<td>Cytek Biosciences, Inc. - Joel Crespo</td>
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**SATURDAY**

Breakfast will be available in the Exhibit area in **Salons A-E** from 7:00 AM to 8:00 AM

**ALL OF THE ORAL PRESENTATIONS WILL BE DELIVERED IN SALONS F-H**

**8:00 AM - 8:15 AM**  Welcome Address: **David Adams** (GLIIFCA President and Swell Guy)

**SESSION 1: AI AND CYTOMETRY (SALONS F-H)**

Moderator: Aaron Rae (Emory University)

<table>
<thead>
<tr>
<th>Time</th>
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<tr>
<td>8:15 AM – 8:25 AM</td>
<td>The Future of Discovery: BD FACSDiscover™ S8 Cell Sorter with BD CellView™ Image Technology, <strong>Katie Tuttle</strong>, BD Biosciences</td>
</tr>
<tr>
<td>8:30 AM - 9:05 AM</td>
<td>Algorithmically performing flow cytometry compensation without requiring compensation controls, <strong>Peng Qiu, Ph. D.</strong>, Georgia Tech</td>
</tr>
<tr>
<td>9:05 AM - 9:40 AM</td>
<td>Location matters: Methods for the characterization of the tumor microenvironment with a spatial context, <strong>Santhoshi Krishnan, Ph. D.</strong>, University of Michigan</td>
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<tr>
<td>9:40 AM – 10:15 AM</td>
<td>Awaiting Abstract</td>
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**THE 2023 CARLETON AND SIGRID STEWART KEYNOTE LECTURE (SALONS F-H)**

Introduction: Matthew Cochran (University of Rochester)

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<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>10:15 AM – 10:45 AM</td>
<td>Coffee Break</td>
</tr>
<tr>
<td>10:45 AM – 11:30 AM</td>
<td>Complexity in flow cytometry data – how much is enough?, <strong>Tim Mosmann, Ph.D.</strong>, University of Rochester Medical Center</td>
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**EXHIBITOR TECH TALKS PART 2 (SALONS F-H)**

Session Chair: Christiane Hassel (Indiana University)

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<th>Time</th>
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<tr>
<td>11:30 AM - 11:35 AM</td>
<td>Exhibitor Tech Talk Introduction</td>
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<tr>
<td>11:35 AM - 11:42 AM</td>
<td>Nexcelom – Patrick Jacobs</td>
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<td>11:42 AM - 11:49 AM</td>
<td>Thermo Fisher Scientific – Natasha Jacobsen</td>
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<tr>
<td>11:49 AM - 11:56 AM</td>
<td>Agilent Technologies</td>
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<tr>
<td>11:56 AM – 12:03 AM</td>
<td>Sony Biotechnology Inc – Anthony Carcio</td>
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</table>
**Lunchtime 12:15PM-1:20PM**

**Roundtable Workshops (Madison Board Room, Middleton, Miliwaukee, Green Bay, LaCrosse)**

Workshop Organizers: David Adams (University of Michigan)  
Galina Petrova (Medical College of Wisconsin)

| 12:30 PM – 1:20 PM | *Multiple parallel roundtable workshops.* |

**Abstract Flash Talks (Salons F-H)**

| 1:20 PM – 1:30 PM | Spectral flow cytometry reveals radiation-induced immune remodeling in human renal cell carcinoma, **Adil Khan**, Roswell Park Comprehensive Cancer Center |
| 1:30 PM – 1:40 PM | The development of an In Vitro Screening System for Chagas Disease mRNA Vaccine Constructs, **Leroy Versteeg**, Baylor College of Medicine |
| 1:40 PM – 1:50 PM | Generation of gd2-car neutrophils from hpscs for targeted cancer immunotherapy of solid tumors, **Aditi Majumder**, University of Wisconsin, Madison |
| 1:50 PM – 2 PM | Video repository for DIY maintenance and repair – FixYourFlowDepot, **David Leclerc**, University of Chicago |
| 2 PM – 2:10 PM | Improving sensitivity of EV detection and measurement using a next generation cytometer and careful attention to instrument calibration and selection of fluorescence probes, **Bill Murphy**, University of Pennsylvania |
| 2:10 PM – 2:20 PM | Side-by-side comparison of compensation bead used in polychromatic flow cytometry, **Debajit Bhomick**, East Carolina University |
| 2:30 PM – 3:00 PM | Coffee Break |

**Session 2: High-content Image-based Single-cell Spatial Screening (Salons F-H)**

Moderator: Jessica Back (Wayne State University)

| 3 PM – 3:10 PM | Optimized Multicolor Panels: Streamline Your Workflows with BioLegend, **Leesa Pennell**, BioLegend |
| 3:55 PM – 4:40 PM | Spatial transcriptomics reveals molecular dysfunction in Parkinson’s disease, **Mike Henderson, Ph.D.**, Van Andel Institute |
| 4:40 PM – 5:30 PM | Integrated single-cell and spatial omics analysis reveals cell-cell interaction markers in cancer and inflammation, **Huy Q. Dinh, Ph. D.**, University of Wisconsin |

**Social Activities (Salons A-E)**

| 5:30 PM – 6:30 PM | Wine and Cheese Happy Hour |
| 7:30 PM - 8:30 PM | GLIFCA 32 Banquet |
| 8:30 PM – 11:00 PM | Post-banquet Scientific Networking |
SUNDAY

Breakfast will be available in the Exhibit area Salons A-E from 8:00 AM to 9:00 AM

BOARD OF DIRECTORS MEETING (GREEN BAY, MILWAUKEE, LACROSSE)

8:00 AM – 8:50 AM GLIIFCA Board of Directors Breakfast

SESSION 3: TECHNOLOGICALLY NOVEL APPLICATIONS OF CYTOMETRY (SALONS F-H)

Moderator: Galina Petrova (Medical College of Wisconsin)

<table>
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<tr>
<th>Time</th>
<th>Session</th>
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<tbody>
<tr>
<td>9:00 AM - 9:10 AM</td>
<td>Revolutionizing Flow Cytometry through On-Demand Controls and Cell Mimics, Amay Dankar, Slingshot Biosciences</td>
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<tr>
<td>9:10 AM – 9:50 AM</td>
<td>Computational Optics of the Tumor Microenvironment, Kevin Eliceiri, Ph. D., University of Wisconsin</td>
</tr>
<tr>
<td>9:50 AM – 10:30 AM</td>
<td>The shape of sickness: connecting bacterial morphology to virulence using image-based flow cytometry, Daniel Vocelle, Ph. D., Michigan State University</td>
</tr>
<tr>
<td>10:30 AM - 11:15 AM</td>
<td>Capturing immune cell interactions with image-enabled cell sorting, Karan Kathuria, Stanford University</td>
</tr>
<tr>
<td>11:15 am – 11:45 AM</td>
<td>Coffee Break</td>
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EXPERT PANEL DISCUSSION: TECHNOLOGICAL ADVANCES IN CYTOMETRY: PARAMETER CASCADE (SALONS F-H)

Panel moderated by: Bartek Rajwa (Purdue University)

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<th>Time</th>
<th>Discussion</th>
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<tr>
<td>11:45 AM - 12:30 PM</td>
<td>Expert Panel Discussion</td>
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<tr>
<td>12:30 PM - 12:35 PM</td>
<td>Closing Remarks</td>
</tr>
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</table>
GLIFCA 32 Roundtable Lunch Workshops

**Topic 1. Core Instrumentation – Complementary Technologies to Cytometry, Jessica B. Back, Ph.D, Wayne State University School of Medicine.**

Flow Cytometry core facilities serve a central role in biological research, often acting as an important conduit between researchers and other instrumentation cores. Because of the wide range of sample types and assays that cycle through flow cores, the technical specialists within these facilities frequently maintain significant depth and breadth of understanding of other, related technologies. As such, these flow cytometry cores may be compelled to offer access to these complementary technologies within the existing core. This roundtable is intended to facilitate discussion related to important facility, technological, and expertise considerations prior to adoption and implementation of complementary technologies within a Flow Cytometry core facility.


Online Core Management Systems are software platforms designed to manage Shared Research Facilities (e.g., individual Core Labs, Centers, and institutions) operations and help them save time and money for core personnel, institutional administrators, and researchers. We will discuss online management systems available on a market and how using these platforms helps with everyday operations including instrument scheduling, billing and invoicing, reporting usage, tracking supplies and inventory, project management and more.

**Topic 3. Contract Work – Clinical Trials, Local Biotech Ecosystem – Alternative Income Streams, Matthew Cochran, University of Rochester Medical School**

Finding and maintaining alternative income streams, such as contracts with pharma, can be a worthwhile goal for many labs. On the other hand this pursuit can be difficult and probably isn’t worth it for every lab. In this roundtable we’ll talk about some of the plusses and minuses to this pursuit so you can make an educated decision regarding whether this path is something you should explore. If you’re already in the midst of the process we’ll discuss strategies we’ve had success with or that you should avoid so we all come out better prepared for the future.

**Topic 4. Nanoscale Cytometry: Analysis, Sorting, and Best Practices related to Nanoparticles, Viruses, EVs, and Exosomes, Daniel Vocelle, Michigan State University**

Are you interested in running submicron particles in your SRL or need to troubleshoot a difficult researcher assay? We will discuss current methods employed at our institutions for the analysis and sorting of small particles. Topics will include; best practices, protocol optimization, instrument set up and controls, and general troubleshooting. Examples of tech notes, protocols, and surveys will be made available.

**Topic 5. Image Cytometry and Cell Sorting, David Adams, University of Michigan**

Looking at the Imagestream, Cytpix, or S8? Now that we can utilize morphologic characteristics alongside standard phenotypic cytometric features in analysis and sorting, what does it add to our assays? How can we best utilize these features to advance our studies? What is the best platform to choose? Join me for a lively discussion regarding the merits of image-based instruments invading our flow labs and how they might best be used.
**Topic 6. Instrument Standardization**, Rachael Sheridan Ph.D., SCYM(ASCP), Van Andel Institute

Standardization and calibration of instruments is an important factor for both research reproducibility and operational continuity. This roundtable will discuss approaches for instrument set up and standardization and factors to consider when choosing an approach for your needs. We will also discuss methods for convincing users to invest time and effort into assay standardization.

**Topic 7. Core Management – A Professional Dissection**, Dagna S Sheerar, SCYM(ASCP)CM, University of Wisconsin

Core managers and directors wear many hats; personnel supervisor, subject matter expert, instrument engineer, financial manager, data analyst, educator, scientific writer, logistics specialist, administrative assistant, event coordinator, scheduler, mentor, and therapist, to name a few. This discussion will focus on varied strategies to keep all these plates safely and efficiently spinning for a successful flow core, with special attention paid to numbers of staff, instruments, services, and customers.


Flow Cytometry can provide many different avenues to pursue for employment. In this roundtable, we will have an open discussion around roles that are available in academia, biotech, industry, and beyond. Take your cytometry skills to a place you may not have been aware that they could be applied.

**Topic 9. Grants- a Practical Approach**, Sherry Thornton, Ph.D., Cincinnati Children’s Hospital

This round table will involve discussions on approaches for applying for grants that can support a shared facility. Discussion will include instrumentation, personnel and center grant approaches as well as potentially novel sources of funding for shared facilities.

**Topic 10. Group Therapy Session for Core issues (Car Talk)**, David Leclerc, University of Chicago

This is the round table where we fix things. Bring your problems whatever they may be, and with the combined powers of the participants, we will find a solution for you. Hardware issues? Staff management problems? You don’t know what instrument you should buy next? We’ll figure it out for you! Where the heart is true, there is always a solution!

**Topic 11. Assay Development and Troubleshooting in a Research Setting**, Eric Schultz, B.S., SCYM(ASCP)CM, Cleveland Clinic

With the advent of high-dimensional instrumentation, assay development has increased in complexity. Come discuss best practices in design and tips for troubleshooting the not-so-perfect assay

**Topic 12. No, go f@%& yourself” is not a correct answer to "Can you help me?"….and other signs of burnout in the workplace**, Ann Marie Deslauriers-Cox, University of Michigan

Burnout in the workplace is on the rise and is caused by unresolved issues including lack of work life balance. At this roundtable we will discuss signs and symptoms, as well as ways to diminish or resolve burnout.
GLIIFCA 32 PRESENTATION ABSTRACTS

**SCIENTIFIC SESSION 1: AI AND CYTOMETRY**

**THE FUTURE OF DISCOVERY: BD FACSDiscover™ S8 CELL SORTER WITH BD CELLVIEW™ IMAGE TECHNOLOGY**

**KATIE TUTTLE (BD BIOSCIENCES)**

The BD FACSDiscover™ S8 Spectral Cell Sorter with BD CellView™ Image Technology was revealed at CYTO last year. The BD CellView™ Image Technology, featured on the January 2022 cover of Science, is a novel high-speed cell imaging technology that empowers scientists to answer previously out of reach biological questions by amplifying the power of cell sorting and analysis through real-time integration of image and flow cytometry data. In this tech talk, Katie Tuttle, PhD will discuss how the CellView™ Image Technology works, what image parameters are available, and possible applications. We invite you to join the discussion and imagine where this high-speed imaging technology could take your research.

**ALGORITHMICALLY PERFORMING FLOW CYTOMETRY COMPENSATION WITHOUT REQUIRING COMPENSATION CONTROLS**

**PENG QIU, PH.D. (GEORGIA TECH)**

When multiple fluorescence channels are used in flow cytometry, detection problems may arise. Due to spectral overlap, the signal of a fluorescence channel may spillover into another channel, causing interference across different channels and obscuring cell type identification and biological interpretations. The effects of spillover can be corrected via a process called compensation, which experimentally determines the amount of spillover among channels using single-stain compensation control samples. However, preparation of the single-stain compensation controls can be cumbersome due to various practical and biological constraints. This presentation will explore the possibility of estimating the spillover without requiring compensation controls, which will lead to huge savings in terms of both experimental and personnel costs, and thus, a significant impact to the research community that routinely uses flow cytometry.

**LOCATION MATTERS: METHODS FOR THE CHARACTERIZATION OF THE TUMOR MICROENVIRONMENT WITH A SPATIAL CONTEXT**

**SANTHOSHI KRISHNAN, PH.D. (UNIVERSITY OF MICHIGAN)**

Spatial profiling has been gaining importance over the understanding of cellular and molecular heterogeneity of the disease microenvironment. Characterization of the interplay between various phenotypic, molecular, and genetic species through multi-omics integration augments the growing requirement for a more personalized approach to therapy. In this talk, I go over some of the work done in the development of methodologies using machine learning and spatial statistics to utilize image-derived features in the quantification of the disease microenvironment, with a spatial context.
Flow cytometry has come a long way from the days when three-color analysis was new and exciting. Biologists have an almost insatiable appetite for more and more channels to define more subtle distinctions between cell populations. However, this vast amount of information is almost an embarrassment of riches, because of the need to first analyze the data to identify and quantify sub-populations, and then to interpret these sub-populations in a biological model. Unlike high-throughput RNA sequence data, in which the gene sequences are mostly predefined, in flow cytometry the cell sub-populations are often defined within the data, and can be difficult to match across different studies.

Many algorithms are now available to help with the initial analysis process. We established the high-resolution SWIFT algorithm, that is particularly effective for identifying rare populations such as antigen-responsive T lymphocytes. This algorithm creates a cluster model that provides a template for assigning many samples, allowing stringent comparisons between samples. This detailed model also provides the information needed to correct for batch effects, while preserving and even enhancing genuine biological differences between groups.

The ability to resolve sub-populations increases as the number of dimensions increases, and unbiased clustering methods can identify previously-unsuspected cell types. The high dimensional data can also identify ‘fingerprints’ of individual subjects – these fingerprints are stable over time. The detailed data can also be used in machine learning algorithms to create classifiers for disease states or potential clinical outcome.

This very high level of resolution creates a conundrum in the interpretation of the clustered data: how should we define a cell sub-population? With very high-dimensional data, even a very small difference in each of several dimensions will allow mathematical separation of cell sub-populations. Are such separations biologically significant? Recent progress in obtaining even higher dimensional marker identification by e.g. CITEseq, and the spectacular advances in single-cell mRNA sequencing, bring this issue into even sharper focus.


Leesa Pennell (BioLegend)

Building a successful multicolor flow cytometry panel requires extensive optimization – fluorophore/marker selection, antibody titrations, and buffer selection, among other factors. BioLegend is here to help with that process!

In this presentation, we will discuss our optimized panels for multicolor immunophenotyping using a full spectrum flow cytometer. We will share representative data and gating strategies that have been designed and optimized by our expert scientists, and highlight some of our new fluorophores that enable high parameter panel design. These pre-optimized panels will remove some of the guesswork from initial panel design, allowing you to advance toward new discoveries more quickly. Finally, we will briefly review our newly-released dry down cocktails for immunophenotyping – a convenient, easy-to-use solution for characterization of human PBMCs.
SINGLE CELL AND SPATIAL ANALYSIS OF UROLOGIC CANCERS
EVAN KELLER, D.V.M., PH.D. (UNIVERSITY OF MICHIGAN)

The recent explosion of high plex methods to evaluate biomolecules at the single cell level in situ has opened the door to identifying novel interactions between tumor cells and their microenvironment, spatial relationships between cell types and signaling processes, and potential biomarkers for prognosis and predictiveness. Using these methods, we have (1) identified spatiotemporal changes in tissue structure, cell composition and signaling associated with androgen deprivation in a murine model; (2) determined putative biomarkers in prostate cancer biopsies that may improve accuracy of tumor grading; and (3) delineated a mechanism through which renal clear cell carcinoma progresses to a renal sarcomatoid cancer subtype. These studies demonstrate how single cell and spatial analytic methods can inform both mechanistic and translational studies.

SPATIAL TRANSCRIPTOMICS REVEALS MOLECULAR DYSFUNCTION IN PARKINSON’S DISEASE
MICHAEL HENDERSON, PH.D. (VAN ANDEL INSTITUTE)

Parkinson’s disease is a progressive disease, initially impacting motor function and eventually leading to dementia in most patients. The symptomatic progression of disease is accompanied by the progression of Lewy pathology throughout the brain. However, until recently, there were limited tools available to identify the cells impacted and the molecular alterations induced by pathology. We took advantage of recent advances in spatial transcriptomics to selectively capture whole-genome transcripts from neurons with and without pathology both in the Parkinson’s disease brain and in a mouse model of Lewy pathology. We demonstrate the power of this approach to identify conserved vulnerable cell types and delineate a conserved pattern of molecular dysfunction associated with Lewy pathology.

INTEGRATED SINGLE-CELL AND SPATIAL OMICS ANALYSIS REVEALS CELL-CELL INTERACTION MARKERS IN CANCER AND INFLAMMATION
HUY Q. DINH, PH. D. (UNIVERSITY OF WISCONSIN)

Previous methods used proteomics to measure cell-cell interactions (CCI), essential molecular features distinguishing normal and diseased cell states. With advancements in single-cell and spatial transcriptomic profiling, we can use bioinformatics to infer intercellular signaling based on RNA measurement, which offers extensive advantages. I’ll present three examples in inflammation and cancer: (i) integrated analysis identifying immunotherapy response markers in head and neck cancers, (iii) scRNA-Seq analysis revealing changes in the tissue immune microenvironment during early high-grade serous ovarian cancer development, and (iii) a cross-species analysis inferring human burn severity markers from zebrafish scRNA-Seq. These illustrate showcases utilizing bioinformatics to identify CCI as potential biomarkers for immune-based therapy and as actionable targets in treating human diseases.

SCIENTIFIC SESSION 3: TECHNOLOGICALLY NOVEL APPLICATIONS OF CYTOMETRY

REVOLUTIONIZING FLOW CYTOMETRY THROUGH ON-DEMAND CONTROLS AND CELL MIMICS
**Amay Dankar (Slingshot Biosciences)**

A major demand in flow cytometry is for robust controls that can be used to reliably compensate, unmix, or gate multicolor samples. In this presentation, Slingshot Biosciences will present our solution to this problem: synthetic cell mimics with the ability to "express" a wide array of desired materials. Our flexible platform can be applied to anything from single stain controls for compensation and unmixing to instrument characterization to fluorescent protein expression, and lastly, to custom biomarker controls for assay validation and batch controls.

**Kevin Eliceiri, PhD**

**Kevin Eliceiri, Ph.D. (University of Wisconsin)**

The cellular microenvironment in disease models is increasingly being recognized as a key contributing factor in disease onset and progression. Particularly in cancer, key features of the cellular microenvironment such as metabolic fluxes and organization of the collagen rich extracellular matrix (ECM) have been demonstrated to be candidate image based biomarkers for cancer invasion and progression. However despite the great promise of these microenvironment image features, their clinical application has been limited for several reasons including a lack of computational methods for extracting these signatures. We will overview our collaborative work to quantitate metabolism and ECM organization in a range of tumor models all using a combination of both intrinsic and extrinsic multiparametric optical signals. These signals include polarization, fluorescence intensity, spectra and lifetime. We will discuss technical approaches and advances for each and early efforts to extend these to clinical pathology. We will also discuss the computational tools being used for this work including open-source software we are developing specifically for this.

**The Shape of Sickness: Connecting Bacterial Morphology to Virulence Using Image-Based Flow Cytometry**

**Daniel Vocelle, Ph.D. (Michigan State University)**

Understanding variation in pathogen virulence is a central goal of evolutionary medicine. In the shape-shifting bacterial pathogen, Pasteuria ramosa, virulence is thought to be mediated by specific bacterial morphotype(s). Accordingly, variation in the virulence of Pasteuria infections arises from variation in the absolute/relative abundance of virulence-inducing morphotypes in Pasteuria populations. Hitherto, testing this hypothesis has been difficult because a lack of fluorescent markers/constructs has prevented the quantification and isolation of morphotypes. We use the Attune Cytpix to overcome these critical barriers to understanding Pasteuria’s virulence, by (a) quantifying the absolute/relative abundance of morphotypes in the population and (b) identifying morphotype-specific autofluorescent signatures to enable cell-sorting.

**Capturing Immune Cell Interactions with Image-Enabled Cell Sorting**

**Karan Raj Kathuria (Stanford University)**

Cell-cell interactions (CCIs) are an understudied yet critical window into the initiation and maturation of immune responses. Current methods to capture cell interactions require a priori knowledge of relevant receptor-ligand pairs and are applicable mostly to cell lines or transgenic animal models. We have developed a method for isolating interacting cell pairs using fluorescence image-enabled cell sorting. This unbiased capture of interacting cells from primary specimens permits rich measurements (e.g. transcriptomics, epigenetics, and proteomics) of cell phenotypes during contact-dependent communication. We validate our
method by independently recovering Treg – CD8 T cell pairs, a well-known interaction necessary for immune regulation. We hope this technical foundation enables discovery of new mechanisms of immune response and regulation.
SPECTRAL FLOW CYTOMETRY REVEALS RADIATION-INDUCED IMMUNE REMODELING IN HUMAN RENAL CELL CARCINOMA

**Adil Khan**¹, **Jacky Chow**¹, **Brianna Wasik**¹, **Alexis Conway**², **Kah Teong Soh**², **Paul Wallace**², **Scott Abrams**¹, **Thomas Schwaab**³, **Anurag Singh**⁴, **Jason Muhitch**¹

¹DEPARTMENTS OF IMMUNOLOGY, ²IMAGE AND FLOW CYTOMETRY, ³UROLOGY, AND ⁴RADIATION MEDICINE, ROSWELL PARK COMPREHENSIVE CANCER CENTER

More than 400 clinical trials are investigating radiation and immunotherapy combinations, yet there has been sparse investigation of the irradiated tumor microenvironment of cancer patients. In this study we performed single cell analysis, spectral flow cytometry and single cell RNA sequencing, to study the impact of high-dose stereotactic body radiation therapy (SBRT) on tumor microenvironment of renal cell carcinoma (RCC) patient tumors. We utilized the CytekTM Aurora spectral flow cytometer to perform analysis on six treatment-naïve and five SBRT-treated RCC tumor samples using a 35-marker panel. Our analysis revealed an increased transition from naïve/stem-like CD8+ T cell populations to more exhausted/effector phenotypes in irradiated tumors. Using FlowSOM unsupervised clustering algorithm, fifteen distinct CD8+ T cell clusters were identified, four of which were significantly increased in SBRT-treated tumors compared to untreated controls. One of the four clusters comprised primarily of naïve-like T cells, one was characterized as within an intermediate/transitory phase, and two were enriched in exhaustion/activation markers. Our single cell RNA sequencing findings further confirmed an increase in transition from a naïve to an exhausted state for CD8+ T cells following radiation treatment. RNaseq findings also revealed an increased expression of CD8 ligands, TRAIL and INFγ, in radiated samples. Analysis of transcriptional data from patients treated with immunotherapy revealed those with high TRAIL and IFNγ expression had longer overall survival. These observations provide an indication of how radiation remolds the human tumor immune landscape and potentially influences the interaction between CD8+ T cells and cancer cells.

THE DEVELOPMENT OF AN IN VITRO SCREENING SYSTEM FOR CHAGAS DISEASE mRNA VACCINE CONSTRUCTS

**Leroy Versteeg**¹,²,³, **Isha Thapar**¹,², **Roman Sukhovershin**⁴, **Maria Elena Bottazzi**¹,²,³, **Jeroen Pollet**¹,²,³, **Edwin Tijhaar**³

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⁴CENTER FOR RNA THERAPEUTICS, HOUSTON METHODIST RESEARCH INSTITUTE,
mRNA-based vaccines have made remarkable progress and are acknowledged for their potential as potent inducers of cell-mediated immunity. The advantages of this platform include the flexibility for multivalency, rapid development and production, and the ability to elicit strong cytotoxic T cell responses. The concept of utilizing mRNA vaccines against Trypanosoma cruzi, the parasite that causes Chagas disease, has been proposed, as cytotoxic T cells can target and eliminate T. cruzi-infected cells. Screening multiple vaccine constructs in vivo can be labor-intensive, time-consuming, and costly. To expedite the mRNA vaccine candidate screening process and reduce the costs of acquisition, we developed a convenient screening system for mRNA vaccine constructs. This in-house system intends to enable the in vitro evaluation of mRNA translation, antigen presentation, and T cell activation using a combination of flow cytometry and Luminex technology. DropArray and Laminar wash technologies were employed to effectively decrease sample volume, assay time and overall assay costs during sample preparation.

We tested our screening technology using an mRNA construct encoding T. cruzi’s Tc24 protein. Briefly, the mRNA construct included a FLAG-tag to facilitate the measurement of intracellular mRNA translation, as well as a SIINFEKL peptide sequence allowing the detection of antigen presentation on MHC class I using specific antibodies. Through the optimization of in vitro mRNA transfection using various transfection agents in a murine dendritic cell line, the Tc24 mRNA construct successfully translated into protein, as assessed by FLAG-tag expression. Additionally, the detection of SIINFEKL presentation on MHC-I indicated that the Tc24 protein underwent effective MHC class I antigen processing and presentation. Next, cytokine analysis of the cell media from a co-culture experiment involving mRNA-transfected dendritic cells and SIINFEKL-specific naïve CD8+ T cells from transgenic OT-1 mice revealed the activation of antigen specific naïve CD8+ T cells by the mRNA construct. Finally, these positive screening results were corroborated in vivo when mice were vaccinated with the Tc24 mRNA construct, resulting in a robust antigen-specific immune response. In conclusion, the developed in vitro screening system provides a valuable and scalable pre-assessment tool for the evaluation and selection of potential mRNA vaccine candidates, before progressing to in vivo studies.

GENERATION OF GD2-CAR NEUTROPHILS FROM HPCS FOR TARGETED CANCER IMMUNOTHERAPY OF SOLID TUMORS

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Chimeric antigen receptor (CAR) T cell and NK cell therapies already been successful in the eradication of lymphoid malignancies. CAR-lymphocytes are incapable to enter the solid tumors and they also lose their activity within immunosuppressive tumor environment. Thus, opportunities exist for new immunotherapies for specific targeting of solid tumors using CAR-weaponized neutrophils which are capable of cytotoxicity and migration into solid tumors. However, generation of CAR neutrophils from peripheral blood represent a significant challenge due to their very short lifespan. Human pluripotent stem cells (hPSCs) are a logical alternative for large-scale production of CAR neutrophils due to their renewability and uniform quality.
In our study, we generated hPSCs with GD2 CARs integrated into AAVS1 locus and differentiated into neutrophils using serum- and xeno-free differentiation system based on modified ETV2 mRNA. Functional assays were performed in vitro and in vivo with GD+ and GD2-negative tumors.

Neutrophils generated from GD2 CAR iPSCs, as compared to wild type (WT), demonstrated superior cytotoxicity in vitro against GD2+ WM266-4 melanoma and CHLA20 neuroblastoma, while no differences of cytotoxicity were observed against GD2-negative SKOV3 ovarian and SK-BR3 breast cancer cells, indicating the specificity of anti-tumor therapeutic effect of CAR neutrophils. To assess in vivo potential of GD2 CAR neutrophils, NCG and NSG mice were inoculated intraperitoneally (IP) with 3x10^5 Luc2-eGFP+ WM266-4 melanoma cells and engraftment was assessed by IVIS bioluminescent imaging. On day 4 post WM266-4 injection, mice were either treated with 107 WT or GD2 CAR neutrophils via IP injection every 7 days. Upon assessment over 30 days, GD2 CAR neutrophil-treated mice showed reduced tumor burden compared to WT neutrophil-treated or untreated mice. Also, NSG mice were inoculated subcutaneously with 5x10^5 Luc2-eGFP+ WM266-4 melanoma cells. On day 14 post WM266-4 injection, mice were either treated with 107 WT or GD2 CAR neutrophils via IV injection twice in a week for 3 weeks. Upon assessment over 30 days, GD2 CAR neutrophil-treated mice showed reduced tumor burden compared to WT neutrophil-treated or untreated mice.

Our studies demonstrate a feasibility of using hPSC-derived CAR-neutrophils for immunotherapies against solid tumor cancers.

**CORE MANAGEMENT**

**VIDEO REPOSITORY FOR DYI MAINTENANCE AND REPAIR – FixYourFlowDepot**

**DAVID LECLERC, M.A.**

**UNIVERSITY OF CHICAGO**

Current practices by instrument manufacturers have made finding information about proper maintenance and repair of Flow Cytometry instrumentation increasingly difficult. Yet this knowledge currently exists within many laboratories and shared service facilities alike. A wealth of knowledge is currently being locked down in our respective facilities and the FixYourFlowDepot (FYFD) YouTube channel aims to facilitate the sharing of this valuable information. Optimally, owners of flow cytometry equipment will be better equipped to understand proper maintenance of their own equipment and resolve issues that should not require a visit from a service engineer.

With limited administrative oversight, FYFD publishes submitted videos sent by flow cytometry users relating to maintenance and repairs of equipment. FYFD does not vet the submissions. A quick overview is done to ensure that the video is minimally understandable. FYFD relies on its viewers to judge the usefulness of the video through the normal means found on the YouTube platform (thumbs up/thumbs down, adding details or warnings about problems in the comment section, ...)

Submissions are made through YouTube (YT) to the FYFD team. The video is taken directly from YT, and the description box is copied in its entirety to the new FYFD entry. This allows the author of the video to keep authorship of the work. FYFD adds verbiage regarding liability and risks to ongoing service contracts. If needed, the author can request assistance with video editing.

The FYFD initiative relies on a sturdy platform that is not going anywhere anytime soon. As such, the collection of entries, along with the discussions generated by viewers, will in due time generate a vast array of
information on the proper maintenance and repairs of different pieces of equipment. This will benefit the field of flow cytometry in many ways: 1 - by helping individual facilities better maintain or repair their own equipment; 2 - improving diagnostics of ongoing issues that can be shared with service engineers for more efficient visits; 3 - supporting manufacturers who should be able to direct the attention of highly trained service engineers to more advanced issues; 4 - supporting the development of a supportive culture in the field of flow cytometry.

**IMPROVING SENSITIVITY OF EV DETECTION AND MEASUREMENT USING A NEXT GENERATION CYTOMETER AND CAREFUL ATTENTION TO INSTRUMENT CALIBRATION AND SELECTION OF FLUORESCENCE PROBES**

**WILLIAM MURPHY, RICHARD SCHRETZENMAIR, SCOTT BORNHEIMER, MOEN SEN, ERICA CARPENTER, JONNI MOORE**

**UNIVERSITY OF PENNSYLVANIA**

Extracellular vesicle (EV) analysis by flow cytometry is growing rapidly and improved tools for consistent sensitive analysis are needed. We evaluated a new instrument, the BD FACSymphony™ A1 Cell Analyzer with BD® Small Particle Detector (SPD), using control particles and biological EVs and tested new reagents to validate this instrument and to establish new SOPs to improve EV detection and measurement.

**Methods:** All studies were performed on the BD FACSymphony™ A1 Cell Analyzer with BD® Small Particle Detector (SPD). The SPD combines a high performance PMT, low noise electronics, and an optical design that splits off a portion of side scatter light and directs it through a centered pinhole to enhance detection of hydrodynamically focused small particles while rejecting stray light. Megamix-Plus SSC beads were used to adjust the SPD picomotor optical alignment to maximize signal and the 200nm bead peak was set to 105 using voltage adjustments. A variety of "standard" particles, including polystyrene (PS) NIST-traceable beads (Thermo Fisher), Exometry™ Rosetta beads, and silica beads were acquired to assess small particle resolution and calibrate the SPD to particle size. Custom fluorescence quantitation beads were used to assess fluorescence detection and calibrate the fluorescence scale. Custom liposomes with and without FITC labeling were tested as a biological surrogate. Biological EVs were labeled with antibodies with conventional and new fluorophores to evaluate signal.

FACSymphony A1 with Small Particle Detector reliably detects biological EVs < 100 nm with reproducible and stable performance over time, accompanied by excellent fluorescence detection BD Horizon RealYellow™ 586 (RY586) dramatically improves detection of small EVs compared to PE by providing excellent fluorescence signal and low background.

- This held for all markers tested: CD41a, CD9, CD81, CD45
- RY586 was designed to improve upon PE with small size, single laser excitation, and high brightness. The small size presumably allows more RY586-labeled antibodies to bind EVs compared to PE-labeled antibodies.

**SIDE-BY-SIDE COMPARISON OF COMPENSATION BEAD USED IN POLychromatic FLOW CYTOMETRY**

**DEBAJIT BHOWMICK1#, SARA KRISTEN LOWE2, MICHELLE LEIGH RATLIFF2#**
These days we can run big panels over 40 fluorochromes, soon maybe over 50 colors. For all poly chromatic experiments, we need to apply compensation or unmixing to make the data useful for any type of analysis either manual or automated. The backbone of this process is the single stains. A wrong compensation matrix can lead to incorrect biological conclusion. To avoid such situation, it is wise to stick to best practices of single stain preparation and follow the rules of compensation strictly. Especially for human samples we need to use plastic beads to generate the single stains as cells are limited. Common knowledge is as long a researcher is following the rules it does not matter what we use for carrier it could be bead or cell. Dr. Roederer clearly concluded this in his 2002 publication. At that time flow field have machines that allow handful of fluorochromes to run together. Fast forward 20 years we still operate under the same assumption that change of carrier does not matter. Unfortunately, no one tested the idea, at the same time multiple paper do recommend researchers that use of cells to prepare single stain is the best option. All these suggestions came from years of experience of these authors. Any experienced flow cytometrist will tell you that they have seen strange artifacts after performing bead based compensation in regular interval. In this work we compared all the commercially available beads with cells for their accuracy on compensation. We found that single stained beads perform worse compared to single stain cells, also found some strange observation which was never reported before. With a small panel we should how bead based compensation can hugely impact the process of dimensionality reduction such as tSNE. This work is a warning for all of us to take a step back and evaluate the best way to prepare single stains before we invest thousands of dollars on big panels to get incorrect, non-reproducible data. Let’s check the quality of the bricks first, before we build the castle...
2023 Tech Talk Abstracts

The Exhibitor Tech Talks will take place Friday evening, September 8th and Saturday morning, September 9th. These sessions are intended to provide our exhibitors, a forum to present new technology, instrumentation, etc. Each presentation lasts approximately 6 minutes.

Beckman Coulter Life Sciences

High-Parameter Analysis Made Easy With Cytobank

Jake Norley (jnорley@beckman.com)

Cytobank software is a cloud-based data analysis platform that allows biologists, with no-coding required, to take advantage of the algorithms that are driving the field of flow cytometry forward, including viSNE, tSNE-CUDA, FlowSOM, CITRUS, etc. The Cytobank platform even offers a proprietary Automatic Gating function that allows the end-users to train a model based on their specific gating strategies and share it, with lab members and collaborators, thus enhancing reproducibility. Cytobank standard and advanced analysis functions, with the added benefit of statistical tools and illustration editing features, empower researchers to perform an end-to-end analysis workflow in one software.

Particle Metrix

Current Advances in Nanoparticle Tracking Analysis - Colocalization of Biomarkers with the New Particle Metrix ZetaView x30 Family

Sven Rudolf Kreutel (kreutel@particle-metrix.com)

During the last decades, Nanoparticle Tracking Analysis (NTA) has emerged as a vital and fast characterization technology for biological nanoparticles like Extracellular Vesicles (EVs), Exosomes and Viruses. While classic NTA scatter operation feeds back particle size and total concentration, the fluorescence detection capability (f-NTA) enables the user to gain specific biochemical information. Statistical determination of signal colocalization on low nano scale particles however, is a challenging task for any analytical instrument including flow cytometers and microscopes. A new laser generation paired with ultra fast switching times between fluorescence channels lays the foundation of colocalization nanoparticle tracking analysis (C-NTA) introduced recently by Particle Metrix. For the first time, we report results of colocalization measurements on reference material as well as real biological nanoparticles based on NTA technology on the new ZetaView® PMX-430 QUATT.

Deepcell

Label-Free Single Cell Imaging and Sorting with the AI-Powered REM-I Platform

Matthew Nakaki (mjnakaki@deepcellbio.com)

Like molecular analytes, cell morphology is a rich source of biological information that is indicative of phenotype and function. To unlock the insights embedded in cell morphology, multi-dimensional morphological traits must be turned into a quantitative, high-dimensional "-ome", the morpholome.
The REM-I platform combines high-resolution brightfield imaging of single cells in flow with deep learning foundation models to analyze cell morphology. The high-dimensional descriptions of cell features are projected onto morphology UMAPs for visualization and unbounded exploration of cell groups. This technology can be used to assess morphological changes at the single cell level, including stem cell differentiation, cellular identity during regeneration and aging, and disease modeling with stem cells.

Come hear about the latest developments on the REM-I platform and learn what the morpholome can reveal!

**MIL TEN YI BIOTEC**

**MAKING SORTING CHILD’S PLAY - MACSQUANT TYTO CELL SORTER**

Allie Guiang ([ALLISONG@MILTENYI.COM](mailto:ALLISONG@MILTENYI.COM))

Need to get your cell sorting sorted? We are changing the FACS with our Tyto cartridge technology and self-service sorter. It's all about effortless efficiency and unleashing the power of gentle, fast, and easy cell sorting. But don't just trust our word for it - let's see what your colleagues in the field are saying. From flow cores to genomics cores, to even metabolomics cores: tune in to learn how this platform is changing the game of cell sorting. Say goodbye to complex and frustrating cell sorting workflows and hello to the Tyto Breeze: making cell sorting child's play.

**BIO-RAD LABORATORIES**

**BUILDING BIGGER BETTER FLOW CYTOMETRY PANELS WITH STARBRIGHT DYES**

Alice Valentin-Torres ([ALICE_VALENTIN-TORRES@BIO-RAD.COM](mailto:ALICE_VALENTIN-TORRES@BIO-RAD.COM))

Bio-Rad recently launched StarBright (“SB”) dyes for flow cytometry, which deliver tunable brightness and unique spectral properties, improved stability and spectral consistency, as well as superior lot-to-lot reproducibility. SB Dyes are bright and have narrow emission spectra, enhancing signal resolution when constructing complex panels. Additionally, SB Dyes can be fixed in either PFA-or alcohol-based fixatives with minimal spectral changes, can be pre-mixed for up to 28 days, and do not require any special buffer during staining.

We present our novel SB Blue and Yellow Dyes along with our previously released Violet and UV dyes to the SB portfolio for use in both conventional and spectral flow cytometry. SB Blue Dyes are bright and allow an expansion of dyes to be used using the 488 laser, whereas SB Yellow Dyes are optimally excited by the 561 laser with reduced excitation from the 488 laser, making large panel design using both the 488 and 561 lasers possible.

**CYTEK BIOSCIENCES, INC.**

**CYTEK CLOUD - STREAMLINE YOUR EXPERIMENTAL WORKFLOW**

Joel Crespo ([JCRESPO@CYTEKBIO.COM](mailto:JCRESPO@CYTEKBIO.COM))
Cytek® Cloud is the new digital ecosystem that supports full spectrum flow cytometry research from panel design to data acquisition. It features two integrated online tools, Panel Builder and Experiment Builder, to streamline your experiment workflow on Northern Lights™, Aurora, and Aurora CS systems.

Sign up today for a free account at cloud.cytekbio.com.

**NEXCELOM**

**T CELL IMMUNOPHENOTYPING ASSAY USING THE CELLACA PLX IMAGE CYTOMETER**

Patrick Jacobs (PATRICK.JACOBS@PERKINELMER.COM)

CAR-T or immune cells frequently undergo phenotypic characterization using flow cytometry during discovery/development for novel therapies and biomanufacturing. We demonstrate rapid immunophenotyping and viability detection of PBMCs stained with Hoechst/CD3/CD4/CD8 or Hoechst/CD3/CD8/RubyDead kits and compared measurements between Cellaca PLX Image Cytometer with three different flow cytometers. Results showed comparable populations between the two systems suggesting image cytometer may streamline immunophenotyping workflows, and quickly move patient samples into downstream processes.

**THERMO FISHER SCIENTIFIC**

**ADVANCEMENTS AND DISTINCTIVE ATTRIBUTES OF THE BIGFOOT CELL SORTER: A BRIEF OVERVIEW**

Natasha Jacobsen (NATASHA.JACOBSEN@THERMOFISHER.COM)

Discover the Bigfoot Cell Sorter, a pioneering platform in cell analysis and cell sorting technology. This presentation highlights its distinctive features, recent hardware and software progress, and advancements in its spectral capabilities. With exceptional versatility, automation, and speed, the Bigfoot transforms cell sorting workflows. Enhanced reliability, user-friendly interfaces, and expanded spectral options streamline cell analysis. Join us to learn more about the distinguishing features and innovations of the Bigfoot Cell Sorter.

**AGILENT TECHNOLOGIES**

**AWAITING ABSTRACT**

**SONY BIOTECHNOLOGY INC**

**ID7000 TM SPECTRAL ANALYZER – DELIVERING INTUITIVE TOOLS FOR HIGHEST DATA QUALITY**

Anthony Carcio (ANTHONY.CARCIO@SONY.COM)

The ID7000 Spectral Cell Analyzer delivers state of the art optics with up-to 7 lasers and 186 detectors offering both flexibility and sensitivity required for multi-parameter spectral flow. In our talk, we will discuss user workflows on the ID7000 Spectral Cell Analyzer highlighting the use of the spectral reference library and instrument standardization for streamlined daily operation.
GLIIFCA 32 SPEAKERS

Huy Q. Dinh, Ph.D, University of Wisconsin

Dr. Dinh received his Bachelor and Master's degree in Computer Science from Vietnam National University, Hanoi, in 2004 and 200, respectively. From there he moved to the University of Vienna to complete his Ph.D. work in Bioinformatics in 2012. He completed his Postdoctoral research in Cancer Epigenomics at the University of Southern California & Cedars Sinai before moving to the University of Wisconsin where he is currently and Assistant Professor in Oncology.

Kevin W. Eliceiri, Ph.D, University of Wisconsin

Dr. Kevin Eliceiri is the Walter H. Helmerich Research Chair and Professor of Medical Physics and Biomedical Engineering at the University of Wisconsin at Madison. He is an Investigator in the Morgridge Institute for Research and member of the Carbone Cancer Center and McPherson Eye Research Institute. He is director of the Center for Quantitative Cell Imaging dedicated to the development and application of optical and computational technologies for cell studies. The Eliceiri lab is the lead developer of several open-source imaging packages including FIJI and ImageJ. His instrumentation efforts involve novel forms of polarization, laser scanning and multiscale imaging. Dr. Eliceiri has authored more than 250 scientific papers on various aspects of optical imaging, image analysis, cancer and live cell imaging.

Michael Henderson, Ph.D, Van Andel Institute

Michael Henderson is a neuroscientist whose focus is on the impact of protein pathologies and genetic risk factors on the development and progression of neurodegenerative diseases. He earned his B.Sc. in biological science from Florida State, followed by his Ph.D. in neuroscience from Yale University. He conducted his doctoral research in the lab of Dr. Sreeganga Chandra, and moved to the University of Pennsylvania for his postdoctoral fellowship in the Center for Neurodegenerative Disease Research with Drs. Virginia Lee and John Trojanowski. In 2020, Dr. Henderson joined Van Andel Institute’s Center for Neurodegenerative Science as an assistant professor.
Evan T. Keller, D.V.M, Ph.D, University of Michigan

Dr. Keller is the Richard and Susan Rogel Professor of Oncology and serves as Director of the Single Cell Spatial Analysis Program (website: singlecellspatialanalysis.umich.edu), Director of Research Core Office in the Office of Vice President of Research, and Associate Director of the Rogel Cancer Center Shared Resources. Dr. Keller obtained a Doctor of Veterinary Medicine (D.V.M.) and Masters of Preventive Veterinary Medicine/Epidemiology (M.P.V.M.) degrees from the University of California, Davis and a doctorate (Ph.D.) in Developmental Biology from the University of Wisconsin, Madison. He is Board Certified in the American College of Veterinary Internal Medicine (Oncology). Dr. Keller is a Professor of Urology and Pathology at the University of Michigan. Dr. Keller has published more than 250 scientific publications. Dr. Keller’s research extends from basic through clinical studies with a focus is on crosstalk between tumor and its microenvironment.

Karan Raj Kathuria, Stanford University

Karan Kathuria is an MD/PhD student in the lab of Dr. Mark M. Davis at Stanford University. As an immunology graduate student, he is interested in how immune cells communicate and the consequences of their interactions.

Peng Qiu, Ph.D, Georgia Tech and Emory University

Dr. Peng Qiu is a Professor in the Wallace H. Coulter Department of Biomedical Engineering at Georgia Tech and Emory University. He received his B.S. from University of Science and Technology of China (2003), his Ph.D. from University of Maryland College Park (2007), and completed his postdoctoral training at Stanford University (2010). Prior to joining Georgia Tech and Emory in 2013, he was an Assistant Professor at University of Texas MD Anderson Cancer Center (2010-2013). Dr. Qiu’s research focuses on bioinformatics and machine learning. He is an ISAC Marylou Ingram Scholar, an AIMBE Fellow, and an Associate Editor of Frontiers in Bioinformatics and PLoS ONE. He received a NSF CAREER Award, and has achieved “Best Performer” in four computational biology challenges on single-cell analysis topics including: AML classification, rare cell type identification, protein localization prediction and spatial transcriptomics prediction.
Santhoshi Krishnan, Ph.D, University of Michigan

Santhoshi N Krishnan is an incoming Postdoctoral scholar in the at the Department of Computational Medicine and Bioinformatics at the University of Michigan. She recently obtained her Ph.D from the Department of Electrical and Computer Engineering at Rice University, working under Dr. Arvind Rao. Her research interests lie in leveraging machine learning and spatial statistical methods to develop robust frameworks that characterize the disease microenvironment, with a special focus on cancer biology. Through her projects, she has been able to establish strong collaborative research relationships with healthcare providers, statisticians, and epidemiologists, with the aim of developing solutions that are in tune with real-world problems.

She also holds a master's degree in Bioengineering from Rice University, where she worked on quantifying the difference in treatment models in nuclear medicine. When not working, she enjoys reading science fiction books, baking, and plans to visit and hike through all the national parks in the Midwest region during her stay there.

Daniel Vocelle, Ph.D, Michigan State University

Dr. Daniel Vocelle is an Assistant Professor in the Department of Pharmacology and Toxicology at Michigan State University. He also holds the position of Assistant Director of the Michigan State University Flow Cytometry Core Facility, where he supports more than 300 active users, over 140 federally funded research projects, and 10 advanced analytical and sorting instruments. Dr. Vocelle is a seasoned Biomolecular Engineer with a dual Ph.D. in Chemical Engineering and Quantitative Biology, and over a decade of multidisciplinary research experience in a range of areas, including Immunology, Genetic Engineering, Exosomes/Nanoparticles, and Single-Cell Genomics. Drawing on these skills and experience, he is an expert in workflow development, assay optimization, and innovating non-traditional flow cytometry applications.
GLIFCA RAFFLE PRIZES AND FIRST TIME ATTENDEE WELCOME BAG ITEMS PROVIDED BY:
GLIIFCA 32 GENERAL INFORMATION

CONFERENCE REGISTRATION DESK
- The registration desk is located in the lobby of the Madison Marriott West:
  - Friday, Sep. 8 – 5:00 pm to 8:00 pm
  - Saturday, Sep. 9 – 8:00 am to 10:00 am
- The conference registration fee includes all coffee breaks, the Friday Opening Reception, Saturday breakfast, lunch, Wine & Cheese reception, and Sunday breakfast.

EXHIBITS
- Scheduled vendors will have booths in the Exhibit area (Salons A-E)
- Please Note: Exhibitor set-up for Salons A-E starting at 12 pm on Sept. 8 with formal opening of Salons A-E at 6:00 pm. Break down starting at 11:45 am on Sunday, Sept. 10
- All activities other than the Core Managers’ Workshops, Roundtable Luncheon, Steering Committee Meeting and Banquet will be located in the Exhibit area (Salons A-E)
- Please frequent the vendor booths, and show your appreciation for the generous financial support provided by the vendors who substantially help “pay the freight” for this meeting

LOCATION OF ALL ORAL PRESENTATIONS (SAT/SUN): SALONS F-H

BREAKFASTS
Free continental breakfast will be provided for all the registrants in the Exhibit area (Salons A-E) on Saturday from 7:00 am to 8:00 am, and on Sunday from 8:00 am to 9:00 am.

Coffee Breaks
- The refreshments will be served in Salons A-E:
  - Friday – 2:30 pm to 3:00 pm (Core Managers’ Meeting; LACROSSE/MILWAUKEE/GREEN BAY)
  - Saturday – 10:15 am to 10:45 am, and 2:30 pm to 3 pm
  - Sunday – 11:15 am to 11:45 am

EXHIBITOR TECH TALKS
- Tech Talk presentations, Salons F-H
  - Friday – 7 pm to 8:15 pm
  - Saturday – 11:30 am to 12:02 pm

SOCIAL ACTIVITIES

OPENING RECEPTION
- 6:00 pm to 9:00 pm, Salons A-E
Use 2 drink tickets for wine and beer (drink tickets can be used at either the Friday Reception, Saturday Happy Hour, or the Saturday Banquet)

Any unused drink tickets can be donated to the Common GLIFCA Drink Pool at the Opening Reception

**SATURDAY LUNCH (12:15 PM TO 1:20 PM)**

A lunch buffet will be provided. Those attending the roundtables may bring their food to the discussions.

**ROUND TABLES**

Join selected roundtable labeled with the title of discussion topic (MADISON BOARD ROOM, MIDDLETON, MILWAUKEE, GREEN BAY, LACROSSE). The attendance at each table is determined from the sign-up sheet at GLIFCA registration desk and is limited to 10 registrants per table.

**SATURDAY WINE & CHEESE HAPPY HOUR**

5:30 pm to 6:30 pm in the Exhibit/Poster area (Salons A-E) with cheese trays (you can use your drink tickets for beer and wine).

**GLIFCA BANQUET (THEME: CELL SUPERHEROES)**

Free to registrants, available to paid guests.

Commences at 7:30 pm (Salons A-E)

Buffet style (salads, entrées, side dishes, and dessert).

Full-service bar available. Use drink tickets for beer and wine, cash for mixed drinks.

DJ with dance music 9:00 pm – 12:00 am; requests encouraged (get up and have fun!)

Any unused drink tickets can be donated to the Common GLIFCA Drink Pool at the GLIFCA Banquet
DRINKS
- Full-service bar will be located in the Exhibit area (Salons A-E) for the Friday opening reception and the Saturday Wine & Cheese reception, and also in Salons A-E for the banquet on Saturday evening
- Three free drink tickets per registrant for beer, wine, and soda only – beer in bottles/cans
- Mixed drinks – cash bar (your cost)

FACILITIES/SERVICES
- Message Board: on easel next to the GLIIFCA Registration Desk
- Xerox copying, faxing, etc.: ask at the Registration Desk

OTHER INFORMATION

GLIIFCA WEBSITE
- http://www.gliifca.org

NAME TAGS AND EVALUATION FORMS:
- Remember! Before leaving, please fill out evaluation form and leave at Registration/Check Out Desk with your name tag

ADDITIONAL ENQUIRIES, COMMENTS, SUGGESTIONS
- Leave message at the GLIIFCA registration desk
- Comments and suggestions – e-mail Laura Johnston at president@gliifca.org

BOARD OF DIRECTORS BREAKFAST MEETING
- Sunday morning (8:00 am to 8:50 am) in GREEN BAY, MILWAUKEE, LACROSSE