Conference Overview
Sponsors
qPCR & Digital PCR Congress
Microfluidics Congress
NGS Tech & Applications Congress
Workshops
qPCR Registration
Microfluidics Registration
NGS Registration

Global Engage

Philadelphia, USA
July 25-26 2017
Workshops available 24th, 27th & 28th

3rd qPCR & DIGITAL PCR CONGRESS
2nd MICROFLUIDICS CONGRESS
NGS TECH & APPLICATIONS CONGRESS

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	qPCR & DIGITAL PCR CONGRESS	MICROFLUIDICS CONGRESS	NGS TECH & APPLICATIONS CONGRESS
8:00-8:50	Registration and Refreshments		
8:50-9:00	**Global Engage Welcome Address:** **Track Chair's Opening Remarks**	**Global Engage Welcome Address:** **Track Chair's Opening Remarks:** **Leyla Esfandiari**, Assistant Professor of Electrical Engineering and Computing Systems, Assistant Professor of Biomedical, Chemical and Environmental Engineering, **University of Cincinnati**	**Global Engage Welcome Address:** **Track Chair's Opening Remarks**
9:00-9:40	**Keynote Address:** **Liquid Biopsies in the Management of Cancer** **Nick Papadopoulos**, Professor and Director of Translational Genetics, **Johns Hopkins University**	**Keynote Address:** **Where From Here?** **George Whitesides**, Woodford L. and Ann A. Flowers University Professor, Department of Chemistry & Chemical Biology, **Harvard University**	**Keynote Address:** **Managing Health and Disease Using Big Data** **Michael Snyder**, Professor and Chair of Genetics; Director, Stanford Center for Genomics and Personalized Medicine, **Stanford University**
9:40-10:15	**Keynote Address:** **Multi-step real time PCR coupled with HRM enables rapid mutation assessment prior to targeted re-sequencing** **Mike Makrigiorgos**, Professor of Radiation Oncology, **Dana Farber Cancer Institute and Harvard Medical School**	**Keynote Address:** **Microfluidic Circulatory System for Biomedicine** **Abraham Lee**, William J. Link Professor and Chair, Department of Biomedical Engineering, **University of California Irvine**	**Live Single Cell and Subcellular Genomics and Functional Genomics** **James Eberwine**, Elmer Holmes Bobst Professor of Systems Pharmacology and Translational Therapeutics, **University of Pennsylvania Perelman School of Medicine**
10:15-10:45	**Solution Provider Presentation:** **6 years in: Bio-Rad and Digital PCR** **Jennifer Jackson**, Market Development Scientist, **Bio-Rad**	**Solution Provider Presentation:** **Title – TBC** **Nick Long**, Vision Research	**Solution Provider Presentation** For sponsorship opportunities please contact Gavin Hambrook/ Nick Best at sponsorship@globalengage.co.uk
10:45-11:55	Morning Refreshments / Even Numbered Poster Presentation Sessions / One-to-One Partnering Meetings		
	Digital PCR: Possibilities & Opportunities	qPCR: Strategies & Developments	Strategy and Technology in Microfluidics	Strategy, Technology and Analysis Methods
		Track Chair: **Rick Haselton**, Professor, **Vanderbilt University**		
11:55-12:20	**Challenges and opportunities for digital PCR in the CLIA laboratory of the Moffitt Cancer Experience** **Anthony Magliocco**, Chair of Anatomical Pathology, **Moffitt Cancer Center**	**ThermaStop™ and ThermaGo™: Innovative Reagents that Enhance PCR Specificity and Fidelity** **Lawrence J. Wangh**, Professor of Biology, **Brandeis University**	**2D and 3D Microfluidic System for Cell and Organ on a Chip Applications** **Jenny Emnéus**, Professor, Department of Micro- and Nanotechnology, **Technical University of Denmark**	**Rapid structural event characterization of clinical cancer samples on the Oxford Nanopore MinION** **Sara Goodwin**, Technology Development Manager, **Cold Spring Harbor Laboratory**
12:20-12:45	**A novel digital PCR approach using HRM analysis – Title TBC** **Stephanie Fraley**, Assistant Professor, **University of California San Diego**	**Adaptive PCR Based on Hybridization Sensing of Mirror-Image L-DNA** **Nicholas Adams**, Research Assistant Professor, **Vanderbilt University**	**Digital microfluidics: from sample preparation to sensing** **Mina Hoorfar**, Professor, Director of the School of Engineering, **University of British Columbia**, Canada	**Single molecule electronic DNA sequencing by synthesis using polymer-tagged nucleotides and nanopore detection** **Jingyue Ju**, Samuel Ruben-Peter G. Viele Professor of Engineering; Professor of Chemical Engineering and Pharmacology; Director, Center for Genome Technology & Biomolecular Engineering, **Columbia University**

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12:45-1:15	Solution Provider Presentation: **Title – TBC** **Senior Representative,** Stilla	Solution Provider Presentation: For sponsorship opportunities please contact Gavin Hambrook/ Nick Best at sponsorship@globalengage.co.uk	Solution Provider Presentation: **Title – TBC** **Senior Representative,** Fluigent	Solution Provider Presentation: For sponsorship opportunities please contact Gavin Hambrook/ Nick Best at sponsorship@globalengage.co.uk
1:15-2:15	Lunch / One-to-One Partnering Meetings			
2:15-2:40	**Using droplet digital PCR for rare mutation validation and determination of copy number variation** **Kateryna Makova,** Professor of Biology, **Pennsylvania State University**	**Simple and Multiplexed Enrichment of Rare DNA Variants via Sequence-Selective and Temperature-Robust Amplification** **David Zhang,** Ted Law Jr. Assistant Professor of Bioengineering, **Rice University**	**Microfluidics-integrated electrodes for single-cell biology** **Carlotta Guiducci,** Assistant Professor, Swiss Federal Institute of Technology, **École Polytechnique Fédérale de Lausanne, Switzerland**	**Developing in situ sequencing chemistry platforms for clinical applications** **Je Lee,** Assistant Professor, Cancer Centre, **Cold Spring Harbor Laboratory**
2:40-3:05	**Utility of digital PCR in management of hematological malignancies** **Rashmi Kanangal Shamanna,** Assistant Professor, **University of Texas MD Anderson Cancer Center**	**Ultrasensitive Measurement of Circulating Tumor DNA via a Highly Multiplexed NGS Assay** **Abhijit Patel,** Assistant Professor, **Yale University**	**Shaping Fluids with FreeStyle Fluidics** **Edmond J. Walsh,** Associate Professor, Osney Thermo-Fluids Laboratory, Department of Engineering Science, **University of Oxford, UK**	**Cap trapper technologies and applications, Cap Analysis of Gene Expression (CAGE) and FANTOM5 project** **Masayoshi Itoh,** Senior Scientist, Division of Genomic Technologies (DGT), **RIKEN Center for Life Science Technologies (CLST)/ Coordinator, RIKEN Preventive Medicine and Diagnostics Innovation Program (PMI), Japan**
3:05-3:30	**Biomarker identification for BCMA BiTE molecules in cyno preclinical studies** **Chi-Ming Li,** Senior Scientist, **Amgen**	**High-Throughput qPCR Applications for miRNA profiling in Large Clinical Studies** **Kahraman Tanriverdi,** Research Associate Professor and Co-Director, High throughput Gene Expression and Biomarker Core, **University of Massachusetts Medical School**	**Catalysing Commercialization at the National Science Foundation** **Rajesh Mehta,** Program Director, Small Business Innovation Research / Small Business Technology Transfer Research (SBIR/STTR), **National Science Foundation**	**Title – TBC** **Mickey Williams** (Reserved), Director, Molecular Characterization Laboratory, **National Cancer Institute**
3:30-4:00	Solution Provider Presentation: **Title – TBC** **Senior Representative,** JN Medsys	Solution Provider Presentation: For sponsorship opportunities please contact Gavin Hambrook/ Nick Best at sponsorship@globalengage.co.uk	Solution Provider Presentation: **Title – TBC** **Senior Representative,** Elveflow	**Mutation enrichment combined with high resolution melting for no-cost pre-screening prior to targeted re-sequencing** **Mike Makrigiorgos,** Professor of Radiation Oncology, **Dana Farber Cancer Institute and Harvard Medical School**

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4:00-4:50 Afternoon Refreshments / Odd Numbered Poster Presentation Sessions / One-to-One Partnering Meetings

4:50-5:15
PCR-based Methods for Respiratory Virus Studies
Jane Kuypers, Director of Respiratory Virology, **University of Washington and Fred Hutchinson**

4:50-5:15
Know Your Limits: Development and Qualification Considerations of PCR Based Limit Tests using Viral Assays
Brenda Kinnes, Associate Principal Scientist, **Genzyme**

4:50-5:15
Shaped Paper Pumps for Microfluidic Devices
Glenn Walker, Associate Professor, Joint Department of Biomedical Engineering, Joint Department of Biomedical Engineering, **University of North Carolina-Chapel Hill and North Carolina State University**

Strategy, Technology and Analysis Methods

4:50-5:15
Topic: Non-invasive prenatal screening
Bernhard Zimmermann, Senior Director of Research and Development, **Natera, Inc.**

5:15-5:30
Young Investigator Presentation:
Considerations for Digital Droplet PCR to Quantitatively Measure miRNA Using a Two-Step Method
Erica Stein, Research Biologist, **National Institute of Standards and Technology (NIST)**

5:15-5:30
Young Investigator Presentation:
Developing Ultra-sensitive PCR Assays and protocols for HIV Vaccine Research
Catherine Kibirige, Clinical Research Scientist, **Imperial College London, UK**

5:15-5:40
Topic: Centrifugal microfluidics using carbon MEMs for medical diagnostics in extreme POC situations, Title - TBC
Marc Madou, Professor of Mechanical and Aerospace Engineering, **University of California Irvine**

5:15-5:40
Title - TBC
Neil Barth, Chief Medical Officer, **Veracyte, Inc.**

5:30-5:55
Analysis of mitochondrial genome stability by qPCR and dPCR methods
Brett Kaufman, Associate Professor, **University of Pittsburgh**

5:40-6:05
Acoustic Nanofluidics
James Friend, Professor, Center for Medical Devices and Instrumentation, Department of Mechanical and Aerospace Engineering, **University of California-San Diego**

5:40-6:05
Topic: NGS for preconception genetic screening
Senior representative (Reserved), **GenePeeks, Inc.**

6:05 Chair's Closing Remarks / End of Day 1 / Networking Drinks Reception

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8:00-8:40 Refreshments / One-to-One Partnering Meetings		
		Track Chair's Opening Remarks: **Sumit Middha**, Principal Computational Biologist, **Memorial Sloan Kettering Cancer Center**
8:40-9:40 **Keynote Address:** **SuperSelective Primers for Multiplex Real-time PCR Assays that Assess the Abundance of Rare Mutations Associated with Cancer** **Fred Kramer,** Professor of Microbiology, Biochemistry & Molecular Genetics, **New Jersey Medical School Rutgers University**	8:40-9:15 **Keynote Address:** **SD Chip for Digital Biological Measurements** **Daniel Chiu,** A. Bruce Montgomery Professor of Chemistry, Endowed Professor of Analytical Chemistry, and Professor of Bioengineering, **University of Washington**	8:40-9:15 **Keynote Address:** **Precision Medicine – Are we on target?** **John D. McPherson,** Professor, Deputy Director and Associate Director for Basic Science, UCD Comprehensive Cancer Center; Professor, Department of Biochemistry and Molecular Medicine, **University of California Davis**
9:40-10:10 **Solution Provider Presentation:** **Title – TBC** **Bjoern Carle,** Product Manager, **Artel** ARTEL Trust Your Results	9:15-9:40 **Scaling Up Droplet-Based Microfluidics for Diagnostics and Drug Manufacturing Applications** **David Issadore,** Assistant Professor, Bioengineering, Electrical and Systems Engineering, **University of Pennsylvania**	9:15-9:40 **Turning tumor mutations into personalized cancer therapies** **Roman Yelensky,** EVP of Bioinformatics and Sequencing, **Gritstone Oncology**
	09:40-10:10 **Solution Provider Presentation:** FISH. FISH & RICHARDSON **We Got a Patent. Now What?** **Joseph Valentino,** Associate, Fish & Richardson **Sushil Iyer,** Associate, Fish & Richardson	9:40-10:10 **Molecular characterization of circulating tumor cells (CTCs) to elucidate drug resistance mechanisms.** **Vipul Bhargava,** Senior Scientist, **Janssen**
10:10-10:35 **Personalized qPCR probe sets for monitoring cancer progression in ctDNA** **George Vasmatzis,** Co-director of the Biomarker Discovery Program, **Mayo Clinic**	10:10-10:40 **Panel Discussion:** **Commercialization of Microfluidics Research – Q&A Panel** **Daniel Levner,** Chief Technology Officer, **Emulate, Inc.**	10:10-10:35 **Topic: Blood-based assays for early cancer detection, Title – TBC** **Amy Sehnert,** Medical Director, **GRAIL, Inc.**
10:35-11:30 Morning Refreshments / Odd Numbered Poster Presentation Sessions / One-to-One Partnering Meetings		
11:30-12:00 **Solution Provider Presentation:** **Title – TBC** **Senior Representative,** New England Biolabs NEW ENGLAND BioLabs	11:30-12:00 **Solution Provider Presentation:** **The Complexity Challenge: Development and Manufacturing of Fully Integrated Sample-to-Result Microfluidic Devices** **Holger Becker,** Co-founder and CSO, **microfluidic ChipShop GmbH, Germany** microfluidic ChipShop	11:30-12:00 **Solution Provider Presentation** For sponsorship opportunities please contact Gavin Hambrook/ Nick Best at sponsorship@globalengage.co.uk
12:00-12:25 **A Comparative Study on Aptamer SELEX Efficiency Using Droplet PCR versus Conventional PCR** **John Burnett,** Assistant Professor, Beckman Research Institute, **City of Hope Cancer Center**	12:00-12:25 **Highly Multiplexed, Two-Stage Isothermal Assay for Molecular Detection at the Point of Care** **Haim Bau,** Professor, Mechanical Engineering and Applied Mechanics (MEAM), **University of Pennsylvania**	12:00-12:25 **Emma Bowden,** Research Advisor, Genomics and Bioinformatics, Oncology Research, **Eli Lilly and Company**
12:25-12:50 **Circulating microRNAs Predict the Initiation of NHL in a Novel In Vivo Model: Impact of Age and Sex via a Systems Biology Approach** **Afshin Beheshti,** Assistant Professor, **Tufts University School of Medicine**	12:25-12:50 **Microfluidics in Pharmaceutical Secondary Manufacturing: Particle Engineering for Long-Acting Injectables** **David Lai,** Process Engineer, **GlaxoSmithKline Pharmaceuticals**	12:25-12:50 **Topic: Using NGS for clinical biomarker development** **Patrik Vitazka,** Director Clinical Genetics & Genomics, Biomarker Technologies, **Bristol-Myers Squibb**

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12:50-1:50 Lunch

1:50-2:15 **Opportunities and Challenges in Next-Generation Screening and Surveillance of Gynecologic Cancers**
John Martignetti, Associate Professor, **Mount Sinai Hospital**

1:50-2:15 **Microfluidic Devices for Cell Capture and DNA Amplification**
Harold Craighead, Professor of Applied and Engineering Physics, **Cornell University**

1:50-2:15 **Integration of NGS data in clinical diagnosis of rare pediatric disorders**
Avni Santani, Director, Clinical Laboratories, Strategic Partnerships and Innovation, **Center for Applied Genomics, The Children's Hospital of Philadelphia**; Assistant Professor of Clinical Pathology, **Perelman School of Medicine, University of Pennsylvania**

2:20-2:50 **qPCR in the diagnosis and prognosis of pediatric high grade osteosarcomas**
Natacha Entz-Werle, Professor of Pediatrics, **University of Strasbourg and Hospital of Strasbourg, France**

2:15-2:40 **Chemistry-Free Levitational Sorting of Cells for Monitoring Health and Disease**
Utkan Demirci, Tenured Associate Professor, **Stanford University School of Medicine, Department of Radiology, Canary Center for Early Cancer Detection**

2:15-2:40 **Standardizing clinical genomic result interpretation in the NGS era: ClinGen's frameworks for curating variant pathogenicity and gene-disease associations for inherited cardiovascular disorders**
Birgit Funke, Associate Professor of Pathology, **Massachusetts General Hospital/Harvard Medical School**

2:40-3:05 **PCR-based Point of Care Diagnostics – Title TBC**
Renee Yura, Precision Medicine Associate Director, **Novartis**

2:40-3:05 **Clinical Microfluidics: Isolation of CTCs and Extracellular Vesicles from Brain Cancer Patients**
Shannon Stott, Assistant Professor of Medicine, **Massachusetts General Hospital**

2:40-3:05 **281 lessons learned from scaling NGS-based expanded carrier screening**
Lisa Edelmann, Associate Professor, Executive Director, Mount Sinai Genetic Testing Laboratory, **Icahn School of Medicine at Mount Sinai**

3:05-3:30 Afternoon Refreshments / Even Numbered Poster Presentation Sessions

3:30-3:55 **Developing a qPCR assay to detect P. acnes**
J Christopher Ellis, Head of Microbiology, **Eli Lilly and Company, USA**

3:30-3:55 **High throughput Label free Microfluidic Technologies for the Isolation and Analysis of Circulating Tumor Cells**
Sunitha Nagrath, Associate Professor, Chemical Engineering, **University of Michigan**

3:30-3:55 **Title – TBC**
Ekta Khurana (Reserved), Assistant Professor of Computational Genomics, **Weill Cornell Medical College**

3:55-4:20 **Title TBC**
Invitation out to s Senior Representative

3:55-4:20 **Microfluidic Systems for Recapitulating Tumor-Immune Cell Interactions**
Jeffrey Borenstein, Laboratory Technical Staff, Technical Director – **Biomedical Engineering Center, Draper**

3:55-4:20 **Beyond the genome – decode the leukemia epigenome dynamics via a novel algorithm and high-throughput sequencing technology**
Sheng Li, Assistant Professor, The Jackson Laboratory for Genomic Medicine, **The Jackson Laboratory Cancer Center, Connecticut**

4:20-4:45 **Title – TBC**
Daniel Levner, Chief Technology Officer, **Emulate, Inc.**

4:45-5:10 **Understanding the impact of lymphocyte cell phenotypic diversity on tumor cell survival via functional profiling**
Tania Konry, Assistant Professor, Department of Pharmaceutical Sciences, **Northeastern University**

5:10 Chair's Closing Remarks & Conference Close

SINGH CENTER DRINKS RECEPTION

As an attendee, you are warmly invited to a drinks reception at 6pm on Monday July 24th at the Singh Center for Nanotechnology – just 2 miles from the congress venue.

Following the first day of workshops, whether qPCR, Microfluidics or NGS Tech, continue your conversations over drinks and tour this outstanding facility, specifically designed for nanotechnology research.

Not attending a workshop, but arriving early in Philadelphia for the conference? Come along and start your networking early.

Full details of the workshops can be found on pages 34-36.

Monday, July 24th 2017

9:00am-1:00pm
Innovations in digital nucleic acid amplification
Dr. Felix von Stetten

2:00pm-6:00pm
Microfluidics and Lab-on-a-chip technologies for commercial product development: strategies, technologies, markets and applications
Holger Becker

2:30pm-6:00pm
NGS Tech & Applications Workshop
Avni Santani
Matthew Lebo
Jennifer Morrissette

Thursday, July 27th & Friday 28th 2017

2 Day Course: MIQE – How to get Good Quality Control in qPCR
Mikael Kubista
CEO, TATAA Biocenter & Head of Department, BTU, CAS

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Global Engage is pleased to announce the 3rd year of the American leg of our successful qPCR & Digital PCR series, which will be co-located with our Microfluidics Congress and NGS Tech & Applications Congress on July 24-26, 2017 in Philadelphia and will attract around 400 attendees.

Bringing together industry and academic experts working in areas such as molecular biology/diagnostics, gene expression, genomics, biomarkers, pathogen detection, mRNA, bioinformatics, and data management, the congress will examine the latest developments, opportunities and applications of both dPCR and qPCR through case studies across diverse areas such as oncology, infectious diseases, vaccines, prenatal diagnostics, clinical applications, microbiology, and other novel applications.

NICK PAPADOPOULOS
Professor and Director of Translational Genetics, Johns Hopkins University

LAWRENCE WANGH
Professor of Biology, Brandeis University

MIKE MAKRIGIORGOS
Professor of Radiation Oncology, Dana Farber Cancer Institute and Harvard Medical School

KATERYNA MAKOVA
Professor of Biology, Pennsylvania State University

SYNOPSIS

DAY 1 – STREAM ONE
Digital PCR: Applications & Possibilities

- Introduction, benefits, and future development of dPCR
- Comparing dPCR to qPCR
- Converting to dPCR and choosing your system
- Digital PCR workflow optimisation
- Validation of dPCR for clinical and research use
- Complimenting digital PCR with other technologies including NGS
- Multiplexing in digital PCR
- Detection of rare/patient-specific mutations
- Applications for precision medicine

DAY 1 – STREAM TWO
qPCR: Strategies & Developments

- Developments in qPCR methods
- MIQE guidelines & standardisation
- qPCR/RT-PCR assay design, optimisation & validation
- Sample preparation & quality control methods
- Detection, quantification and sequencing of RNA
- Automation of qPCR methods
- Bioinformatics and data analysis
- Multiplexing
- Parallel sequencing
- Point of Care diagnostics developments

DAY 2 – STREAM ONE
Healthcare Case Studies

- Clinical/Diagnostic applications
- Companion diagnostics
- Clinical test validation
- Oncology
  - Rare variant detection
  - Mutation detection
  - Monitoring therapy response
  - Early relapse detection
- Neurological disorders
- Prenatal diagnostics
- Infectious diseases
- Biomarker discovery
- Micro RNA/ncRNA/siRNA applications
- Gene expression and analysis
- Single cell analysis
- Liquid Biopsies

CONFIRMED SPEAKERS

FRED KRAMER
Professor of Microbiology, Biochemistry and Molecular Genetics, Public Health Research Institute, Rutgers University

JANE KUYPERS
Director of Respiratory Virology, University of Washington and Fred Hutchinson Cancer Research Center

JOHN MARTIGNETTI
Associate Professor, Icahn School of Medicine at Mount Sinai

NICHOLAS ADAMS
Research Assistant Professor, Vanderbilt University

KATERYNA MAKOVA
Professor of Biology, Pennsylvania State University

JOHN BURNETT
Assistant Professor, Beckman Research Institute, City of Hope Cancer Center

BRENDA KINNES
Associate Principal Scientist, Genzyme

DAVID ZHANG
Assistant Professor of Bioengineering and Principle Investigator and the Nucleic Acid Bioengineering Lab, Rice University

LAWRENCE J. WANGH
Professor of Biology, Brandeis University

NATACHA ENTZ-WERLE
Professor of Pediatrics, University of Strasbourg and Hospital of Strasbourg, France

BRETT KAUFMAN
Associate Professor, University of Pittsburgh

BJOERN CARLE
Product Manager, Artel

AFSHIN BEHESHTI
Assistant Professor, Tufts University School of Medicine

ERICA STEIN
Research Biologist, National Institute of Standards and Technology (NIST)

MIKE MAKRIGIORGOS
Professor of Radiation Oncology, Dana Farber Cancer Institute and Harvard Medical School

ABHIJIT PATEL
Assistant Professor, Yale University

CHRISTOPHER ELLIS
Head of Microbiology, Eli Lily and Company

CATHERINE KIBIRIGE
Clinical Research Scientist, Imperial College London, UK

FREDERICK HASELTON
(Track Chair)
Professor of Biomedical Engineering, Vanderbilt University

KAHRAMAN TANRIVERDI
Research Associate Professor and Co-Director, High Throughput Gene Expression and Biomarker Core, University of Massachusetts Medical School

ANTHONY MAGLIOCCO
Chair of Anatomical Pathology, Moffitt Cancer Center

NICK PAPADOPOULOS
Professor and Director of Translational Genetics, Johns Hopkins University

RASHMI KANAGAL-SHAMANNA
Assistant Professor, Department of Hematopathology and Molecular Diagnostics, University of Texas MD Anderson Cancer Center

GEORGE VASMATZIS
Co-director of the Biomarker Discovery Program, Mayo Clinic

CHI-MING LI
Senior Scientist at Amgen

RENEE YURA
Precision Medicine Associate Director, Novartis

STEPHANIE FRALEY
Assistant Professor, University of California San Diego

REMI DANGLA
CEO, Stilla Technologies

NICOLE NICHOLS
Group Leader, Amplification Applications and Product Development, New England BioLabs

JENNIFER JACKSON
Market Development Scientist, Bio-Rad

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8:00-8:50 Registration & Refreshments

8:50-9:00 **Global Engage Welcome Address and Morning Chair's Opening Remarks**

9:00-9:40

KEYNOTE ADDRESS:
NICK PAPADOPOULOS

Professor and Director of Translational Genetics, Johns Hopkins University

Liquid Biopsies in the Management of Cancer

- Somatic mutations are cancer specific biomarkers that reveal the presence of cancer when present in cell free DNA present in liquid biopsies.
- For most of the clinical application, the number of circulating tumor DNA molecules with somatic mutations is very small compared to that of DNA molecules with wild type sequence making their detection challenging requiring the development of sensitive methods.
- We developed a very sensitive dPCR based method that utilizes NGS for the detection of rare tumor-derived mutations in bodily fluids.
- Detection of mutations in a combination of liquid biopsies form different bodily fluids can increase the sensitivity of detection of certain tumor types.

9:40-10:15

KEYNOTE ADDRESS:
MIKE MAKRIGIORGOS

Professor of Radiation Oncology, Dana Farber Cancer Institute and Harvard Medical School

Multi-step real time PCR coupled with HRM enables rapid mutation assessment prior to targeted re-sequencing

Targeted re-sequencing often entails discrete amplification and ligation steps during sample preparation that increase both cost and time to results. We provide novel forms of real time PCR that reduce the effort for sample preparation while also providing rapid assessment of mutation status prior to targeted re-sequencing. The new method incorporates implementation of mutation enrichment via COLD-PCR or NaME-PrO together with high resolution melting. Application in circulating DNA from clinical cancer samples will be presented.

10:15-10:45

SOLUTION PROVIDER PRESENTATION:
JENNIFER JACKSON

Market Development Scientist, Bio-Rad

6 years in: Bio-Rad and Digital PCR

Bio-Rad entered the field of digital PCR in 2011 with its Droplet Digital PCR platform, the QX100. Since then we have learned enormously about the different capabilities of this powerful technology and have strived to provide solutions to even more interesting and challenging applications. In this presentation, we will discuss our past and present solutions and the tools we have developed to accelerate both discovery and research as well our near future endeavors.

10:45-11:55 Morning Refreshments / Poster Presentations / Scheduled One-to-One Meetings

DIGITAL PCR: POSSIBILITIES & OPPORTUNITIES

11:55-12:20

ANTHONY MAGLIOCCO

Chair of Anatomical Pathology, Moffitt Cancer Center

Challenges and opportunities for digital PCR in the CLIA laboratory of the Moffitt Cancer Experience

The Moffit Cancer Center is one of the largest NCI designated comprehensive free standing cancer centers in the USA. The center has developed one of the most advanced personalized cancer medicine treatment programs in the world. This program is supported by a comprehensive and advanced CLIA molecular diagnostics. Digital PCR assays are currently being developed for several clinical applications including TKI resistance monitoring in patients with advanced lung cancer. The challenges and opportunities in deploying digital PCR into clinical practice will be discussed.

qPCR: STRATEGIES & DEVELOPMENTS

TRACK CHAIR:
RICK HASELTON

Professor, Vanderbilt University

11:55-12:20

LAWRENCE J. WANGH

Professor of Biology, Brandeis University

ThermaStop™ and ThermaGo™: Innovative Reagents that Enhance PCR Specificity and Fidelity

ThermaStop™ and ThermaGo™ are chemically modified oligonucleotides that bind to Taq polymerase in a temperature-dependent manner and thereby increase both the specificity and the fidelity of the enzyme, without decreasing its activities. ThermaStop™ and ThermaGo™ have been found to improve the performance of several commonly used polymerases from several manufactures and have proven easy to optimize for most symmetric, asymmetric, and LATE-PCR assays. ThermaStop™ also enhances reverse transcriptase, the enzyme used to copy RNA into DNA and therefore significantly improves one-step and two-step RT-PCR. ThermaStop™ and ThermaGo™ are being marketed by ThermaGenix, Inc.

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12:20-12:45

STEPHANIE FRALEY

Assistant Professor, University of California San Diego

A digital high resolution melt platform enables single molecule sensitive, large-scale sequence profiling

Sensitive and quantitative profiling of nucleic acids in heterogeneous samples is critical for precision medicine. dPCR is used for quantitative detection but is limited to a few specific targets at a time. My lab has combined dPCR with high resolution melt (digital HRM, dHRM) and machine learning to accomplish single molecule sensitive, large-scale sequence profiling of complex samples. Specifically, we have used dHRM to fingerprint and quantify individual pathogenic bacteria in mock polymicrobial blood samples in under 4 hours. Our device reduces reaction volumes by 99.995% and achieves a greater than 200-fold increase in dynamic range of detection compared to traditional qPCR HRM approaches. Type I and II error rates are significantly reduced compared to intercalating dye-based dPCR. This technology could accelerate infectious disease diagnosis.

12:20-12:45

NICHOLAS ADAMS

Research Assistant Professor, Vanderbilt University

Adaptive PCR Based on Hybridization Sensing of Mirror-Image L-DNA

This talk describes a fundamentally simpler and more robust PCR design that dynamically controls thermal cycling by more directly monitoring primer annealing and target melting during the reaction. This is achieved by optically sensing the hybridization state of mirror-image L-DNA analogs of the reaction's primers and targets. Because the properties of L-DNA enantiomers parallel those of natural D-DNAs, the L-DNA reagents indicate the ideal cycling conditions without interfering with the reaction. This hybridization-sensing approach eliminates the requirement for thermal calibrations and timed cycling programs and adapts to variations in sample contents that impact DNA hybridization, enabling efficient PCR directly in complex specimens such as patient urine samples. These advantages make PCR-based nucleic acid analysis simpler, more robust, and more accessible outside of laboratory settings.

12:45-1:15

SOLUTION PROVIDER PRESENTATION: REMI DANGLA

CEO, Stilla Technologies

Monitoring EGFR mutations in lung cancer patients using multiplex Crystal Digital PCR

- Presentation of Crystal Digital PCR
- Multicolor assay development
- EGFR Detection monitoring in lung Cancer Patients

STILLA

12:45-1:15

SOLUTION PROVIDER PRESENTATION

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1:15-2:15 Lunch / Scheduled One-to-One Meetings

2:15-2:40

KATERYNA MAKOVA

Professor of Biology, Pennsylvania State University

Using droplet digital PCR for rare mutation validation and determination of copy number variation

- Droplet digital PCR can be successfully used to validate rare
- mutations in heterogeneous genetic samples (e.g., mitochondrial DNA heteroplasmy)
- Droplet digital PCR can be used to discover copy number variation in ampliconic genes on the human Y chromosome.
- Combined with duplex sequencing, droplet digital PCR provides an important tool for studies of mutation

2:15-2:40

DAVID ZHANG

Ted Law Jr. Assistant Professor of Bioengineering, Rice University

Simple and Multiplexed Enrichment of Rare DNA Variants via Sequence-Selective and Temperature-Robust Amplification

Rare DNA sequence variants hold important biological and clinical information, but are challenging for existing PCR and NGS methods to profile in an inexpensive, multiplexed, simple-to-implement, and sequence-general way. Here, we present Blocker Displacement Amplification (BDA), a temperature-robust PCR method that selectively amplifies all sequence variants within a roughly 20nt window by 1000-fold over wildtype sequences. BDA achieves similar enrichment performance across anneal temperatures from 56°C to 64°C. This temperature robustness reduces the need for empirical optimization, especially for multiplexed assays, and furthermore enables the use of inexpensive and portable thermocycling instruments for rare DNA variant detection. We have validated BDA on multiple different PCR platforms, DNA polymerases, and sample types including clinical cell-free DNA samples collected from the blood plasma of lung cancer patients.

Conference Overview
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2:40-3:05

RASHMI KANANGAL-SHAMANNA

Assistant Professor, Department of Hematopathology and Molecular Diagnostics, University of Texas MD Anderson Cancer Center

Utility of digital PCR in management of hematological malignancies

The talk illustrates the principles, validation and clinical utility of digital PCR in monitoring of residual leukemias and lymphomas. This talk also illustrates how digital PCR can overcome some of the common difficulties in molecular profiling of hematological malignancies.

2:40-3:05

ABHIJIT PATEL

Assistant Professor, Yale University

Ultrasensitive Measurement of Circulating Tumor DNA via a Highly Multiplexed NGS Assay

- Our group has developed a highly multiplexed PCR-based library preparation method that utilizes a molecular lineage tagging strategy to enable measurement of mutant DNA at allele fractions below 0.1%.
- We have used this assay to identify and quantify circulating tumor DNA fragments in more than 2000 clinical plasma samples from over 400 patients.
- Data will be presented from ongoing studies to establish the clinical utility of this technology, with a particular focus on monitoring of therapeutic response.

3:05-3:30

CHI-MING LI

Senior Scientist, Amgen

Biomarker identification for BCMA BiTE molecules in cyno preclinical studies

My talk will focus on specific applications of ddPCR technology in biomarker identification and validation in preclinical studies, including (1) Identification of biomarkers for plasma cells (PC) using RNA-Seq, (2) Validation of ddPCR-based assays for PC biomarker assessment, (3) Application of the biomarker assays in cyno PK/PD studies for BCMA BiTE molecules

3:05-3:30

KAHRAMAN TANRIVERDI

Research Associate Professor and Co-Director, High throughput Gene Expression and Biomarker Core, University of Massachusetts Medical School

High-Throughput qPCR Applications for miRNA profiling in Large Clinical Studies

- Although profiling miRNAs in large cohorts has a potential to identify potential biomarkers and therapeutic targets these studies can be very expensive. Next Generation Sequencing (NGS) thought to be the best way to profile all miRNAs but RT-qPCR is still cheaper and more sensitive method especially for low abundant miRNA targets.
- High-Throughput RT-qPCR applications are the solution for cheaper, faster, easier and more reproducible data generation from large clinical cohorts for miRNA and even for mRNA profiling.
- Recent interest on extracellular RNAs (exRNAs) increased the need of fast, cost-effective and sensitive methods for profiling small non coding RNAs such as miRNAs in biofluids in large clinical cohorts. Again, High-Throughput RT-qPCR applications are a good solution for this type of studies.

3:30-4:00

SOLUTION PROVIDER PRESENTATION:
SENIOR REPRESENTATIVE

JN Medsys

Title TBC

jnmedsys

3:30-4:00

SOLUTION PROVIDER PRESENTATION

For sponsorship opportunities please contact Gavin Hambrook/ Nick Best at sponsorship@globalengage.co.uk

16:00-16:50 Afternoon Refreshments / Poster Presentations / Scheduled One-to-One Meetings

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4:50-5:15

JANE KUYPERS

Director of Respiratory Virology, University of Washington and Fred Hutchinson Cancer Research Center

PCR-based Methods for Respiratory Virus Studies

Rapid and accurate detection of respiratory viruses is important to guide antiviral therapy, prevent nosocomial spread, provide surveillance, and decrease hospital costs and lengths of stay. Real-time PCR assays provide not only rapid and sensitive detection, but also quantification of respiratory viruses. However, the sequence diversity within some respiratory viruses poses challenges for the development of robust qPCR methods that detect all genotypes with equal efficiency. Digital PCR, which does not rely on amplification efficiency, may perform better than qPCR for quantitation of viruses with high sequence diversity. We compared the accuracy of reverse transcription-qPCR and reverse transcription-digital PCR for quantification of human rhinovirus RNA using a consensus primer/probe set targeting the 5′ non-coding region. When using consensus primers and probes, digital PCR outperformed qPCR.

4:50-5:15

BRENDA KINNES

Associate Principal Scientist, Genzyme

Know Your Limits: Development and Qualification Considerations of PCR Based Limit Tests using Viral Assays

Development and qualification strategies when designing a PCR based limit test

- System Suitability Considerations during development
- Using Qualification data to help set preliminary limits
- Case Scenario #1: Infectious Helper Virus Detection Assay using Traditional qPCR
- Case Scenario #2: Replication Competent AAV Detection Assay using Melt Curve Analysis

5:15-5:30

YOUNG INVESTIGATOR PRESENTATION: ERICA STEIN

Research Biologist, National Institute of Standards and Technology (NIST)

Considerations for Digital Droplet PCR to Quantitatively Measure miRNA Using a Two-Step Method

- Practical rules on how to create and identify appropriate controls for the assay.
- Optimization of assay conditions to incorporate spike-in controls after identifying targets of interest.
- Application of assay principles to perform critical analysis on clinical samples to quantitatively detect miRNA.

5:15-5:30

YOUNG INVESTIGATOR PRESENTATION: CATHERINE KIBIRIGE

Clinical Research Scientist, Imperial College London, UK

Developing Ultra-sensitive PCR Assays and protocols for HIV Vaccine Research

- We have developed PCR assays that detect down to 3 copies of HIV-1 DNA/RNA with >90% reliability.
- In a pilot study using archival cells (PBMCs) from HIV-infected men with <20 copies HIV-1 RNA/ml plasma. HIV-1 RNA was detected significantly more frequently in cells from a high inflammation group (21/27; 78%) compared to a low inflammation group (7/27; 26%; p=.0003).
- We are using the assays to characterize the viral-inhibition assay (VIA) used in IAVI vaccine clinical trials to assess the impact of anti-HIV CD8 responses in the context of CD4 T-cell HIV transcription. We are assessing HIV levels in archival samples to establish and correlate the HIV levels measured by these assays to previous assessments. This will enhance our vaccine design efforts.

5:30-5:55

BRETT KAUFMAN

Associate Professor, University of Pittsburgh

Analysis of mitochondrial genome stability by qPCR and dPCR methods

Mitochondrial DNA (mtDNA) mutations are a common cause of primary mitochondrial disorders, and have also been implicated in a broad collection of conditions, including aging, neurodegeneration, and cancer. Prevalent among these pathogenic variants are mtDNA deletions, which show a strong bias for the loss of sequence in the major arc between, but not including, the heavy and light strand origins of replication. Because individual mtDNA deletions can accumulate focally, occur with multiple mixed breakpoints, and in the presence of normal mtDNA sequences, methods that detect broad-spectrum mutations with enhanced sensitivity and limited costs have both research and clinical applications. In this study, we evaluated semi-quantitative and digital PCR-based methods of mtDNA deletion detection using double-stranded reference templates or biological samples. Our aim was to describe key experimental assay parameters that will enable the analysis of low levels or small differences in mtDNA deletion load during disease progression, with limited false-positive detection. We determined that the digital PCR method significantly improved mtDNA deletion detection sensitivity through absolute quantitation, improved precision and reduced assay standard error.

5:55	Chair's Closing Remarks and End of Day One
5:55-6:55	Networking Drinks Reception

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8:00-8:35 Registration & Refreshments

8:35-8:40 **Morning Chair's Opening Remarks**

8:40-9:40

KEYNOTE ADDRESS:
FRED KRAMER

Professor of Microbiology, Biochemistry & Molecular Genetics. New Jersey Medical School Rutgers University

SuperSelective Primers for Multiplex Real-time PCR Assays that Assess the Abundance of Rare Mutations Associated with Cancer

PCR assays are the most rapid, most sensitive, and least expensive way to assess the abundance of mutant DNA fragments present in liquid biopsies. "SuperSelective" PCR primers, due to their unique design, are extraordinarily specific, able to selectively initiate the synthesis of amplicons on ten mutant DNA fragments in the presence of 1,000,000 wild-type DNA fragments. Sets of SuperSelective primers, each possessing unique 5'-tag sequences, enable the amplicons generated from each mutant to be distinguished by differently colored molecular beacon probes. And the inclusion of primers for a wild-type reference gene fragment enables the abundance of each type of mutant DNA fragment to be assessed by determining the difference between its threshold value and the threshold value of the reference gene.

9:40-10:10

SOLUTION PROVIDER PRESENTATION:
BJOERN CARLE

Product Manager, Artel

ARTEL
Trust Your Results

The Importance of Pipetting Technique when Using Micropipettes

Mechanical action micropipettes are ubiquitous in laboratories and are used for many routine tasks, including the quantitative measurement and dispensing of analytical samples and reagents. As concentrations of biological and chemical components in the prepared samples for analyses and assays are volume-dependent, incorrectly performed pipetting steps will directly impact the transferred volumes, and hence, the test results. The design and construction of piston-operated air-displacement pipettes render their performance susceptible to the pipetting technique used by the operator of such devices, as well as the environment in which they are operated. This presentation evaluates a number of techniques that influence the accuracy and precision of the pipetted volume and solutions on how the operator may control all of these parameters.

10:10-10:35

GEORGE VASMATZIS

Co-director of the Biomarker Discovery Program, Mayo Clinic

Personalized qPCR probe sets for monitoring cancer progression in ctDNA

We have identified promising new way to monitor and treat recurrence of cancer using liquid biopsies from blood tests.
Our approach utilizes personalized monitoring using specific junctions found in patient's tumor tissue and then developing patient specific PCR assays to measure their level in the blood. There are several advantages using this approach versus mutational panels.

- These personalized assays will be more sensitive because of the ability to design specific primers to amplify these junctions that would not amplify regions from normal genomes.
- We have the ability to choose the junctions according to a particular therapy that we want to monitor.
- We have the ability to chose junctions related to different clones of the disease.

The major disadvantage is that regulatory agencies, would have to agree to develop specific assays for every patient.

10:40-11:30 Morning Refreshments / Poster Presentations / Scheduled One-to-One Meetings

11:30-12:00

SOLUTION PROVIDER PRESENTATION:
NICOLE NICHOLS

Group Leader, Amplification Applications and Product Development, New England BioLabs

Novel enzyme engineering, assay development and data visualization approaches to build a simplified and robust qPCR portfolio

qPCR reagents enable discoveries across a multitude of disciplines. Although they are ubiquitous, they are not all created equal. We took a systematic approach in the design and development of our recent Luna qPCR portfolio, creating a novel data visualization method that drove our development efforts. We also engineered a new, thermostable, warmstart RT that supports robust performance of the Luna one-step RT-qPCR products, even in multiplex and cell-direct applications.

NEW ENGLAND BioLabs

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12:00-12:25

JOHN BURNETT

Assistant Professor, Beckman Research Institute, City of Hope Cancer Center

A Comparative Study on Aptamer SELEX Efficiency Using Droplet PCR versus Conventional PCR

Nine parallel rounds of cell-based SELEX were performed for CCR7-specific RNA aptamers using conventional open PCR (oPCR) and droplet digital (ddPCR). High throughput sequencing (HTS) revealed striking differences between the enrichment of sequences from oPCR and ddPCR libraries – likely owing to intrinsic amplification bias from oPCR. Indeed, SELEX using ddPCR yielded a significantly larger molecular diversity compared to the same SELEX workflow using oPCR. Similar binding affinities in aptamer candidates were observed from selected aptamers within both selection pools, suggesting that ddPCR could retain aptamer species that were potentially eliminated in oPCR from amplification bias. By characterizing the types of sequences and aptamer clusters lost in oPCR selection due to amplification bias, this study demonstrates the integral benefits of using ddPCR for aptamer SELEX.

12:25-12:50

AFSHIN BEHESHTI

Assistant Professor, Tufts University School of Medicine

Circulating microRNAs Predict the Initiation of NHL in a Novel In Vivo Model: Impact of Age and Sex via a Systems Biology Approach

Extensive epidemiological data have demonstrated an exponential rise in the incidence of non-Hodgkin lymphoma (NHL) that is associated with increasing age, starting from young adulthood. We propose that there are predictable, age-dependent circulating microRNA (miRNA) signatures in the host that influence NHL development. To investigate this we utilized a novel murine model for spontaneous DLBCL initiation. We determined a list of 10 circulating miRNAs in the serum present in DLBCL forming mice that are not present in the control mice starting from 2 months of age quantified through Droplet Digital PCR system. It was determined that there is a key miRNA signature circulating throughout a host prior to the formation of a tumor. We were able to determine an age-based key functional circulating miRNA signature associated with NHL that occurs in the blood. Furthermore, this can potentially be used as a simple biomarker to predict future lymphoma development and allow for advanced novel therapeutic strategies to prevent lymphomagenesis

12:50-1:50 Lunch

1:50-2:15

JOHN MARTIGNETTI

Associate Professor, Mount Sinai Hospital

Opportunities and Challenges in Next-Generation Screening and Surveillance of Gynecologic Cancers

The talk summarizes our experiences built upon qPCR, ddPCR and NGS in the detection of cancer-specific mutations in blood and uterine lavage fluid to develop biomarkers for gynecologic cancer screening, surveillance and prognosis of patients. ddPCR-based biomarkers demonstrated improved sensitivity over current FDA-approved tests and tracked with overall survival. Unexpectedly, while earliest recognition of disease existence may open the window for improved survival and quality of life in these and other cancers, our studies also identified realities that will have to be overcome before translation to the clinic.

2:15-2:40

NATACHA ENTZ-WERLE

Professor of Pediatrics, University of Strasbourg and Hospital of Strasbourg, France

qPCR in the diagnosis and prognosis of pediatric high grade osteosarcomas

The survival of pediatric high grade osteosarcoma is stable worldwide since two decades. The management of those cancers is really lacking new approaches to classify closely the patients and adapt thereafter the treatments. The objectives of the qPCR developments was to determine the impact of the tumor molecular profile in the initial biopsy, in the tumor resection after neoadjuvant chemotherapy and their molecular correlations with survival and the tumor histological response after treatment. The qPCR panel based on genes of bone dedifferentiation and cell proliferation was used in the large tumor cohorts of the French national protocols treated pediatric osteosarcomas (OS94 and OS2006). This molecular stratification was associated with a significant impact on survival and provides evidence that this approach is a useful tool.

2:40-3:05

RENEE YURA

Precision Medicine Associate Director, Novartis

PCR-based Point of Care Diagnostics – Title TBC

3:05-3:30 Afternoon Refreshments / Poster Presentation Sessions

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3:30-3:55

CHRISTOPHER ELLIS

Head of Microbiology, Eli Lilly and Company, USA

Rapid Detection of P. acne Using Quantitative Polymerase Chain Reaction (qPCR) Method

Propionibacterium acne (P.acne), a member of the phylum Actinobacteria, is named for its ability to produce propionic acid. P. acne is a commensal bacterium that lives deep within hair follicles and pores of the skin. It is the causative agent of serious diseases such as eye inflammation, endocarditis, and implant associated infections. Because of its known pathogenicity it is important to be able to rapidly detect and identify P. acne in bioreactor contamination events during the manufacture of drug products such as monoclonal antibodies. However, detection of P. acne using traditional cultivation techniques has proven challenging because of its extremely slow growth. Therefore, it is highly desirable to develop a rapid and sensitive method for P. acne detection. Here we will describe the development of a quantitative polymerase chain reaction (qPCR) method capable for rapid detection of P. acne with great sensitivity and specificity.

3:55-4:20

Invitation out to a Senior Representative

Title TBC

4:20 Chair's Closing Remarks and Conference Close

Global Engage is pleased to announce the 2nd Microfluidics Congress: USA, which will be held on July 24-26, 2017 in Philadelphia, Pennsylvania. The event will be co-located with the 3rd qPCR & Digital PCR Congress: USA and the 2017 NGS Tech & Applications Congress and will attract around 400 attendees.

Microfluidics is a rapidly developing area of research, and scientists are continually discovering the wide range of possibilities the technology can provide. At the intersection of engineering, physics, chemistry, nanotechnology, and biotechnology, microfluidics is revolutionizing the way patients are diagnosed, monitored and treated, and is unlocking the potential for reduced reagent consumption and thus, cost.

GEORGE WHITESIDES
Woodford L. and Ann A. Flowers University Professor, Department of Chemistry & Chemical Biology, Harvard University

JENNY EMNÉUS
Professor, Department of Micro- and Nanotechnology, Technical University of Denmark

ABRAHAM LEE
William J. Link Professor and Chair, Department of Biomedical Engineering, University of California Irvine

CARLOTTA GUIDUCCI
Assistant Professor, Swiss Federal Institute of Technology, École Polytechnique Fédérale de Lausanne, Switzerland

SYNOPSIS

STRATEGY AND TECHNOLOGY IN MICROFLUIDICS

- Droplet microfluidics
- Digital microfluidics
- Centrifugal microfluidics
- Dielectrophoresis
- Paper-based systems
- Optofluidics
- Intertial microfluidics
- Acoustofluidics
- Electrokinetics
- Gas microflows
- Sensing technologies
- Modelling and simulation
- Microfabrication
- Sample preparation
- 3-D printing of microfluidic devices
- Technology patent law

CASE STUDIES AND APPLICATIONS IN MEDICAL RESEARCH

- Point-of-care diagnostics and disease monitoring
- Isolation and analysis of CTCs
- Single cell analysis
- Synthetic biology
- Organ-on-a-chip platforms
- Lab-on-a-chip
- DNA analysis
- Biomaterials and tissue engineering
- Biomarker analysis
- Drug delivery
- Proteomics
- Cell sorting
- High throughput screening

CONFIRMED SPEAKERS

GEORGE WHITESIDES
Woodford L. and Ann A. Flowers University Professor, Department of Chemistry & Chemical Biology, Harvard University

ABRAHAM LEE
William J. Link Professor and Chair, Department of Biomedical Engineering, University of California Irvine

MINA HOORFAR
Professor, Director of the School of Engineering, University of British Columbia, Canada

EDMOND J. WALSH
Associate Professor, Osney Thermo-Fluids Laboratory, Department of Engineering Science, University of Oxford, UK

RAJESH MEHTA
Program Director, Small Business Innovation Research / Small Business Technology Transfer Research (SBIR/STTR), National Science Foundation

GLENN WALKER
Associate Professor, Joint Department of Biomedical Engineering, Joint Department of Biomedical Engineering, University of North Carolina-Chapel Hill and North Carolina State University

HOLGER BECKER
Co-founder and CSO, microfluidic ChipShop GmbH, Germany

JENNY EMNÉUS
Professor, Department of Micro- and Nanotechnology, Technical University of Denmark

MARC MADOU
Professor of Mechanical and Aerospace Engineering, University of California Irvine

CARLOTTA GUIDUCCI
Assistant Professor, Swiss Federal Institute of Technology, École Polytechnique Fédérale de Lausanne, Switzerland

JAMES FRIEND
Professor, Center for Medical Devices and Instrumentation, Department of Mechanical and Aerospace Engineering, University of California-San Diego

UTKAN DEMIRCI
Associate Professor of Radiology and Electrical Engineering, Stanford University

DANIEL CHIU
A. Bruce Montgomery Professor of Chemistry, Endowed Professor of Analytical Chemistry, and Professor of Bioengineering, University of Washington

DAVID ISSADORE
Assistant Professor, Bioengineering, Electrical and Systems Engineering, University of Pennsylvania

HAIM BAU
Professor, Mechanical Engineering and Applied Mechanics (MEAM), University of Pennsylvania

TANIA KONRY
Assistant Professor, Department of Pharmaceutical Sciences, Northeastern University

HAROLD CRAIGHEAD
Professor of Applied and Engineering Physics, Cornell University

SUNITHA NAGRATH
Associate Professor, Chemical Engineering, University of Michigan

JEFFREY BORENSTEIN
Laboratory Technical Staff, Technical Director - Biomedical Engineering Center, Draper

SENIOR REPRESENTATIVE
Fluigent

SHANNON STOTT
Assistant Professor of Medicine, Massachusetts General Hospital, Harvard Medical School

DAVID LAI
Process Engineer, GlaxoSmithKline Pharmaceuticals

JOSEPH VALENTINO
Associate, Fish & Richardson

SUSHIL IYER
Associate, Fish & Richardson

DANIEL LEVNER
Chief Technology Officer, Emulate, Inc.

SENIOR REPRESENTATIVE
Elveflow

LEYLA ESFANDIARI
(Track Chair)
Assistant Professor of Electrical Engineering and Computing Systems, Assistant Professor of Biomedical, Chemical and Environmental Engineering, University of Cincinnati

NICK LONG
Vision Research / Ametek

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8:00-8:50 Registration & Refreshments

8:50-9:00 **Global Engage Welcome Address and Morning Chair's Opening Remarks:** **Leyla Esfandiari,** Assistant Professor of Electrical Engineering and Computing Systems, Assistant Professor of Biomedical, Chemical and Environmental Engineering, University of Cincinnati

9:00-9:40

KEYNOTE ADDRESS:
GEORGE WHITESIDES

Woodford L. and Ann A. Flowers University Professor, Department of Chemistry & Chemical Biology, Harvard University

Where From Here?

This talk will be a brief overview of current trends in the field of microfluidics, and focus on some technologies that are developing particularly rapidly now, and speculation on what might come next.

9:40-10:15

KEYNOTE ADDRESS:
ABRAHAM LEE

William J. Link Professor and Chair, Department of Biomedical Engineering, University of California Irvine

Microfluidic Circulatory System for Biomedicine

Microfluidic systems for organ-on-a-chip and single cell capturing, enrichment and analysis from biological samples will be introduced. Our microfluidic organ-on-a-chip platform can enable the delivery of biological constituents through a physiological vasculature network, mimicking the physiological circulation of the human body. The critical bottleneck is to engineer the microenvironment for the formation of 3D tissues and organs and to also perfuse the tissue vascular network for on-chip microcirculation. On the other hand, microfluidics play an important role in the recent advances in liquid biopsy and the ability to specifically capture rare cells such as circulating tumor cells. These two technologies may go hand-in-hand to connect in vitro screening to in vivo screening with great potential in the development of personalized medicine and point-of-care diagnostics.

10:15-10:45

SOLUTION PROVIDER PRESENTATION:
NICK LONG

Ametek / Vision Research

Title TBC

VISION RESEARCH

AMETEK MATERIALS ANALYSIS DIVISION

10:45-11:55 Morning Refreshments / Even Numbered Poster Presentations / Scheduled One-to-One Meetings

11:55-12:20

JENNY EMNÉUS

Professor, Department of Micro- and Nanotechnology, Technical University of Denmark

2D and 3D Microfluidic System for Cell and Organ on a Chip Applications

2D/3D microfluidic systems will be presented, applied in different biomedical and environmental biosensing- and organ-on-a-chip applications. These are designed with two basic modules: (1) a motherboard equipped with fully integrated pumping, valving and sample/waste reservoirs. (2) An exchangeable microfluidic chip designed to fit the desired application. 2D chips are equipped with a 12-channel planar electrode array explored for intra and extracellular events using amperometric and/or impedimetric detection. 3D systems are equipped with different scaffolds for support and culturing of cells, having: (a) Structured perfusable channel network, enabling delivery of necessary nutrients and oxygen to the interior of the scaffolds. (b) Secondary more arbitrary random porous network that can enclose a hydrogel phase with a "nearby" source of important cell factors, supporting the growth and differentiation of cells. (c) Ability to conduct or sense electrical currents.

12:20-12:45

MINA HOORFAR

Professor, Director of the School of Engineering, University of British Columbia, Canada

Digital microfluidics: from sample preparation to sensing

Portable sensors and biomedical devices are influenced by high precision control of microfluidic systems, low-cost fabrication techniques, detection and analysis capabilities. The integration of sensing devices into the chip is still a major problem in microfluidic devices. This presentation focuses on design and fabrication of a precise liquid handling system for flow-thru biosensors using open and closed digital microfluidic (DMF) systems. Real-time on-chip detection of biological species in the biosensor is demonstrated using both optical detection of individual stained cells as well as measuring capacitance variation of a cluster of biological cells passing through the readout site. Adding sample preparation, filtering and purification sites, the proposed biosensor can be used for total analysis or single cell analysis assays. Featuring low-cost hardware with high capacitance measurement resolution and rapid chip fabrication techniques, the proposed biosensor design has the potential to be commercialized as viable solution for life-science research and clinical diagnostics.

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12:45-1:15

SOLUTION PROVIDER PRESENTATION:
SENIOR REPRESENTATIVE
Fluigent
Title - TBC

1:15-2:15 Lunch

2:15-2:40

CARLOTTA GUIDUCCI

Assistant Professor, Swiss Federal Institute of Technology, École Polytechnique Fédérale de Lausanne, Switzerland

Microfluidics-integrated electrodes for single-cell biology

Integrated microelectrode technologies play a crucial role in lab-on-chip development since electric fields can be effectively used to sense, manipulate and move molecules and cells at the microscale. Nevertheless, high-throughput implementations of already assessed techniques are constrained by the design limitations entailed by planar electrodes in microfluidic configurations. These could be overcome by placing vertical electrodes along the micro-channel sidewalls or as free-standing structures inside channels. We recently reported a new microprocessing approach to achieve arrays of singularly-addressable vertical elements generating highly-confined electric fields. We have demonstrated the possibility to manipulate and analyse single cells on the basis of their electrical properties. We successfully employed our approach to characterize the electrical signature of T lymphocytes activation.

2:40-3:05

EDMOND J. WALSH

Associate Professor, Osney Thermo-Fluids Laboratory, Department of Engineering Science, University of Oxford, UK

Shaping Fluids with FreeStyle Fluidics

Interfacial tension replaces gravity as a dominant force as things get smaller. FreeStyle Fluidics exploits this physical principle which enables microfluidics networks to be formed on a surface in a few seconds. By varying wall shapes passive flows can be initiated in a controlled way. This new approach to the manufacture of microfluidic systems brings with it many advantages in cell based assays. Advantages include; enabling users to go from microfluidic network design to operation in minutes, fully-open for accessibility, passive or active pumping can be employed, biocompatible with human cell lines without additional treatment, and it also removes the air bubble challenges of traditional microfluidics. The simplicity and low cost of the method makes it suitable for high throughput applications. Here, the method will be demonstrated with applications in human and bacterial cells.

3:05-3:30

RAJESH MEHTA

Program Director, Small Business Innovation Research / Small Business Technology Transfer Research (SBIR/STTR), National Science Foundation

Catalysing Commercialization at the National Science Foundation

The talk will provide a brief overview of the Small Business Innovation Research (SBIR)/ Small Business Technology Transfer Research (STTR) program at the National Science Foundation (NSF). NSF awards nearly $190 million annually to startups and small businesses through this program, transforming scientific discovery into products and services with commercial and societal impact. The non-dilutive grants support research and development (R&D) across all areas of science and technology – including Microfluidics - helping companies de-risk technology for commercial success. The talk will also showcase some of the recent grantees in the microfluidics technology space.

3:30-4:00

Solution Provider Presentation:
SENIOR REPRESENTATIVE
Elveflow
Title – TBC

4:00-4:50 Afternoon Refreshments / Odd Numbered Poster Presentations / Scheduled One-to-One Meetings

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4:50-5:15

GLENN WALKER

Associate Professor, Joint Department of Biomedical Engineering, Joint Department of Biomedical Engineering, University of North Carolina-Chapel Hill and North Carolina State University

Shaped Paper Pumps for Microfluidic Devices

- Rational design of paper pumps to control flow rate
- Programmable flow behavior
- Application to a point-of-care immunoassay

5:15-5:40

MARC MADOU

Professor of Mechanical and Aerospace Engineering, University of California Irvine

Centrifugal microfluidics using carbon MEMs for medical diagnostics in extreme POC situations,
Title – TBC

5:40-6:05

JAMES FRIEND

Professor, Center for Medical Devices and Instrumentation, Department of Mechanical and Aerospace Engineering, University of California-San Diego

Acoustic Nanofluidics

Acoustic waves have found new utility in microfluidics, providing an enormously powerful ability to manipulate fluids and suspended particles in fluid systems. In this talk, we cover some fundamental concepts of acoustic wave generation and propagation often overlooked in the literature, and follow it with exploration of new phenomena observed at the nanoscale. In fact, the usefulness of acoustic waves at the micro-scale is even more compelling at the nano-scale, in ways not predicted by classical theory. Particle deagglomeration, fluid pumping, pattern formation, and other curious physical phenomena will be shown in the context of potentially useful applications. Along the way, the fascinating underlying physics tying together the acoustics, fluid dynamics, and free fluid interface in these systems will be described.

6:05 Chair's Closing Remarks and End of Day One / Networking Drinks Reception

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8:00-8:40 Refreshments

8:40-9:15

KEYNOTE ADDRESS:
DANIEL CHIU

A. Bruce Montgomery Professor of Chemistry, Endowed Professor of Analytical Chemistry, and Professor of Bioengineering, University of Washington

SD Chip for Digital Biological Measurements

- We will describe workings of SD chip, especially towards POC applications.
- We will present results of SD chip based digital PCR.
- We will discuss single-cell measurements enabled by the SD chip.

9:15-9:40

DAVID ISSADORE

Assistant Professor, Bioengineering, Electrical and Systems Engineering, University of Pennsylvania

Scaling up droplet-based microfluidics for diagnostics and drug manufacturing applications

The transformative growth in microelectronics in the latter half of the 20th century was fueled fundamentally by the ability to simultaneously miniaturize and integrate complex circuits onto monolithic chips. The impact of this growth has been profound– computing is pervasive and portable, communication is instant and global, and information is ubiquitously gathered and shared. My research aims to harness these same electrical engineering approaches, which have enabled the microelectronic revolution, to solve high impact problems in medical diagnostics. To accomplish this goal my lab develops hybrid microchips, where microfluidics are built directly on top of semiconductor chips. In this talk I will focus mainly on my most recent work at Penn on 'digital assays.' Digital assays — in which ultra-sensitive molecular measurements are made by performing millions of parallel experiments in picoliter droplets — have generated enormous enthusiasm due to their single molecule resolution and robustness to reaction conditions. These assays have incredible untapped potential for disease diagnostics, environmental surveillance, and biosafety monitoring, but are currently confined to laboratory settings due to the instrumentation necessary to generate, control, and measure tens of millions of independent droplets. To overcome this challenge, we are developing a hybrid microelectronic / microfluidic chip to 'unlock' droplet-based assays for mobile use. Our microDroplet Fluorescence Detector (μDFD) takes inspiration from cellular networks, in which phones are identified by their carrier frequency and not their particular location. In the same way, but on a much smaller scale, we screen millions of droplets per second using only a conventional smartphone camera. In collaboration with physicians at The Abramson Cancer Center, we are demonstrating the power of this approach by developing a multiplexed exosome-based point of care diagnostic for the early detection of pancreatic cancer. Additionally, we harness these high throughput droplet manufacturing technologies to scale-up drug micro and nano-materials.

9:40-10:10

SOLUTION PROVIDER PRESENTATION:

JOSEPH VALENTINO

Associate, Fish & Richardson

SUSHIL IYER

Associate, Fish & Richardson

We Got a Patent. Now What?

In this presentation, we will talk about the benefits that a patent bestows upon its owner. Specifically we will discuss the following:

- How the owner can use their technical ingenuity to generate revenue through a patent
- What it takes to get a patent
- Ways in which the patent can be lost
- What inventors and patent owners can do to better secure their patents

FISH.
FISH & RICHARDSON

10:10-10:40

PANEL DISCUSSION:

Commercialization of Microfluidics Research – Q&A Panel

PANELIST:
DANIEL LEVNER

Chief Technology Officer, Emulate, Inc.

10:40-11:30 Morning Refreshments / Odd Numbered Poster Presentations / Scheduled One-to-One Meetings

Conference Overview

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NGS Registration

11:30-12:00

SOLUTION PROVIDER PRESENTATION:

HOLGER BECKER

Co-founder and CSO, microfluidic ChipShop GmbH, Germany

The Complexity Challenge: Development and Manufacturing of Fully Integrated Sample-to-Result Microfluidic Devices

A clear technological trend in all application areas of microfluidics is the utilization of single-use disposable microfluidics-enabled cartridges to perform the respective analytical/diagnostic assay in a sample-to-result fashion. As a consequence of this development, the requirements with regards to the complexity of cartridge design and function have massively increased in recent years. In addition, also the reagents required to perform these protocols have to be integrated, either in liquid and/or dried form, in order to reduce contamination risk and to simplify the instrument which operates the cartridge. In this talk, we will present strategies to develop such complex cartridges as well as highlight technological challenges. With several examples for such microfluidics-enabled cartridges we will exemplify the technical solutions.

12:00-12:25

HAIM BAU

Professor, Mechanical Engineering and Applied Mechanics (MEAM), University of Pennsylvania

Highly Multiplexed, Two-Stage Isothermal Assay for Molecular Detection at the Point of Care

- The wide array of pathogens responsible for infectious diseases complicates causative pathogens identification with single-plex tests.
- To address the need for point-of-care highly multiplexed tests, we propose two-stage, isothermal amplification assay, comprising first-stage RPA that amplifies all targets in the sample First-stage amplicons are aliquoted to second stage reactors, each specialized for a specific target, to undergo LAMP. The assay is implemented in a microfluidic chip. LAMP amplicons are detected in-situ with colorimetric dye or with a fluorescent dye and a Smartphone. The test can be carried out with minimal or no instrumentation.
- We demonstrated high level of multiplexing (≥16); high sensitivity (i.e., 1 PFU of ZIKV) and specificity; speed (<40 min); ease of use; and ability to cope with minimally-processed samples.

12:25-12:50

DAVID LAI

Process Engineer, GlaxoSmithKline Pharmaceuticals

Microfluidics in Pharmaceutical Secondary Manufacturing: Particle Engineering for Long-Acting Injectables

GlaxoSmithKline (GSK) is pursuing a Manufacturing Technology Vision and Roadmap to deliver quality and affordable products to patients through simplified and robust manufacturing. In drug product manufacturing, the Active Pharmaceutical ingredient (API) is processed into a consumable form for patients. While injectable API are often in soluble form, Long-Acting Injectables (LAI) are often particle suspensions. The size of a particle plays a role in pharmacokinetics and LAI longevity. GSK applied droplet microfluidics to generate tunable monodisperse pure API and API/Excipient particles for exquisite size control unattainable by conventional API micronization processes in both precision and accuracy. GSK plans to expand its microfluidics capability in breadth to manufacturing hydrophilic and hydrophobic compounds, in depth to increase scale, and beyond to improve candidate selection and high-throughput screening.

12:50-1:50 Lunch

1:50-2:15

HAROLD CRAIGHEAD

Professor of Applied and Engineering Physics, Cornell University

Microfluidic Devices for Cell Capture and DNA Amplification

We have fabricated microfluidic devise for the capture of selected cells by size or affinity binding. The genetic material from a captured cell or group of cells can be immobilized in the device and amplified by whole-genome amplification or selected amplification. The small amount of original genetic material can be efficiently amplified and handled, and there are indications that the can reduce the amplification bias that may occur or small DNA samples.

2:15-2:40

UTKAN DEMIRCI

Tenured Associate Professor, Stanford University School of Medicine, Department of Radiology, Canary Center for Early Cancer Detection

Chemistry-Free Levitational Sorting of Cells for Monitoring Health and Disease

Micro- and nano-scale technologies can have a significant impact on medicine and biology in the areas of cell manipulation, diagnostics and monitoring. At the convergence of these new technologies and biology, we research for enabling solutions to the real world problems at the clinic. Emerging nano-scale and microfluidic technologies integrated with biology offer innovative possibilities for creating intelligent, mobile medical lab-chip devices that could transform diagnostics and monitoring, tissue engineering and regenerative medicine. In this talk, we will present an overview of our laboratory's work in these areas focussed on applications in magnetic levitation methods for assembling cells and label free sorting of rare cells from whole blood. Cells consist of micro- and nano-scale components and materials that contribute to their fundamental magnetic and density signatures. Previous studies have claimed that magnetic levitation can only be used to measure density signatures of nonliving materials. Here, we demonstrate that both eukaryotic and prokaryotic cells can be levitated and that each cell has a unique levitation profile. Furthermore, our levitation platform uniquely enables ultrasensitive density measurements, imaging, and profiling of cells in real-time at single-cell resolution. This method has broad applications, such as the label-free identification and sorting of CTCs and CTM with broad applications in drug screening in personalized medicine.

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2:40-3:05

SHANNON STOTT

Assistant Professor of Medicine, Massachusetts General Hospital Cancer Center, Harvard Medical School

Clinical Microfluidics: Isolation of CTCs and Extracellular Vesicles from Brain Cancer Patients

As a tumor grows, whole cancer cells can be released into the blood stream, albeit at a very low frequency. These rare circulating tumor cells (CTCs) have the potential to be a readily accessible source of genetic and functional information about the patient's cancer. On a smaller scale, each cancer cell can release thousands of tiny particles into the blood stream, referred to as exosomes and microvesicles, Through a collaborative effort between bioengineers, biologists, and clinicians, my laboratory at Massachusetts General Hospital has developed microfluidic devices to isolate these rare circulating biomarkers from whole blood. Data from these devices will be presented with a focus on our recent effort to characterize clusters of CTCs as well as extracellular vesicles from cancer patient blood. Through the microfluidic isolation of blood based biomarkers from patients, our goal is to obtain complementary data to the current standard of care to help better guide treatment.

3:05-3:30

SUNITHA NAGRATH

Associate Professor, Chemical Engineering, University of Michigan

High throughput Label free Microfluidic Technologies for the Isolation and Analysis of Circulating Tumor Cells

Circulating tumor cells (CTCs) are shed from the primary tumor into the peripheral blood. CTCs are emerging as important biomarkers with high clinical relevance. Enumeration of CTCs may have several clinical uses, including determination of prognosis in patients with established malignancy, or even detection of previously undiagnosed cancer. However, due to the limitation of sensitivity and specificity of current technologies for CTC isolation, the full potential of CTCs has yet to be realized. Furthermore, emerging research show that a small number of cells have stem cell-like nature in various cancers and those are called cancer stem cells (CSC) which may arise from differentiated cancer cells through EMT and have the potential to self-renew and are pluripotent. Emerging microfluidic technologies are promising for isolating both CTCs and CSCs with a high yield and specificity. We present novel integrated nano microfluidic technologies that enable both functional and genomic assays beyond enumeration. We developed an inertial microfluidic-based separation technique for high throughput and label-free isolation of CTCs yields the highest throughput with high CTC recovery and high blood cell removal among all the label-free technologies. The isolated CTC populations were further analyzed for single cell multiplex gene expression analysis.

3:30-3:55 Afternoon Refreshments / Even Numbered Poster Presentations

3:55-4:20

JEFFREY BORENSTEIN

Laboratory Technical Staff, Technical Director - Biomedical Engineering Center, Draper

Microfluidic Systems for Recapitulating Tumor-Immune Cell Interactions

Immunotherapies for cancer are advancing rapidly, as is the need for innovative approaches toward recapitulating the tumor microenvironment and its interactions with the immune system. Here we present microfluidics-based approaches toward the development of systems incorporating tumor samples in a precision-controlled perfusion chamber that enables observation and manipulation of tumor-infiltrating lymphocytes and their interactions with the tumors in real-time. Development of these technologies requires significant advances in microfluidic device fabrication and flow control systems in an integrated system capable of multiplex evaluation of tumor biopsy samples. These systems represent a powerful tool for enabling the study of emerging immunotherapies and their efficacy in tumor killing, and ultimately will permit ex vivo determination of patient-specific therapies on tumors prior to clinical administration.

4:20-4:45

DANIEL LEVNER

Chief Technology Officer, Emulate, Inc.

Organ-on-chip,

Title – TBC

4:45-5:10

TANIA KONRY

Assistant Professor, Department of Pharmaceutical Sciences, Northeastern University

Understanding the impact of lymphocyte cell phenotypic diversity on tumor cell survival via functional profiling

Evaluation of the subtypes, numbers and functionality of cells is a complex scientific and biotechnological challenge. Cellular functional phenotype studies of live cells could advance our fundamental understanding of the bio systems, equally important for monitoring in healthy as well as in disease conditions. Many analytical technologies developed to date to analyze cellular phenotype are based on averaging of measured parameters masking the specific phenotypic state of these cells. Averaging these measurements prevents to detect rare subsets of cells as such cells contribute only a minor component of the total measurement. More importantly, those techniques do not allow continues or dynamic monitoring of parameters or cell-cell interactions, thus providing only a snapshot of the event which provides a little insight into the steps that led to the result. Our research program is focused on the development of a novel biotechnology platform for high-throughput quantitative in vitro characterization of single cell functions that reflect the state of the biological system in dynamics. The transformative nature of this platform is expected to introduce a powerful and novel approach for monitoring live cell functional phenotype, secretions, morphology, proliferation as well as cell-cell interactions and communications studies, which can be applied to a myriad of applications including therapy evaluation. This technological capability will provide exceptional insights into disease pathogenesis and immunity, including the detection (and discrimination) of cell phenotypes, high-throughput analysis of antibody or other immune-therapy responses in large studies.

5:10 Conference Close

Global Engage is pleased to announce the 2017 NGS Tech & Applications Congress, which will be held on July 24-26, 2017 in Philadelphia, Pennsylvania. The event will be co-located with the 3rd qPCR & Digital PCR Congress: USA and the 2nd Microfluidics Congress USA and will attract around 400 attendees.

Over the past decade, advances in sequencing technology and significant cost reductions have been instrumental to clinical research. Scientists are continuing to develop new sequencing techniques, tools and methods of analysis, and subsequently discovering new applications in clinical research. NGS has already revolutionized the way genomics research is conducted, and with the advent of new methods such as nanopore, it is an exciting time to be in the field.

MICHAEL SNYDER
Professor and Chair of Genetics; Director, Stanford Center for Genomics and Personalized Medicine, Stanford University

AMY SEHNERT
Medical Director, GRAIL, Inc.

JOHN D. MCPHERSON
Professor, Deputy Director and Associate Director for Basic Science, UCD Comprehensive Cancer Center; Professor, Department of Biochemistry and Molecular Medicine, University of California Davis

ROMAN YELENSKY
EVP of Bioinformatics and Sequencing, Gritstone Oncology

SYNOPSIS

DAY 1 – Strategy, Technology and Analysis Methods

- Nanopore sequencing
- Library preparation
- DNA amplification
- ChIP-seq
- Whole genome sequencing
- Targeted resequencing
- Exome sequencing
- De novo genome assembly
- Single-cell genomics

DAY 2 – Applications of NGS

- Challenges of clinical implementation
- Personalized medicine
- Clinical diagnostics
- Data interpretation
- Targeted therapy
- Genetic screening
- Genotyping
- Biomarker discovery
- Gene expression profiling

CONFIRMED SPEAKERS

MICHAEL SNYDER
Professor and Chair of Genetics; Director, Stanford Center for Genomics and Personalized Medicine, Stanford University

SARA GOODWIN
Technology Development Manager, Cold Spring Harbor Laboratory

JAMES EBERWINE
Elmer Holmes Bobst Professor of Systems Pharmacology and Translational Therapeutics, University of Pennsylvania Perelman School of Medicine

JE LEE
Assistant Professor, Cancer Centre, Cold Spring Harbor Laboratory

MASAYOSHI ITOH
Senior Scientist, Division of Genomic Technologies (DGT), RIKEN Center for Life Science Technologies (CLST)/ Coordinator, RIKEN Preventive Medicine and Diagnostics Innovation Program (PMI), Japan

JINGYUE JU
Samuel Ruben-Peter G. Viele Professor of Engineering; Professor of Chemical Engineering and Pharmacology; Director, Center for Genome Technology & Biomolecular Engineering, Columbia University

JOHN D. MCPHERSON
Professor, Deputy Director and Associate Director for Basic Science, UCD Comprehensive Cancer Center; Professor, Department of Biochemistry and Molecular Medicine, University of California Davis

ROMAN YELENSKY
EVP of Bioinformatics and Sequencing, Gritstone Oncology

AVNI SANTANI
Director, Clinical Laboratories, Strategic Partnerships and Innovation, Center for Applied Genomics, The Children's Hospital of Philadelphia; Assistant Professor of Clinical Pathology, Perelman School of Medicine, University of Pennsylvania

BIRGIT FUNKE
Associate Professor of Pathology, Massachusetts General Hospital/Harvard Medical School

LISA EDELMANN
Associate Professor, Executive Director, Mount Sinai Genetic Testing Laboratory, Icahn School of Medicine at Mount Sinai

AMY SEHNERT
Medical Director, GRAIL, Inc.

SHENG LI
Assistant Professor, The Jackson Laboratory for Genomic Medicine, The Jackson Laboratory Cancer Center, Connecticut

MIKE MAKRIGIORGOS
Professor of Radiation Oncology, Dana Farber Cancer Institute and Harvard Medical School

TAE LEE (Track Chair)
Investigator – Single Cell Genomics, GlaxoSmithKline Pharmaceuticals

VIPUL BHARGAVA
Senior Scientist, Janssen

BERNHARD ZIMMERMANN
Senior Director of Research and Development, Natera, Inc.

NEIL BARTH
Chief Medical Officer, Veracyte, Inc.

PATRIK VITAZKA
Director Clinical Genetics & Genomics, Biomarker Technologies, Bristol-Myers Squibb

SUMIT MIDDHA
(Track Chair)
Principal Computational Biologist, Memorial Sloan Kettering Cancer Center

GENEPEEKS (Reserved)
Senior Representative

MICKEY WILLIAMS
(Reserved)
Director, Molecular Characterization Laboratory, National Cancer Institute

EMMA BOWDEN
Research Advisor, Genomics and Bioinformatics, Oncology Research, Eli Lilly and Company

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8:00-8:50 Registration & Refreshments

8:50-9:00 **Global Engage Welcome Address and Morning Chair's Opening Remarks**

9:00-9:40

KEYNOTE ADDRESS:

MICHAEL SNYDER

Professor and Chair of Genetics; Director, Stanford Center for Genomics and Personalized Medicine, Stanford University

Managing Health and Disease Using Big Data

- Genome Sequencing can be used to predict disease risk
- Longitudinal omics profiles can be used to follow health and disease
- Wearables provide useful phenotypic information and can catch early disease onset

9:40-10:15

JAMES EBERWINE

Elmer Holmes Bobst Professor of Systems Pharmacology and Translational Therapeutics, University of Pennsylvania Perelman School of Medicine

Live Single Cell and Subcellular Genomics and Functional Genomics

- RNA-seq of single live aged human neuronal cells that have been isolated from neurosurgically resected tissue
- Genomics of subcellular domains shows regulation of subcellular biology to produce a coordinated cellular response
- Single cell functional genomics highlights the role of the transcriptome in the complex orchestration of the symphony of cellular regulation

10:15-10:45

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Nick Best at sponsorship@globalengage.co.uk

10:45-11:55 Morning Refreshments / Even Numbered Poster Presentations / Scheduled One-to-One Meetings

11:55-12:20

SARA GOODWIN

Technology Development Manager, Cold Spring Harbor Laboratory

Rapid structural event characterization of clinical cancer samples on the Oxford Nanopore MinION

Structural events (SVs) are widely recognized as contributing to cancer pathogenesis, patient prognosis and therapeutic response. DNA sequencing can provide molecular cytogenetic information, which in turn provides improved patient classification and can direct sub-type specific therapies. Despite recent advancements in Next-Generation Sequencing (NGS) approaches, clinical genetic sequencing often takes weeks before actionable results are generated due to the substantial investment in infrastructure required for most sequencing pipelines. The Oxford Nanopore MinION device can provide clinicians with a tool to generate rapid low-coverage structural variation profiles, equivalent to cytogenetic examination in a point-of-care setting. We have developed a pipeline for generating copy number variant (CNV) profiles from clinical cancer samples in 24 hours from purified DNA to analysis. Using clinically derived acute myeloid leukemia (AML) samples model we have been able to generate >500k short reads on during a single MinION run. Sequencing is followed by CNV analysis by Ginkgo. The profiles generated are virtually identical to CNVs profiles derived from both karyotypes and in MiSeq sequencing. Upcoming advancements in the nanopore chemistry will be able to provide sufficient through put to detect important translocation and inversion events in addition to CNVs. The low overhead cost and rapid turnaround time make the MinION a competitive option for point-of-care sequencing. With the added benefit of long read methods the MinION is well suited for clinical SV profiling.

12:20-12:45

JINGYUE JU

Samuel Ruben-Peter G. Viele Professor of Engineering; Professor of Chemical Engineering and Pharmacology; Director, Center for Genome Technology & Biomolecular Engineering, Columbia University

Single molecule electronic DNA sequencing by synthesis using polymer-tagged nucleotides and nanopore detection

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12:45-1:15

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1:15-2:15 Lunch

2:15-2:40

JE LEE

Assistant Professor, Cancer Centre, Cold Spring Harbor Laboratory

Developing in situ sequencing chemistry platforms for clinical applications

- It is challenging to identify functional biomarkers through quantifying molecular and genetic signatures without high-resolution spatial or architectural information.
- Modern NGS-based methods enable limited spatial and temporal reconstruction of singe cell variations, tissue heterogeneity, and cell history tracking; however, they suffer from various drawbacks in terms of the sensitivity, the scalability, and the applicability in translational medicine.
- We will describe a progress in Fluorescent In Situ Sequencing (FISSEQ) for studying astrocytoma in vitro and in patients, fundamental limitations, and approaches for genome-wide FISSEQ tomography in model organisms. Finally, we will discuss approaches to update clinical histology using NGS chemistry, so that sequential staining can generate practical gene expression cluster- and mutation-specific atlases in a clinical setting.

2:40-3:05

MASAYOSHI ITOH

Senior Scientist, Division of Genomic Technologies (DGT), RIKEN Center for Life Science Technologies (CLST)/ Coordinator, RIKEN Preventive Medicine and Diagnostics Innovation Program (PMI), Japan

Cap trapper technologies and applications, Cap Analysis of Gene Expression (CAGE) and FANTOM5 project

The cap trapper is a reliable technology based on simple chemical reaction to capture cap structure at the 5' end of matured mRNAs. Based on the technology, we have developed full length cDNA preparation method and CAGE for the analysis of comprehensive transcription start sites and for measurement of promoter and enhancer activities. Here, I will introduce the cap trapper based transcriptome analysis technologies involving CAGE, full length mRNA analysis using NGS, and the findings of FANTOM5 project.

3:05-3:30

RESERVED

MICKEY WILLIAMS

Director, Molecular Characterization Laboratory, National Cancer Institute

3:30-4:00

MIKE MAKRIGIORGOS

Professor of Radiation Oncology, Dana Farber Cancer Institute and Harvard Medical School

Mutation enrichment combined with high resolution melting for no-cost pre-screening prior to targeted re-sequencing

With the continuous reduction in sequencing costs, sample preparation for targeted re-sequencing presents a bottle-neck to highly efficient sequencing. We provide a novel sample preparation method that (a) provides higher sensitivity for detection of rare mutations; and (b) reduces the cost of both sample preparation and re-sequencing. The method is based on implementation of NaME-PrO, a new mutation enrichment method, together with high resolution melting. Application in circulating DNA from clinical cancer samples will be presented.

4:00-4:50 Afternoon Refreshments / Odd Numbered Poster Presentations / Scheduled One-to-One Meetings

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CLINICAL DIAGNOSTICS

TRACK CHAIR:
TAE LEE
Investigator – Single Cell Genomics, GlaxoSmithKline Pharmaceuticals

4:50-5:15

BERNHARD ZIMMERMANN
Senior Director of Research and Development, Natera, Inc.
Title – TBC

5:15-5:40

NEIL BARTH
Chief Medical Officer, Veracyte, Inc.

5:40-6:05

SENIOR REPRESENTATIVE
GenePeeks, Inc.
Topic: NGS for preconception genetic screening
Title – TBC

6:05 Chair's Closing Remarks and End of Day One / Networking Drinks Reception

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8:00-8:40 Refreshments

8:40 **Morning Chair: Sumit Middha,** Principal Computational Biologist, Memorial Sloan Kettering Cancer Center

8:40-9:15

KEYNOTE ADDRESS:

JOHN D. MCPHERSON

Professor, Deputy Director and Associate Director for Basic Science, UCD Comprehensive Cancer Center; Professor, Department of Biochemistry and Molecular Medicine, University of California Davis

Precision Medicine – Are we on target?

Precision Medicine (PM) promises to align individual patients with optimal therapy by considering specific genomic variation and alterations. This is currently best exemplified in oncology where the landscape of somatic mutations in an individual's tumor can be used to guide therapeutic drug selection targeting specific mutated genes or altered pathways. Advances in sequencing technology now make the comprehensive identification of somatic mutations very feasible. Dramatic responses to targeted therapy are seen but inconsistencies exist with relapse is frequent. We must build on the successes but must also acknowledge that the mechanisms underlying disease are recalcitrant to linear thinking of individual genes. A more holistic approach is needed to gain insight into the complex interplay of mutations and pathways within each individual tumor or disease state.

9:15-9:40

ROMAN YELENSKY

EVP of Bioinformatics and Sequencing, Gritstone Oncology

Turning tumor mutations into personalized cancer therapies

Each patient's tumor genome is different from their normal cells and this difference creates tumor-specific neo-antigens (TSNAs), which can be targeted by the immune system. Gritstone Oncology is exploiting this tumor vulnerability in a therapeutic immunization strategy. The approach includes NGS to identify candidate TSNAs, proteomics and machine learning to predict which TSNAs can activate T cells, the manufacture of a personalized TSNA-based vaccine, and delivery in a combination regimen.

9:40-10:10

VIPUL BHARGAVA

Senior Scientist, Janssen

Molecular characterization of circulating tumor cells (CTCs) to elucidate drug resistance mechanisms.

Prostate cancer represents the most common malignancy in males. Two androgen receptor (AR)-targeted therapies, enzalutamide and abiraterone acetate, have been approved for treatment of metastatic castration resistant prostate cancer (CRPC). Many patients respond to these agents; however, they ultimately progress and acquire resistance to these therapies. To characterize resistant phenotypes that emerge following treatment with antiandrogens, we isolated and characterized circulating tumor cells (CTCs) from CRPC patients at varying timepoints on therapy. By comparing drug-sensitive and drug-resistant CTC samples, we identified dysregulated signaling pathways that could confer resistance to AR-targeted therapies. Experiments in cell culture models demonstrate that these pathways do indeed mediate resistance to enzalutamide. Importantly, we demonstrated that CTC sequencing from drug resistant patients could facilitate the development of effective patient centric therapeutics.

10:10-10:35

AMY SEHNERT

Medical Director, GRAIL, Inc.

Blood-based assays for early cancer detection,
Title – TBC

10:35-11:30 Morning Refreshments / Odd Numbered Poster Presentations / Scheduled One-to-One Meetings

11:30-12:00

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12:00-12:25

EMMA BOWDEN
Research Advisor, Genomics and Bioinformatics, Oncology Research, Eli Lilly and Company

12:25-12:50

PATRIK VITAZKA
Director Clinical Genetics & Genomics, Biomarker Technologies, Bristol-Myers Squibb

Using NGS for clinical biomarker development,
Title – TBC

12:50-1:50 Lunch

COMPLEXITIES IN DATA INTERPRETATION CASE STUDIES

1:50-2:15

AVNI SANTANI
Director, Clinical Laboratories, Strategic Partnerships and Innovation, Center for Applied Genomics, The Children's Hospital of Philadelphia; Assistant Professor of Clinical Pathology, Perelman School of Medicine, University of Pennsylvania

Integration of NGS data in clinical diagnosis of rare pediatric disorders

Prof. Santani will share insights in the integration of NGS data in clinical diagnostics, using exome sequencing as an example. She will address the development of a comprehensive interpretation pipeline for exome sequencing, discuss challenges with maintaining compliance in the dynamic genomics space, and present results from exome sequencing.

2:15-2:40

BIRGIT FUNKE
Associate Professor of Pathology, Massachusetts General Hospital/Harvard Medical School

Standardizing clinical genomic result interpretation in the NGS era: ClinGen's frameworks for curating variant pathogenicity and gene-disease associations for inherited cardiovascular disorders

- Adaptation of the ACMG/AMP variant classification rules for inherited cardiomyopathy
- Application of a structured matrix to evaluate gene-disease relationships for hypertrophic cardiomyopathy

2:40-3:05

LISA EDELMANN
Associate Professor, Executive Director, Mount Sinai Genetic Testing Laboratory, Icahn School of Medicine at Mount Sinai

281 lessons learned from scaling NGS-based expanded carrier screening

Pan-ethnic comprehensive carrier screening has the highest yield when a sequence-based approach is used to interrogate the coding regions of genes with supplementation by additional methodologies for regions of the genome in which sequencing is not adequate. The infrastructure necessary to build a high-throughput next generation sequencing (NGS) carrier screening panel with a rapid turnaround time includes an automated workflow, extensive sequencing capacity and a multifaceted bioinformatics solution that allows for batch analysis, export and reporting through the LIMS. Through extensive literature and database review, physician input and population genetics research, we selected a panel of 281 autosomal recessive and X-linked diseases for inclusion in our expanded carrier screen. However, we are able to run to return data on any subset of genes within the panel. To date, the laboratory has performed testing on more than 100,000 samples and depending on the size of the panel, there is between 4 and 64% positive rate for at least one pathogenic variant with 9.2% representing novel frameshifts, nonsense variants or splice site changes. The rate of carrier couples identified with the 281 gene panel is about 1 in 60 inclusive of X-linked carrier. We have also identified about 45 individuals who are expected to manifest symptoms of disease and another 45 with incompletely penetrant homozygous or compound heterozygous genotypes. Our data indicate that expanded screening using an NGS sequencing strategy to identify carriers of autosomal recessive and X-linked disorders is a more effective method for carrier identification than founder-based genotyping and current technologies with customized and automated workflows allow for high-throughput workflow with relatively rapid turn-around-times that are essential in a reproductive setting.

3:05-3:30 Afternoon Refreshments / Even Numbered Poster Presentations

3:30-3:55

RESERVED

EKTA KHURANA

Assistant Professor of Computational Genomics, Weill Cornell Medical College

Title - TBC

3:55-4:20

SHENG LI

Assistant Professor, The Jackson Laboratory for Genomic Medicine, The Jackson Laboratory Cancer Center, Connecticut

Beyond the genome - decode the leukemia epigenome dynamics via a novel algorithm and high-throughput sequencing technology

High-throughput sequencing profoundly expands the potential for comprehensive understanding of cancer dynamics on whole-genome, transcriptome, and epigenome landscape. We developed a series of computational methods and software – methylKit, edmr, and methclone – for DNA methylation sequencing data analysis, to comprehensively detect the significant DNA methylation aberration and epigenetic heterogeneity during disease progression. We applied these approaches to study the epigenetic heterogeneity and dynamics of acute myeloid leukemia (AML) relapse - a longitudinal research of the allelic diversity of the global DNA methylation for a cohort of 138 AML patients. We found that epigenetic allele burden was linked to inferior clinical outcome. Epigenetic dynamics was related to hypervariable transcriptional regulation. This research demonstrates that epigenetic heterogeneity as an important feature of AML with functional and clinical impacts.

4:20 Conference Close

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WORKSHOP

tataabiocenter

2 Day Course: MIQE – How to get Good Quality Control in q PCR

Are you working with qPCR? Do you have control of the quality in all the steps of the analysis procedure? This course will go deep into the MIQE guidelines, describe the important steps in RNA and DNA analysis with qPCR and how you should work to fulfil the guidelines. To follow the guidelines will give you a better control of the quality of your results. The course is theoretical with a few practical computer-based exercises. The course content includes:

Background about the MIQE guidelines
- What are the MIQE guidelines?
- Why are they important?

What to think about when doing experimental design

How to do nucleic acid extraction and quality control of extracts
- Different approaches for nucleic acid extraction
- How can we check the quality of extracted samples?
- How do we identify inhibitory samples?

The Reverse Transcription reaction
- Different priming strategies for reverse transcription
- Pros and cons for different strategies

How to do primer and probe design
- How to search for gene sequences
- Which are the factors that affect design?
- How do we avoid primer dimer formation?
- Other important considerations for primer design
- How to design hydrolysis probes
- Practical exercises in primer design

How to optimize qPCR assays
- Which factors affect the PCR?
- Which factors can be optimized?

How to validate qPCR assays, LOD and LOQ
- How to determine LOD and LOQ
- Precision estimation
- Which controls to use

Data analysis
- How does qPCR software process the data?
- How to evaluate curves and set threshold

Normalization
- Different ways to normalize
- How to find stable reference genes

How to do relative quantification
- Quantification methods and equations
- How to interplate calibration

Absolute quantification strategies
- What is a suitable standard?
- How to do absolute quantification

Mikael Kubista
Course Leader
CEO, TATAA Biocenter & Head of Department, BTU, CAS

Dr Kubista is the head of the department of gene expression at the institute of Biotechnology of the Czech Academy of Sciences, and founder and CEO of the TATAA Biocenter (www.tataa.com). He was one of the pioneers contributing to the development of quantitative real-time PCR (qPCR) and introduced qPCR for single cell expression profiling. He led the development of reagents for high throughput single cell expression profiling and quality control at TATAA. He also developed qPCR tomography for intracellular expression profiling. Kubista co-authored the Minimum Information for Publication of Quantitative. Real-Time PCR Experiments (MIQE) guidelines, was partner of the SPIDIA project, and is member of the CEN and ISO workgroups drafting the forthcoming guidelines on pre-analytics.

Course Information
Dates: 27th & 28th July 2017
Cost Academic: $499.00
Cost Industry: $699.00

WORKSHOP

microfluidic ChipShop

Monday, July 24th – 2:00pm-6:00pm
Singh Centre for Nanotechnology,
3205 Walnut St, Philadelphia, PA 19104, USA
Cost: $200.00

Microfluidics and Lab-on-a-chip technologies for commercial product development: strategies, technologies, markets and applications

The course will provide a broad overview of Lab-on-a-Chip (LOC) technologies as an enabling technology for new product development in diagnostics and the life sciences. Emphasis is put on the complete development process for commercial microfluidics-enabled products, covering aspects of development strategies, manufacturing technologies, application cases, markets as well as aspects of commercialisation and latest trends in the academic world. Recent product examples will be presented as well as lessons learned during all stages of the development and commercialization process of LOC-enabled devices.

Learning Objectives

- Understand the role of microfluidics technology in the development of new products.
- Learn about development and modularisation strategies in product development.
- Understand different microfabrication methods for low and high volume production.
- Understand economic aspects in the development and manufacturing of Lab-on-a-chip devices and systems.
- Learn about examples of successful and unsuccessful microfluidic product introductions.
- Understand the current state of the markets and obstacles in the commercialization process.
- Get an overview on current trends in LOC research.

Topics and Course Organisation

- Introduction
- Challenges in product development
- Case studies
- Commercialization issues
- Materials and microfabrication methods
- Application and products
- Design Advice
- Conclusions

Holger Becker
Course Leader
Co-founder and CSO, microfluidic ChipShop GmbH

Dr Holger Becker is co-founder and CSO of microfluidic ChipShop GmbH. He obtained physics degrees from the University of Western Australia/Perth and the University of Heidelberg and obtained a PhD in Physics from University Heidelberg in 1995. Between 1995 and 1997 he was a Research Associate at Imperial College with Prof. Andreas Manz. In 1998 he joined Jenoptik Mikrotechnik GmbH. Since then, he founded and led several companies in the field of microsystem technologies in medicine and the life sciences, for which he received various awards. He led the Industry Group of the German Physical Society between 2004 and 2009, and is the current chair of the SPIE "Microfluidics, BioMEMS and Medical Microsystems" conference, co-chair of MicroTAS 2013 and Industrial Committee Chair for MicroTAS 2016. He serves on the Editorial Board of "Lab-on-a-Chip", "Microelectronic Engineering" as well as acting as a regular reviewer of project proposals on a national and international level.

WORKSHOP

Monday, July 24th 2017 - 9:00am-1:00pm
Singh Centre for Nanotechnology,
3205 Walnut St, Philadelphia, PA 19104, USA
Cost: $200.00

qPCR & Digital PCR Workshop

Innovations in digital nucleic acid amplification

Introduction

- Digital PCR and related statistics
- Overview on commercial systems for digital nucleic acid amplification

Innovations

- Digital nucleic amplification using standard laboratory devices
- Microfluidic integration of droplet generation, amplification and detection into one single device
- Mediator Probe PCR for improved signal to–noise–ratio, multiplexing and SNP detection
- Protocols for amplification-compatible lysis of single cells and bacteria in droplets

Life lab/Demonstrators

- Microfluidic chip for droplet generation, digital amplification and detection based on standard laboratory devices
- Microfluidic integration of a complete workflow into one single cartridge: From nasal swab sample to digital amplification

Dr. Felix von Stetten
Associate Director of Hahn-Schickard

WORKSHOP

Monday, July 24th 2017 – 2:30pm-6:00pm
Singh Centre for Nanotechnology,
3205 Walnut St, Philadelphia, PA 19104, USA
Cost: $200.00

NGS Tech & Applications Workshop

Basic Principles of NGS Assay Design and Validation (Avni Santani)
This talk will review the basic methodologies used in current NGS based diagnostic testing including enrichment, sequencing, analysis for germline testing. Emphasis will be placed on assay design and compliance including pre-analytic, analytical and post analytical phases and test validation.

Basic principles of informatics (Matt Lebo)
This talk is focused on the informatics approaches used in NGS analyses and interpretation. Specific emphasis will revolve around the clinical implementation of these assays. Topics discussed will include data processing steps, variant detection, annotation, filtration, and interpretation of genomic variants. Examples of software applications and important considerations will also be presented.

Precision Medicine using NGS (Jennifer Morrissette)
This talk will review the complex interpretations of clinical cancer sequencing. Topics discussed will include the utility of fine needle aspirations for diagnostic specimens, tumor heterogeneity, the effect of amplification on variant detection, mutational tumor burden and interpretation of potentially germline variants in somatic sequencing. The connection of genomics with precision medicine will be discussed in the context of clinical pathways in oncology inclusive of genomic results.

Avni Santani
Director, Clinical Laboratories, Strategic Partnerships and Innovation, Center for Applied Genomics, The Children's Hospital of Philadelphia; Assistant Professor of Clinical Pathology, Perelman School of Medicine, University of Pennsylvania

Matthew Lebo
Director of Bioinformatics, Assistant Laboratory Director, Partners Healthcare, Personalized Medicine, Laboratory for Molecular Medicine; Instructor of Pathology – Brigham and Woman's Hospital and Harvard Medical School

Jennifer Morrissette
Assistant Professor of Clinical Pathology and Laboratory Medicine, University of Pennsylvania Perelman School of Medicine, Clinical Director, Center for Personalized Diagnostics Scientific Director, Clinical Cytogenetics

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