Global Engage

Digital PCR

NGS

Microfluidics

qPCR

4BIO SUMMIT: USA

SAN FRANCISCO, USA

September 13-14 2018

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WARM WELCOME

Global Engage

Global Engage is pleased to announce the **4BIO Summit: USA**. Combining the **4th qPCR & Digital PCR Congress** and the **3rd Microfluidics Congress**, this summit will bring together over 180 industry and academic experts and will provide an interactive networking forum as well as the opportunity to keep up to date with the cutting edge of research in your field.

qPCR & Digital PCR Congress

Designed for academic experts working in areas such as molecular biology/diagnostics, liquid biopsies, gene expression, genomics, biomarkers, pathogen detection, and miRNA analysis, these tracks 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, clinical applications, microbiology, and other novel applications. With increasing numbers of real-time PCR users purchasing digital PCR due to the reduction in its cost, absolute quantification, improved sensitivity, precision and greater robustness; and with the qPCR and Digital PCR market predicted to grow to $4.94 billion by 2021, this conference provides a timely opportunity to learn first-hand about dPCR whilst also keeping up to date with latest developments and strategies in qPCR. The conference will provide an interactive networking forum to both further develop and answer your queries through a vibrant exhibition room full of technology providers showcasing their technologies and other solutions, poster presentation sessions, and expert led case study presentations from a 30-strong speaker faculty examining topics on 3 separate tracks.

Microfluidics Congress

At the intersection of engineering, physics, chemistry, nanotechnology and biotechnology, microfluidics holds great promise for the advancement of human healthcare. As a rapidly developing are of research, this technology looks to revolutionize the way patients are diagnosed, monitored and treated, and is unlocking the potential for reduced reagent consumption and thus, cost. With two dedicated tracks, these interactive sessions bring together experts working across multiple key fields in microfluidics, and will showcase case studies examining the latest advancements in the development of microfluidic devices and their application in diagnostics and disease monitoring and detection. Talks will cover lab-ona- chip fabrication, development of paper based systems, and droplet, digital and acousto-microfluidics, as well as pointof-care diagnostics, single cell analysis, circulating tumor cell capture and analysis, high throughput screening, and next generation micro and nanofluidics. This meeting will allow you to keep up to date with the cutting edge of research and the opportunity to make lasting connections with academics, entrepreneurs and businesses in your field.

NGS Research

Numerous presentations at both Congresses incorporate the important role that sequencing plays, and how it is being used to compliment the other technologies.

EXPERT SPEAKERS INCLUDE:

CARL WITTWER
Professor of Pathology, University of Utah

HESTIA MELLERT
Director, Molecular Development, Biodesixl

HANLEE JI
Associate Professor and Senior Associate Director, Genome Technology Center, Stanford University

LUKE LEE
Professor of Bioengineering, UC Berkeley

ADELA BEN-YAKAR
Professor, University of Texas at Austin

JUAN SANTIAGO
Professor, Sanford University

CONFERENCE SYNOPSIS

DAY 1 / TRACK 1
DIGITAL PCR: POSSIBILITIES & OPPORTUNITIES

- 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 / TRACK 2
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 1 / TRACK 3
MICROFLUIDICS: STRATEGY & TECHNOLOGY

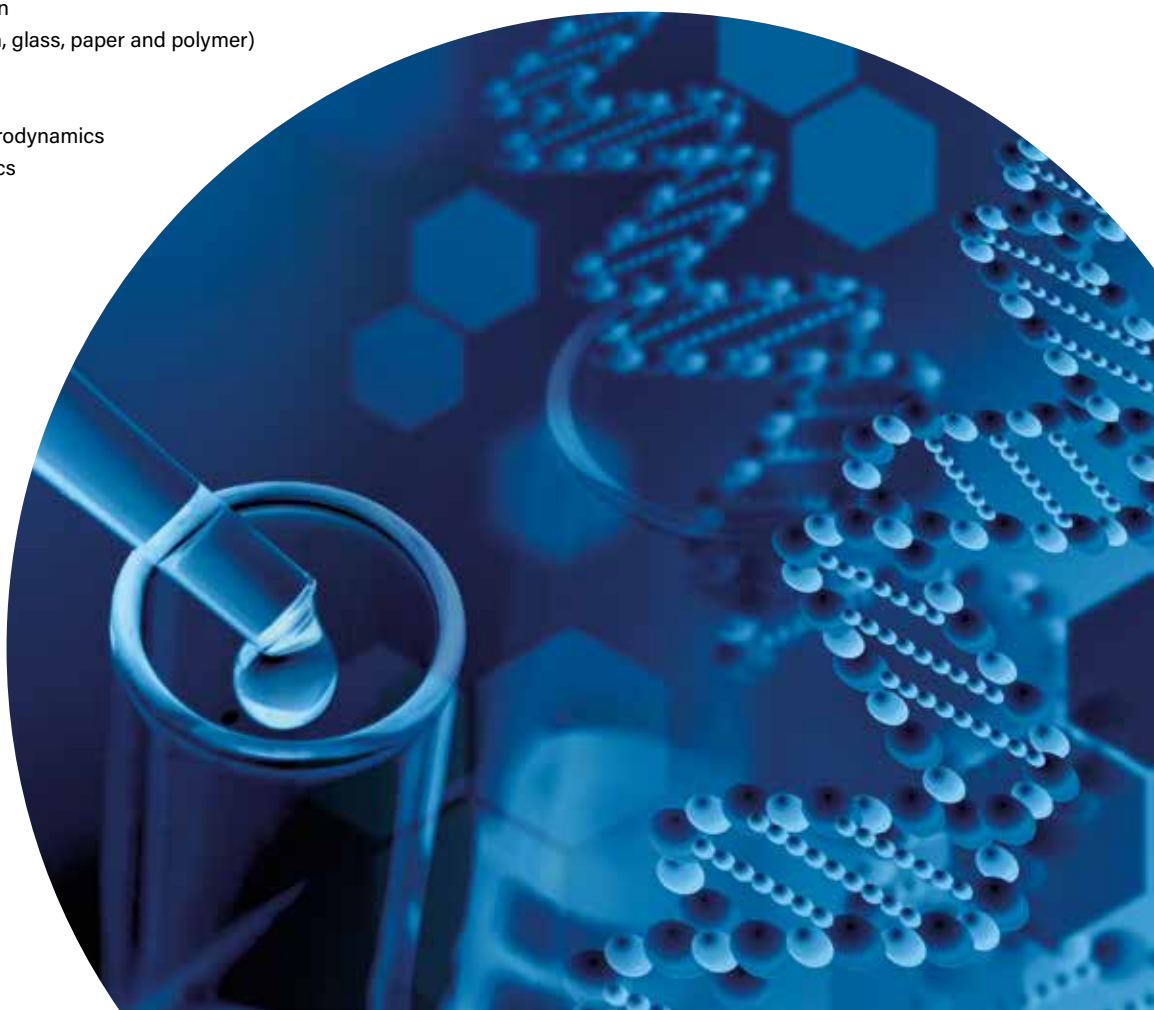
- Lab-on-a-Chip microfabrication
- Substrate development (silicon, glass, paper and polymer)
- 3D printing
- Digital microfluidics
- Electrokinetics and electrohydrodynamics
- Acoustofluidics and Optofluidics
- Droplet microfluidics
- Centrifugal microfluidics
- Advances in MEMs

DAY 2 / TRACK 1
QPCR / DIGITAL PCR: HEALTHCARE CASE STUDIES

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

DAY 2 / TRACK 2
MICROFLUIDICS: ANALYSIS & DIAGNOSTIC APPLICATION CASE STUDIES

- Point-of-care diagnostics
- Molecular diagnostics
- CTC capture and analysis
- High-throughput screening
- Disease monitoring
- Single cell and cellular signalling analysis
- DNA analysis in nanofluidics



CARL WITTWER
Professor of Pathology, University of Utah

JOEL TELLINGHUISEN
Emeritus Professor, Vanderbilt University

OLIVIER THAS
Professor of Biostatistics at Ghent University, Belgium, Honorary Professor at the University of Wollongong, Australia

SETH CROSBY
Director, Genome Technology Access Center, Washington University in St Louis

SENIOR REPRESENTATIVE
Stilla Technologies

HESTIA MELLERT
Director, Molecular Development, Biodesix

HIMANSHU SETHI
Associate Director, R&D, Natera

KEITH PEDEN
Chief, Laboratory of DNA Viruses, FDA

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

DAN WEISENBERGER
Assistant Professor of Research, University of Southern California

YUAN CAO
Postdoctoral Research Fellow, Rutgers New Jersey Medical School

JEAN-CHRISTOPHE AVARRE
Head of the High Throughput qPCR Platform and Research Group Leader, University of Montpellier, France

WILLIAM LEENDERS
Associate Professor, Radboud UMC, The Netherlands

YU LI
Molecular Diagnostics and Genomics Team, CDC

HANLEE JI
Associate Professor and Senior Associate Director, Genome Technology Center, Stanford University

JULIANN CHMIELECKI
Associate Director, Translational Science, AstraZeneca

RACHEL TAM
Senior Scientist, Genentech

JOHN MARTIGNETTI
Professor, Icahn School of Medicine at Mount Sinai

TIMOTHY ROSE
Professor and Co-Director of the Center for Global Infectious Disease Research, University of Washington and Seattle Children's Hospital

TARA SIGDEL
Assistant Professor, University of San Francisco

MARIE KORABECNA
(Chair)
Associate Professor, Charles University, Czech Republic

FENYONG LIU
Professor, Infectious Diseases, University of California Berkeley

MARINE JEANMOUGIN
Postdoctoral Research Fellow, Department of Molecular Oncology, Institute for cancer research, Oslo University hospital

KEITH JEROME
Professor, Fred Hutchinson Cancer Research Center and University of Washington

RICHARD FAIR
Professor, Duke University

ADELA BEN-YAKAR
Professor, University of Texas at Austin

DAEYON LEE
Professor of Chemical and Biomolecular Engineering, University of Pennsylvania

GREG NORDIN
Professor, Brigham Young University

TODD THORSEN
Technical Staff, MIT Lincoln Laboratory

LUKE LEE
Professor of Bioengineering, UC Berkeley

JUAN SANTIAGO
Professor, Stanford University

KEVIN DORFMAN
Minnesota University

BRIAN CUNNINGHAM
Professor, University of Illinois at Urbana-Champaign

ANDERSON SHUM
Associate Professor, University of Hong Kong

JAMES STURM
Stephen R. Forrest Professor of Electrical Engineering, Princeton

ASHLEIGH THEBERGE
Assistant Professor, University of Washington

CHEN CHIA-HUNG
National University of Singapore

JEFF WANG
Professor of Mechanical and Biomedical Engineering, John Hopkins University

SUVAJYOTI GUHA
Staff Fellow: Mechanical Engineer, FDA

PIOTR GARSTECKI
Professor, CTO, Polish Academy of Science

SINDY TANG
Assistant Professor, Stanford University

8:00-8:50 Registration & Refreshments

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

QPCR & DIGITAL PCR

9:00-9:40

KEYNOTE ADDRESS:
CARL WITTWER
Professor of Pathology, University of Utah
Rapid diagnostics – extreme PCR and high speed melting

- PCR can be performed in 15-30 seconds with good specificity, efficiency, and yield.
- Genotyping by melting analysis can be performed in <5 seconds.
- The advantages of rapid point-of-care diagnostics will change the balance of testing away from reference labs in the future.

9:40-10:20

KEYNOTE ADDRESS:
KEITH JEROME
Professor, Fred Hutchinson Cancer Research Center and University of Washington
Digital PCR in clinical virology

Digital PCR offers advantages over qPCR suggesting it might prove useful in clinical virology laboratories. We have applied the Bio-Rad droplet digital PCR system to several diagnostic virology applications. These studies confirm the precision of dPCR quantitation, and reveal that dPCR is more resistant to inhibition than traditional qPCR. The precision of dPCR is especially useful in ratiometric assays, such as for the diagnosis of chromosomally integrated HHV-6. Conversely, for applications such as cytomegalovirus quantitation, the improved precision does not clearly translate to clinical benefit. Precise quantitation may be more useful in research studies, such as evaluation of the HIV reservoir during eradication efforts. Current dPCR instruments have lower throughput than more mature qPCR platforms, and therefore traditional qPCR continues to play a role in diagnostic virology.

10:20-10:50

SPONSORED PRESENTATION:
SENIOR REPRESENTATIVE
Bio-Rad
Title TBC

MICROFLUIDICS

9:00-9:40

KEYNOTE ADDRESS:
RICHARD B. FAIR
Lord-Chandran Professor of Engineering, Duke University
Digital Microfluidics as a Platform for Biomedical Research and Rapid Diagnostics

Digital microfluidic lab-on-a-chip technology has been shown to be a competitive platform for developing diagnostic protocols that impact patient care. In most diagnostic applications, a key challenge has been the on-chip preparation of physiological samples. In this talk we present methods for selectively extracting target cells from physiological samples for the purpose of rapid identification. We also present methods for on-chip processing of nucleic acid molecules for use in qPCR and DNA sequencing. Finally, results from studies of the application of digital microfluidics to biomedical research are discussed, which include synthetic biology and epigenetics.

9:40-10:20

KEYNOTE ADDRESS:
ADELA BEN-YAKAR
Professor, University of Texas at Austin
Topic: Developing a large scale microfluidic system for high-throughput screening of C. elegans disease models and regeneration studies

10:20-10:50

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10:50-12:00 Morning Refreshments / Poster Presentations / One-to-One Meetings

DIGITAL PCR: POSSIBILITIES & OPPORTUNITIES

12:00-12:25

JOEL TELLINGHUISEN

Emeritus Professor, Vanderbilt University

Is precise partition volume (monodispersity) required for good results in dPCR? Actually, no!

Most dPCR methods and instrument manufacturers have placed heavy emphasis on monodispersity in partition volume, the goal being to decrease volume variability to as close to zero as possible. Emphasizing this goal can add significantly to instrument expense and is completely unwarranted, as is shown through theoretical considerations and Monte Carlo simulations. For example, even 50% volume dispersion leads to only ~10% loss of precision for average copy number per partition □ < 1 and can even improve precision for □ > 4. Such large polydispersity does lead to significant bias, but this bias can be corrected easily through calibration with known reference materials. Accordingly, establishing reliable references should be a priority in dPCR going forward, with higher throughput and lower expense achievable in instrumentation by relaxing monodispersity demands.

12:25-12:50

OLIVIER THAS

Professor of Biostatistics at Ghent University, Belgium, Honorary Professor at the University of Wollongong, Australia

Data Analysis Pipelines and Tools for dPCR Experiments

Absolute quantification of targets based on the digital dPCR obervations, typically relies on the Poisson assumption. Whereas the calculations are straightforward for a single dPCR run on a single sample, correct calculations become more complicated when replicated runs are available, or when copy number variation (CNV) is the focus. Moreover, computations should not only result in estimates of copy number of CNV, but standard errors or confidence intervals are also needed for reporting. Appropriate setting of the threshold is also important, as it may affect the results. In this talk I will give an overview of data analysis pipelines and easy-to-use applets that have been developed at Ghent University.

QPCR: STRATEGIES & DEVELOPMENTS

12:00-12:25

KEITH PEDEN

Chief, Laboratory of DNA Viruses, FDA

Topic: qPCR readouts for viruses

12:25-12:50

SETH CROSBY

Director, Genome Technology Access Center, Washington University in St Louis

16S - why not leverage ALL the hypervariable regions?

MVRSION is a computational system which exploits all nine 16S hyper variable regions. We use Fluidigm Juno to amplify and index the nine regions in up to 192 samples per run. These are sequenced and analyzed in parallel, using the MVRSION computational protocol. Both accuracy and economy exceed other methods, such a QIIME.

STRATEGY AND TECHNOLOGY IN MICROFLUIDICS

12:00-12:25

SUVAJYOTI GUHA

Staff Fellow: Mechanical Engineer, FDA

Overview of FDA's Regulatory Requirements: Medical devices

- Brief discussion about the regulatory requirements for medical devices
- Our 2018-2020 strategic priorities
- Brief discussion about some microfluidics specific examples
- Introduction to our microfluidics program

12:25-12:50

DAEYON LEE

Professor of Chemical and Biomolecular Engineering, University of Pennsylvania

Towards Commercialization of Microfluidic-based Particles for Biomedical Applications

The advent of microfluidics has led to unprecedented advances in the synthesis of functional particles for biomedical applications. The ability to precisely manipulate the flow of multiphasic fluids in microchannels enable production of highly uniform liquid droplets and gas bubbles with complex morphology. Despite these exciting development, there remains some key challenges that must be addressed to enable successful commercialization of these technologies. In this talk, I will discuss our recent contributions in producing "designer" microparticles for drug delivery, diagnostics and regenerative medicine applications. The importance of understanding and harnessing the fundamental interfacial phenomena to engineer the structure and functionality of these particles will be described. I will also discuss our recent efforts to scale-up the production of particles via parallelization in solvent-resistant microfluidic devices.

12:50-1:20

SPONSORED PRESENTATION:
SENIOR REPRESENTATIVE
Stilla Technologies
Title TBC

12:50-1:20

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12:50-1:20

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1:20-2:20 Lunch / One-to-One Partnering Meetings

2:20-2:45

HESTIA MELLERT

Director, Molecular Development, Biodesix

Development, Commercialization and On-market Improvement to Liquid Diagnostic Tests in Lung Cancer

Time to treatment can have significant impact on progression of lung cancer. However, multiple factors impact the delivery of molecular diagnostic test results from traditional tissue biopsies. This presentation will focus on the Biodesix GeneStrat test, which is a blood-based test that uses a series of ddPCR assays to detect DNA (EGFR, KRAS, BRAF) and RNA variants (EML4-ALK, ROS1, RET). In this report we will describe on-market test improvements as well as on-going feasibility and product development projects.

2:20-2:45

FRED KRAMER

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

Extraordinarily Sensitive, Multiplex PCR Assays that Assess the Abundance of Rare Mutations Associated with Cancer, Utilizing Liquid Biopsy Samples

PCR assays are the most rapid and least expensive way to assess the abundance of mutant DNA fragments present in liquid biopsies. Uniquely designed PCR primers, in combination with fidelity enhancing agents, enable the selective synthesis of amplicons from extremely rare mutant DNA fragments, without amplifying the far more abundant related wild-type DNA fragments. The inclusion of unique tag sequences on the 5´ ends of the primers, enable the amplicons generated from each mutant to be distinguished from each other by differently colored molecular beacon probes. Amplicons generated from different mutations that signify the same therapeutic approach can bear the same 5´-tag sequence. Consequently, frequent liquid biopsies that identify newly arisen mutations enable the care of each patient to be adjusted over time, improving outcomes.

2:20-2:45

GREG NORDIN

Professor, Brigham Young University

Miniaturizing 3D Printed Microfluidics: Status and Trends

While there is great interest in 3D printing for microfluidic device fabrication, the challenge has been to achieve feature sizes that are in the truly microfluidic regime (<100 µm). The fundamental problem is that commercial tools and materials have not been developed to address the unique needs of microfluidic device fabrication. Consequently, we have created our own stereolithographic 3D printer and materials that are specifically tailored to meet these needs. We show that flow channels as small as 18 µm x 20 µm can be reliably fabricated, as well as compact active elements such as valves and pumps. With these capabilities, we demonstrate highly integrated 3D printed microfluidic devices that measure only a few millimeters on a side, and that integrate to separate chip-to-world interfaces through high density interconnects (up to 88 interconnects per square mm) that are directly 3D printed as part of a device chip. These advances open the door to 3D printing as a replacement for expensive cleanroom fabrication processes, with the additional advantage of fast (30 minute), parallel fabrication of many devices in a single print run due to their small size.

2:45-3:10

DAN WEISENBERGER

Assistant Professor of Research, University of Southern California

DNA Methylation Analysis Using Digital MethyLight Technology

DNA methylation changes are frequently observed in all human cancers, and can be also identified in patient blood. Here we describe the development of Digital MethyLight technology, a digital PCR application of MethyLight, sensitively detecting DNA methylation in primary tissues and fluids. We have identified and quantitated single-molecule, cancer-specific DNA hypermethylation events in plasma and serum samples from patients with cancer. This technology has promise in cancer detection and surveillance.

2:45-3:10

HIMANSHU SETHI

Associate Director, R&D, Natera

Non-Invasive Cancer Recurrence Detection and Therapy Monitoring using a highly sensitive patient-specific multiplex PCR NGS-based assay

Liquid biopsy-based detection and monitoring of tumor-specific somatic mutations in cell-free DNA has great potential to improve patient care by detecting cancer early, assisting adjuvant therapy decision-making, determining treatment effects and assessing the need for follow-up intervention. We have developed a highly sensitive and specific novel approach to detect the presence and ability to quantify circulatory tumor DNA in plasma by looking for personalized cancer signatures in plasma. We recently described our ability to detect ctDNA presence longitudinally in patients with non-small cell lung cancer (NSCLC) and now have productized and validated this personalized approach for detection of tumor DNA in plasma for research use only (RUO).

2:45-3:10

MATTHEW BEGLEY (Reserved)

Professor, UC Santa Barbara

Topic: Advancing portable device manufacture for field applications utilizing 3D printing

3:10-3:40

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3:10-3:40

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3:10-3:40

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SENIOR REPRESENTATIVE

Elveflow

Title TBC

3:40-4:05

MARINE JEANMOUGIN

Postdoctoral Research Fellow, Department of Molecular Oncology, Institute for cancer research, Oslo University hospital

Standardization of DNA methylation droplet digital PCR for urine-based detection of bladder cancer

Droplet digital PCR (ddPCR) has great potential for DNA methylation analyses of liquid biopsies. However, the lack of consensus regarding how to perform standardized methylation-specific ddPCR experiments has been challenging. To increase the accuracy of ddPCR DNA methylation analyses we have developed both (i) a robust internal control for DNA methylation analyses by droplet digital PCR and (ii) an in-house algorithm for automated dichotomization of droplets. Drawing on this robust methodology, our group aim to develop a non-invasive urine-based test for bladder cancer. Suitable DNA methylation biomarkers for bladder cancer detection and monitoring have been identified from methylome sequencing and are currently being validated in urine samples using ddPCR.

3:40-4:05

YUAN CAO

Postdoctoral Research Fellow, Rutgers New Jersey Medical School

MTB/XDR Assay: a point-of-care assay for detecting extensively drug resistant TB

- MTB/XDR assay is a reflex assay for rapid detection of extensive drug resistance in Mycobacterium tuberculosis positive samples.
- Combining conventional fluorophores and large-Stokes-shift fluorophores, the MTB/XDR assay uses 10 probes to detect 8 genes for susceptibility or resistance to isoniazid, fluoroquinolones, amikacin and kanamycin.
- The assay detects resistance mutations in clinical samples with 92.7% to 98.1% sensitivity, and 99.6% or greater specificity, depending on the drug being tested.

3:40-4:05

TODD THORSEN

Technical Staff, MIT Lincoln Laboratory

Microfabricated Platforms for Microbiome Culture: From Artificial Mouths to Guts

Humans support an estimated 100 trillion microorganisms that occupy ecological niches in and on our bodies (i.e. mouth, skin, gut). These microbial populations, often referred to as microbiomes, have a complex symbiotic relationship with the human host. For example, the gut microbiome has recently been shown to directly affect the brain through multiple mechanisms, including the synthesis of short chain fatty acids that tighten the blood/brain barrier, and production of metabolites that directly alter neurotransmitters like serotonin. In this talk, I will discuss our recent work in the development of microfabricated platforms to support the growth and characterization of these complex microbiome populations, including a mouth-on-a-chip platform to study oral biofilms as well as an artificial gut that emulates the environment of the colon.

4:05-5:05 Afternoon Refreshments / Poster Presentations / One-to-One Meetings

5:05-5:30

JAY F. DORSEY

Associate Professor, Department of Radiation Oncology, Smilow Center for Translational Research, University of Pennsylvania School of Medicine

Topic: dPCR profiling of EGFRvIII

5:05-5:30

JEAN-CHRISTOPHE AVARRE

Head of the High Throughput qPCR Platform and Research Group Leader, University of Montpellier, France

MelTree: A novel workflow for the automated identification of a large number of variants using high resolution melting

Nucleic acid characterization by High Resolution Melting (HRM) is a simple, flexible, low-cost and powerful technique for identifying sequence variations, making it attractive for a broad range of diagnostic and research applications. However, current procedures for analyzing HRM curves are not suited for large data sets. For this reason, we have developed an innovative tool, called MelTree, which enables the simultaneous discrimination of a large number of variants. MelTree relies on the establishment of a melting profile library and offers a fully automated analysis workflow. Its relevance will be demonstrated with two different applications: i) the simultaneous discrimination of 19 nontuberculous mycobacterial species, and ii) the detection/identification of five pathogens responsible for abortive diseases in cattle with a multiplex diagnostic test.

5:05-5:30

SINDY TANG

Assistant Professor, Stanford University

Microfluidics for applications in single-cell studies

This talk describes our recent work on using microfluidics for single-cell studies, specifically on phenotyping antibiotic resistance with single-cell resolution, and on studying single-cell wound repair.

5:30-5:55

WILLIAM LEENDERS

Associate Professor, Radboud UMC, The Netherlands

Quantitative highly multiplexed next generation sequencing of RNA using single molecule molecular inversion probes. A drug repurposing test?

Treatment of patients with targeted drugs has been firmly implemented in clinical oncology. For most of these drugs companion diagnostic biomarkers are available. Mostly these biomarkers are based on DNA sequencing and, less frequently, immunohistochemistry. In clinical practice overtreatment with targeted drugs, due to unpredictable intrinsic or induced resistance, is a huge problem. There is therefore a great need for methods that predict treatment response. Here a novel technology will be presented that is based on targeted RNA profiling that simultaneously gives information on expression levels of over 200 'actionable' genes, concomitant with mutation detection and splice variant detection. The test can run up to 400 patient samples simultaneously. The profiles contain important information on the biological pathways that are associated with cancer progression and may guide oncologists in treatment decision making.

5:30-5:55

YU LI

Lead, Molecular Diagnostics and Genomics Team, CDC

Developments and validations of pan-lyssavirus RT-qPCR assays for rabies diagnostics

5:30-5:55

DINO DI CARLO (Reserved)

Associate Professor, UC Los Angeles

Topic: Nonlinear fluid dynamics in microfluidic devices and applications in portable diagnostic and analysis systems

5:55-6:20

SENIOR REPRESENTATIVE (Reserved)
LGC
Title TBC

5:55-6:20

JEFFREY EDWARDS (Reserved)
Neuroscience Center; Associate Director Department. of Physiology and Developmental Biology, Brigham Young University
Quantitative single cell PCR in combination with whole-cell electrophysiology, particularly brain synaptic plasticity studies

5:55-6:20

ANDERSON SHUM
Associate Professor, University of Hong Kong
Topic: All-aqueous emulsions for cellular separation and analysis

6:20	Chair's Closing Remarks / End of Day 1
6:20-7:20	Networking Drinks Reception

8:30-8:55 Refreshments

8:35-8:40 **Chair's Opening Remarks: Marie Korabecna,** Associate Professor, Charles University, Czech Republic

QPCR & DIGITAL PCR

8:40-9:20

KEYNOTE ADDRESS:
HANLEE JI
Associate Professor and Senior Associate Director, Genome Technology Center, Stanford University
Topic: Digital PCR without probes to detect mutations in blood

9:20-9:55

FENYONG LIU
Professor, Infectious Diseases, University of California Berkeley
Topic: Viral qPCR Diagnostic Assays

9:55-10:25

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MICROFLUIDICS

8:40-9:20

KEYNOTE ADDRESS:
LUKE LEE
Professor of Bioengineering, UC Berkeley
Topic: Advancing personalized medicine through microfluidic biosensors and point-of-care diagnostics

9:20-9:55

KEYNOTE ADDRESS:
JUAN SANTIAGO
Professor, Stanford University
Separating and analyzing nuclear versus cytoplasmic nucleic acids from single cells

Single cell analyses have become powerful tools in the study of heterogeneous cell populations such as tumors and developing embryos. However, simultaneous analysis of nuclear versus cytoplasmic fractions from single cells remains a challenge as these easily cross-contaminate. We present a microfluidic system that can fractionate and deliver nucleic acid fractions from the nucleus (nucNA) versus the cytoplasm (cytNA) from single cells to independent downstream analyses. We perform selective electrical lysis which disrupts a cell's cytoplasmic membrane, while leaving the nucleus relatively intact. We then extract, purify, preconcentrate, and transport cytNA using isotachophoresis (ITP), while keeping the cell nucleus in a trap. We will present a next generation sequencing analyses including unique data showing correlation analyses of cytRNA vs. nucRNA in a method we term single-cell integrated nucRNA and cytRNA-sequencing (SINC-seq). The data shows high correlation for cell-cycle-related genes; and a damped correlation for RNA processing and splicing genes.

9:55-10:25

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10:25-11:35 Morning Refreshments / Poster Presentations / One-to-One Meetings

11:35-12:25

50 MINUTE PANEL DISCUSSION:

The Challenges of Clinical Implementation

- Practical restrictions
- Reliability considerations
- FDA approval process
- What applications are ready for which technologies
- Case study evidence/Clinical trials

Invitation to Senior Representatives x4

11:35-12:00

PIOTR GARSTECKI

Professor, CTO, Polish Academy of Science

Microfluidics against antibiotic resistant infections

- Antimicrobial resistance (AMR) constitutes one of the most imminent and most important threats to global health.
- Diagnostics is one of the more important methods for effective combat against AMR, as it may effectively help to reduce the number of infections, and reduce the emergence and spread of AMR via using better informed, targeted treatments.
- Microfluidics brings in the tools for i) single cell resolution, ii) lots of reactions/bioprocesses from a single sample, and iii) more efficient processing of the reaction volumes.
- These advantages can effectively be used to construct systems for rapid, point-of-care detection of multiple genes that signal AMR in patients being admitted to hospitals, and in providing full information about the susceptibility of pathogens against a broad spectrum of clinically relevant antibiotics.

12:00-12:25

BRIAN CUNNINGHAM

Professor, University of Illinois at Urbana-Champaign

Multiplexed Smartphone Detection of Infectious Diseases with Microfluidic Loop-Mediated Isothermal Amplification

New tools are needed to enable rapid detection and identification of infectious viral and microbial pathogens in a variety of point-of-care applications that impact human and animal health. We report the design, construction, and characterization of a platform for multiplexed analysis of disease-specific DNA sequences that utilizes a smartphone camera as the sensor in conjunction with a handheld instrument that interfaces the phone with a silicon-based microfluidic chip. Utilizing specific nucleic acid sequences for four equine respiratory pathogens and four bloodborne human viral pathogens, we demonstrated the ability of the system to use a single 15-µL droplet of test sample to perform selective positive/negative determination of target sequences, and concentration estimation in 30 minutes. The system achieves detection limits comparable to those obtained by laboratory-based instruments.

12:25-12:55

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12:25-12:55

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12:55-1:50 Lunch

1:50-2:15

JULIANN CHMIELECKI

Associate Director, Translational Science, AstraZeneca

Use of digital PCR technologies to define patient populations and mechanisms of resistance to osimertinib, a 3rd generation EGFR-TKI

2:15-2:40

RACHEL TAM

Senior Scientist, Genentech

Topic: Digital PCR and NGS for cfDNA analysis

2:40-3:05

JOHN MARTIGNETTI

Professor, Icahn School of Medicine at Mount Sinai

The detection of pre-cancer by targeted liquid biopsy: Tumor-specific mutations detected one year before endometrial cancer diagnosis by uterine lavage

- The "liquid biopsy" has been overwhelmingly focused on issues related to advanced disease in already diagnosed patients under active treatment.
- A targeted sampling technique, the uterine lavage, allows for enriched and focused collection of analytic material to diagnose endometrial and ovarian cancers.
- We provide the first demonstration that future, tumor-specific mutations can be identified in an asymptomatic individual without clinical or pathologic evidence of cancer.

1:50-2:15

JEFF WANG

Professor of Mechanical and Biomedical Engineering, John Hopkins University

All-in-one Droplet Microfluidics for Molecular Diagnostics

One major challenge in implementing complex bioanalytical assays such as genetic detection in a high-throughput manner is to develop a fluid control system that is simple yet fully functional. Manipulation of droplets on a microchip promises easier, more flexible, and more functionally integrated liquid control, than does continuous flow microfluidics. The talk focuses on the development of a droplet microfluidic platform for the detection of biomarkers for human diseases such as cancer and infectious using crude biosamples, as well as for agriculture for high-throughput marker assisted selection (MAS). The framework for the droplet microfluidics in our biomarker analyses is based on two main themes. The emulsion-based picolitre droplet platform provides new ways to measure and digitally analyze biomolecules with high sensitivity and quantification accuracy. This platform also facilitates combinatorial, high-throughput screening of biomarkers. Meanwhile, the surface-based microliter droplet platform provides an opportunity to develop miniaturized diagnostic systems fully integrated with sample preparation and. Such platform may function as portable bench-top environments that dramatically shorten the transition of a bench-top assay into a point-of-care format.

2:15-2:40

KEVIN DORFMAN

Minnesota University

Physics of Genome Mapping in Nanochannels

Genome mapping in nanochannels is an emerging method for obtaining large-scale genomic information at the single molecule level. In this method, large pieces of contiguous genomic DNA, hundreds of kilobase pairs in length, are labeled with a sequence-specific fluorescent probe while the backbone is labeled with a second color. Upon injection into a nanochannel, the labeled molecule stretches due to confinement and the locations of the probes are read by fluorescence microscopy. I will present our experimental and theoretical progress towards understanding the thermodynamics and hydrodynamics of DNA when it is confined in a nanochannel, as well as how this knowledge can be used to improve genome mapping technology.

2:40-3:05

JAMES STURM

Stephen R. Forrest Professor of Electrical Engineering, Princeton

High-Throughput Leukocyte and CTC Harvesting from Whole Blood by Continuous-Flow Deterministic Lateral Displacement (DLD)

Many steps in analytical and therapeutic medicine involve fractionating blood into its constituent components. Of special interest is the harvesting of leukocytes and/or circulating tumor cells (CTCs), with applications ranging from diagnosis and monitoring to isolating cells from blood for transfection for CAR-T cell immunotherapy. The Deterministic Lateral Displacement (DLD) continuous-flow fractionation method is in principle well-suited to these tasks, but its ability to harvest desired cells and reject unwanted ones both traditionally decline rapidly at the high flow rates needed for high throughput applications. In this talk I will show how and why the novel design of the post-shape in DLD arrays can overcome these limitations, so that flow speeds on the chip can be increased in excess of 1 meter/second, while maintaining the yield of desired cells without loss of viability and maintaining the rejection of unwanted cells. Processing rates in excess of 100 ml/hr of blood in one chip appear feasible.

3:05-3:30

TIMOTHY ROSE

Professor and Co-Director of the Center for Global Infectious Disease Research, University of Washington and Seattle Children's Hospital

Consensus-Degenerate Hybrid Oligonucleotide Primer (CODEHOP) PCR for diagnosis of distantly related, emerging and novel pathogens

- CODEHOP PCR primers derived from amino acid motifs highly conserved within members of a protein family are highly effective in the identification and characterization of distantly related family members
- CODEHOP-based PCR has been used to detect and identify distantly related members of large virus families, including herpesviruses, papillomaviruses, retroviruses, paramyxoviruses and adenoviruses.
- Coupling CODEHOP PCR with sequence-based detection systems, such as single-strand conformation polymorphism, sloppy molecular beacons or DNA sequencing, provides new approaches for highly sensitive, broad-based diagnosis of viral infections in point-of-care or laboratory settings.

3:30-4:00

TARA SIGDEL

Assistant Professor, University of San Francisco

Assessment of Targeted Transcriptional Profiling of Kidney Transplant Biopsies stored in different conditions through qPCR and Nanostring technology

- Assessment of RNA integrity of RNA stored in FFPE vs RNA isolated from kidney biopsy stored in RNA-stabilizing solution
- Correlational; analysis of gene expression values in between the two tissue specimen stored in two different conditions
- Correlational analysis of gene expression values calculated from QPCR vs Nanostring technology
- Utility of FFPE kidney biopsies in biomarker validation

3:05-3:30

ASHLEIGH THEBERGE

Assistant Professor, Department of Chemistry, University of Washington

Studying cell signaling in complex environments using open microfluidics

Small molecule and protein signals provide a rich vocabulary for cellular communication. To better understand these signaling processes in both normal and disease states, we have designed new open microfluidic platforms for cell culture and analysis. Open microfluidics - the manipulation of fluids in channels with at least one open air interface - enables increased accessibility and greatly simplifies device fabrication. This talk will highlight our recent work studying the interplay between cell types in urologic disease and asthma.

3:30-4:00

CHEN CHIA-HUNG

Assistant Professor, National University of Singapore

Single Cell Clinical Enzyme Analysis for Precision Medicine by Using Continuous Flow Microfluidics

In this study, a continuous flow microfluidic device was developed to detect secreted multiplexed protease activities at single cell resolution. The individual cells from patient samples are encapsulated within water-in-oil droplets for single cell multiplexed protease assay. We modified FRET (fluorescence resonance energy transfer)-based substrates to accommodate different fluorescent pairs with distinct excitation and emission wavelengths to obtain multiple signals from droplets containing single cells. To infer a quantitative profile of multiple proteolytic activities from single cells, we applied the computational method Proteolytic Activity Matrix Analysis (PrAMA). The capability to determine multiple protease activities at single cell resolution has the potential to characterize tumor progress of individual patients.

4:00 Conference Close / Afternoon Refreshments

MAKING A POSTER PRESENTATION

Poster presentation sessions will take place in breaks and alongside the other breakout sessions of the conference. Your presentation will be displayed in a dedicated area, with the other accepted posters from industry and academic presenters. We also issue a poster eBook to all attendees with your full abstract in and can share your poster as a PDF after the meeting if you desire (optional). Whether looking for funding, employment opportunities or simply wanting to share your work with a like-minded and focused group, these are an excellent way to join the heart of this congress.

In order to present a poster at the congress you need to be registered as a delegate. Please note that there is limited space available and poster space is assigned on a first come first served basis (subject to checks and successful registration). We charge an admin fee of $100 to industry delegates to present, that goes towards the shared cost of providing the poster presentation area and display boards, guides etc. This fee is waived for those representing academic institutions and not for profit organizations.

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