

Conference Summary

Agenda Overview

Sponsors

Venue

qPCR & Digital PCR
Congress

Synthetic Biology
& Gene Editing
Congress

Microfluidics
Congress

NGS Tech &
Applications Congress

4BIO Registration



— London, UK —
4-5 December 2017



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4BIO Registration

4BIO

SUMMIT: EUROPE

Global Engage's 4Bio summit hosts the 5th qPCR and Digital PCR Congress, 4th Synthetic Biology and Gene Editing Congress, 3rd Microfluidics Congress: Europe and NGS Tech & Applications Congress. Featuring 100 expert speakers 4Bio is expected to attract over 550 attendees and 100 poster presentations.



QPCR & DIGITAL PCR CONGRESS: EUROPE

4-5 December 2017, LONDON

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.



GLOBAL SYNTHETIC BIOLOGY & GENE EDITING CONGRESS: EUROPE

4-5 December 2017, LONDON

Synthetic biology continues to be an exciting and rapidly developing area in the life sciences with the potential to revolutionise many aspects of society. As technologies and strategies continue to mature, this conference provides a space for experts in academia and industry to network and share ideas and the opportunity for successful start-ups to showcase the commercial potential of synthetic biology. With a focus on healthcare and investment, this interactive meeting will allow you to keep up to date with cutting edge of research and tool development, access to case studies on drug discovery, therapeutics and technologies, and the opportunity to make connections with academics, entrepreneurs, investors and businesses in your field.



MICROFLUIDICS CONGRESS: EUROPE

4-5 December 2017, LONDON

With a continually expanding range of applications, microfluidics is proving itself a vital field in the advancement of human health. This congress brings together experts working in the development and application of microfluidic devices, including point-of-care diagnostics, single cell analysis, lab-on-a-chip applications, droplet microfluidics and next generation microfluidics. With a focus on medical research, this conference will showcase case studies examining the latest developments in the technologies and techniques advancing medical research in areas as disease monitoring, diagnostics and organ-on-a-chip.



NGS TECH & APPLICATIONS CONGRESS: EUROPE

4-5 December 2017, LONDON

Over the past decade, advances in sequencing technology and significant cost reductions have been instrumental to genomics research. Scientists are continuing to develop new sequencing techniques, tools and methods of analysis, and subsequently discovering new applications in medical research. NGS has already revolutionised 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.

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qPCR & DIGITAL PCR CONGRESS

SYNTHETIC BIOLOGY & GENE EDITING CONGRESS

MICROFLUIDICS CONGRESS

NGS TECH & APPLICATIONS
CONGRESS

08:00-09:00

Registration / Refreshments / Global Engage Welcome Address and Morning Chair's Opening Remarks

09:00-9:40

Keynote Address:

Applying PCR methods for improved diagnostics - Title TBC
Yiu-Lian Fong, Global Head of Diagnostic Innovation, Janssen and Johnson & Johnson Innovation, UK

09:40-10:15

Keynote Address:

Digital PCR for high accuracy measurement of DNA Reference Materials
Kerry Emslie, Senior Research Scientist, National Measurement Institute, Australia

10:15-10:45

Solution Provider Presentation:

Single Cell Analysis with the Naica System
Alexandra Martin, Application Specialist, Stilla Technologies



09:00-09:40

Keynote Address:

Improving Bio Design Reliability and Reproducibly through the use of Foundries
Richard Kitney, Professor of BioMedical Systems Engineering, Imperial College London

09:40-10:15

Keynote Address:

Strategies for the future: the research and commercial landscape - Title TBC
Lionel Clark
 Co-chair of the Synthetic Biology Leadership Council

10:15-10:45

Solution Provider Presentation:

Discover Innovative Technologies to Rapidly Generate Synthetic Genes and Proteins
Malathi Raman, European Product Manager, Takara Bio Europe, St Germain en Laye, 78100, France



09:00-9:40

Keynote Address:

Optical Tools for Ultra High-Throughput Cellular Analysis
Andrew de Mello, Professor of Biochemical Engineering & Chairman, ETH Zurich

09:40-10:15

Keynote Address:

Microfluidic platforms to study gas-liquid interactions
Eugenia Kumacheva, Professor, University of Toronto

10:15-10:45

Solution Provider Presentation:

True lab-on-a-chip devices: Complexity and Manufacturing challenges
Holger Becker, Co-founder and CSO, microfluidic ChipShop GmbH



09:00-9:40

Keynote Address:

Title TBC
Richard McCombie, Professor, Cold Spring Harbor Laboratory, USA

09:40-10:15

Keynote Address:

Recent progress in genomics
Jason Betley, Senior Director, Technology Development, Illumina

10:15-10:45

Solution Provider Presentation:
Improving exome sequencing, targeted sequencing, and low frequency variant detection with better coverage uniformity, higher on-target rates, and unique molecular identifiers
Xiangyu Rao, NGS Field Application Manager, Europe, Integrated DNA Technologies



10:45-11:55

Morning Refreshments / Even Numbered Poster Presentation Sessions / One-to-One Partnering Meetings

Digital PCR: Possibilities
& Opportunities

Track Chair:

Gary Pestano
 Vice President, Development and Operations, Biodesix

11:55-12:20

Prospects for digital PCR in absolute quantification of DNA and RNA

Ward De Spiegelaere, Assistant Professor, Gent University, Belgium

qPCR: Strategies & Developments

Track Chair:

Marie Korabecna, Associate Professor, Charles University, Czech Republic

11:55-12:20

Optimized design of broadly detecting qPCR Primers and Probes using a conservation and hybridization prediction algorithm, 'ConSort'
Jonas Blomberg, Emeritus Professor of Clinical Virology, Uppsala University, Sweden

Genomic Engineering

11:55-12:20

Engineering orthogonal synthetic timer circuits in bacteria
Georg Fritz, Independent Group Leader, LOEWE Center for Synthetic Microbiology, Philipps-University Marburg

Applications of Synthetic Biology in Healthcare & Research

11:55-12:20

Rational Design and Redesign of Natural Product Pharmaceuticals
Paul Race, Senior Lecturer, University of Bristol

Strategy and Technology in Microfluidics

11:55-12:20

Droplet based microfluidic applications in biotechnology (TBC)
Dave Weitz, Mallinckrodt Professor of Physics and Applied Physics, Harvard University

NGS Tech & Applications Congress'

11:55-12:20

Bioelectronics applications with nanostructures
Marija Drndic, Fay R. and Eugene L. Langberg Professor of Physics, University of Pennsylvania, USA

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Application of digital PCR for quantification of minority targets in human disease and antimicrobial resistance monitoring
Gerwyn Jones, Senior Researcher, LGC, UK

12:20-12:45

T oligo-primed polymerase chain reaction (TOP-PCR) and its applications
Kuo-Ping Chiu, Associate Professor, National Taiwan University, and Associate Research Fellow, Genomics Research Center, Academia Sinica, Taiwan

12:20-12:45

Synthetic Biology via continuous directed evolution
Mark Isalan, Reader in Gene Network Engineering, Imperial College London

12:20-12:45

Control of the T-cell fate by a chromatin-based timing control switch
Hao Yuan Kueh, Assistant Professor, University of Washington

12:20-12:45

Centrifugal Microfluidics: Recent developments
Nils Paust, Head of Division of Microfluidic Platforms, Hahn Schickard

12:20-12:45

Pushing the limits of mutation detection in circulating tumour DNA
Iwanka Kozarewa, Senior Scientist – Translational Science, IMED Oncology, AstraZeneca, UK

12:20-12:45

Solution Provider Presentation

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Nick Best at sponsorship@globalengage.co.uk

12:45-13:15

Solution Provider Presentation:
Admix™: Custom lyophilised RT-PCR reagents for point-of-use applications
Martin A Lee, CEO, Fluorogenics Limited

12:45-13:15



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12:45-13:15

Solution Provider Presentation

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Nick Best at sponsorship@globalengage.co.uk

12:45-13:15

Solution Provider Presentation:
Title TBC
Senior Representative, Elveflow

12:45-13:15



Early Career Researcher Presentation:
Topic: Sample & library prep; single-cell RNA-seq – Title TBC
Marta Grzelak, Senior Scientific Associate, CRUK Cambridge Institute Genomics Core, UK

12:45-13:00

Solution Provider Presentation:
Population scale sequencing by cost-efficient targeted NGS
Vinzenz Lange, Chief Technology Officer, DKMS Life Science Lab

13:00-13:15

13:15-14:15

Lunch / One-to-One Partnering Meetings

Track Chair:
Ward De Spiegelaere, Assistant Professor, Gent University, Belgium

Track Chair:
Catherine Kibirige, Clinical Research Scientist, Imperial College London, UK

Droplet PCR for liquid biopsy analysis
Hakan Jonsson, Assistant Professor, KTH Royal Institute of Technology, Sweden

14:15-14:40

Discordance between replicate qPCR reactions
Jan Ruijter, Assistant Professor, University of Amsterdam, The Netherlands

14:15-14:40

The synthetic frontier – unravelling the complexity of biology
Cälin Guet, Assistant Professor, IST Austria

14:15-14:40

Bacterial RNA structures as drug targets
Günter Mayer, Professor, University of Bonn

14:15-14:40

Iso-acoustic focusing organizes cells and liquids based on their acoustic properties
Per Augustsson, Assistant Professor in Biomedical Engineering, University of Lund

14:15-14:40

Spatial maps of cancer transcriptomes reveal an unexplored landscape of heterogeneity
Joakim Lundeberg, Professor in Gene Technology, KTH Royal Institute of Technology; Director of the Genomics Platform, Science for Life Laboratory, Sweden

14:15-14:40

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Circulating tumor DNA detection from heparin plasma samples by droplet digital PCR
Nasrin Sarafan-Vasseur,
 Liquid Biopsy Scientific Leader, Research Team on Oncology (IRON), INSERM and University of Rouen, France

Multiple hotspot mutations scanning by single droplet digital PCR
Charlotte Proudhon,
 Circulating Biomarkers Team Leader, Institut Curie, France

Solution Provider Presentation:
Title TBC
Senior Representative,
 JN Medsys

jnmedsys

Optimization of Molecular Procedures with Two-Dimensional Strandness-Dependent Electrophoresis
Jon Jonsson, Professor and Chair of Biochemistry and Molecular Biology, University of Iceland, and Medical Director, National University Hospital, Iceland

High Resolution melting: a novel workflow for the automated identification of a large number of variants
Jean-Christophe Avarre,
 Head of the High Throughput qPCR Platform and Research Group Leader, University of Montpellier, France

Solution Provider Presentation:
Screening of tick-borne pathogens in European ticks using High-throughput real-time PCR on the Biomark™ HD System
Sara Moutailler,
 PhD. Researcher at ANSES, Animal Health Laboratory, JRU BIPAR, Vectotiq Team

FLUIDIGM

Inducible and deterministic forward programming of human pluripotent stem cells into somatic cell types
Mark Kotter, Principal Investigator, University of Cambridge

Escherichia coli HGT: a novel high glucose throughput chassis, engineered for large scale production and derived from systems biology studies
Ralf Takors, Professor, Director of the Institute of Biochemical Engineering, University of Stuttgart

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Genome and epigenome editing for cardiovascular disease
Jean-Sebastien Hulot,
 Professor of Medicine, Pharmacology, Institute of Cardiometabolism & Nutrition, UMRS Inserm

Taking Inspiration from Nature for the Generation of Novel Antibiotics
Chris Willis, Professor of Organic Chemistry, University of Bristol

Solution Provider Presentation:
Microfluidic functionalities and microfabrication technologies for Point-of-Care testing and Cell Culturing
Monica Brivio,
 Strategic R&D Manager, Micronit Microtechnologies

micronit
microtechnologies

OSTEMERs - new opportunities for micro- and nanofluidics
Wouter Metsola Van Der Wijngaart

Porous Microfluidic Sensors for Field Use Applications
Elain Fu, Assistant Professor in Bio Engineering, Oregon State University

Solution Provider Presentation:
Microfluidic functionalities and microfabrication technologies for Point-of-Care testing and Cell Culturing
Monica Brivio,
 Strategic R&D Manager, Micronit Microtechnologies

micronit
microtechnologies

Massively parallel single cell immune sequencing for immunotherapy discovery
Adrian W. Briggs, Head of Molecular Biology, Receptor Discovery, Juno Therapeutics, USA

How TOP-PCR can help NGS
Kuo Ping Chiu, Associate Research Fellow, Genomics Research Center, Academia Sinica, Taiwan

Solution Provider Presentation:
Title TBC
Senior Representative,
 Perkin Elmer

PerkinElmer
For the Better

16:00-16:50

Afternoon Refreshments / Odd Numbered Poster Presentation Sessions / One-to-One Partnering Meetings

Life beyond the pixels: single-cell phenotyping using machine learning, dPCR, and image analysis methods
Peter Horvath,
 Distinguished Professor and Group Leader, Institute of Molecular Medicine Finland and Hungarian Academy of Sciences, Finland

High through-put DNA methylation analysis of LungCancer - plasma cfDNA for biomarker development
Andreas Weinhausel,
 Associate Professor, University of Natural Resources and Applied Life Sciences, and Senior Scientist, Austrian Institute of Technology, Austria

Next-generation RNA circuits in living cells
Alfonso Jaramillo, Professor of Synthetic Biology, University of Warwick

Using Synthetic Biology and CRISPR/Cas9 bacterial genome engineering for drug development
Gareth Cooper,
 Investigator, Biological Technologies UK R&D, Advanced Manufacturing Technologies, GlaxoSmithKline

Multiplexed DNA Malaria Sensing using Origami Paper Folding in Uganda
Jon Cooper, Professor, University of Glasgow

Methylation-sensitive profiling of genomic CpG sites using TOP-seq
Saulius Klimasauskas,
 Director and Chief Scientist, Institute of Biotechnology, Vilnius University, Lithuania

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17:15-17:45	Solution Provider Presentation For sponsorship opportunities please contact Gavin Hambrook/ Nick Best at sponsorship@globalengage.co.uk	17:15-17:45	Solution Provider Presentation For sponsorship opportunities please contact Gavin Hambrook/ Nick Best at sponsorship@globalengage.co.uk	17:15-17:30	Early Career Researchers Presentation: Transcriptional activation of endogenous transcription factors using novel all-in-one dCAS9-SAM system Antonella Fidanza, University of Edinburgh (Scottish Centre for Regenerative medicine, UK)	17:15-17:30	Early Career Researchers Presentation: Synthetic Phage Biosensors for Pathogen Detection and Eradication Victor Rodrigo Ibarra Chavez, PhD Student, University of Glasgow	17:15-17:45	3D-Printed Bio-Microfluidics Nirveek Bhattacharjee, Postdoctoral Fellow, Folch Lab, University of Washington	17:15-17:45	MitoRS, a method for high throughput, sensitive, and accurate detection of mitochondrial DNA variants Julien Marquis, Genomics Specialist, Nestlé Institute of Health Sciences, Switzerland
17:45-18:10	Clinical utility of ddPCR in the management of patients with castration resistant prostate cancer Daniel Wetterskog, Senior Scientist, Institute of Cancer Research, UK	17:45-18:10	Targeted transcriptome profiling using single molecule Molecular Inversion Probes William Leenders, Associate Professor of Tumor Targeting, Radboud UMC, The Netherlands	17:30-17:45	Early Career Researchers Presentation: Rational engineering of Tal-effector recombinases for genome editing Jumai Abioye, PhD Student, University of Glasgow	17:30-17:45	Early Career Researchers Presentation: Engineering of minimal chassis as delivery system to dissolve biofilms Maria Lluch Senar, Staff Scientist, Center for Genomic Regulation				
18:10-18:35	Droplet-based PCR for the clinical follow up of cancer patients Valerie Taly, Group Leader, University of Paris Descartes, France	18:10-18:35	Explaining biocide tolerance of Gram negative bacteria - using SyBr Green qPCR as a versatile tool to develop and support hypotheses Lucy Bock, Senior Scientist/Project Team Leader, Technology Development Group, Public Health England, UK	17:45-18:10	Site-directed RNA with ADARs and engineered riboproteins Thorsten Stafforst, Group Leader, Institute for Biochemistry, Universität Tübingen	17:45-18:10	Secretion of heterologous proteins from Bacillus subtilis: from the cradle to the grave Colin Harwood, Professor of Synthetic Biology, Newcastle University	17:45-18:10	Laser printed flat optics metasurfaces for microfluidics integration Anders Kristensen, Professor, Technical University of Denmark	17:45-18:10	GeneHancer and VarElect: disease interpretation of whole genome sequence variants Simon Fishilevich, Senior Data Scientist, Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel
18:35	Chair's Closing Remarks / End of Day 1										
18:35-19:35	Networking Drinks										
				18:10-18:35	Artificial C3P3 transcriptional engine for synthetic gene therapy Philippe Jais, President and Chief Scientific Officer, Eukarys		18:10-18:35	Development of a new generation personal bio-detection system Daniel McCluskey, Chief Engineer, Applied R&D: Biodetection, University of Hertfordshire	18:10-18:35	VariantValidator: a web application to accurately validate and convert between HGVS nomenclature and Variant Call Format Raymond Dalglish, Professor of Human Genetics, University of Leicester, UK	

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SYNTHETIC BIOLOGY & GENE EDITING CONGRESS

MICROFLUIDICS CONGRESS

NGS TECH & APPLICATIONS
CONGRESS

08:00-08:40

Refreshments / Morning Chair's Opening Remarks

Track Chair:

Lucy BockSenior Scientist/Project
Team Leader, Technology
Development Group, Public
Health England, UK

Keynote Address:

**Challenges and opportunities for digital PCR in the CLIA
laboratory of the Moffitt Cancer Experience****Anthony Magliocco**, Chair of Anatomical Pathology, Moffitt
Cancer Center, USA

09:00-9:40

Keynote Address:

Design, Construction, and Analysis of a Minimal Bacterial Cell
John Glass, Professor & Leader of the Synthetic Biology and
Bioenergy Group, J. Craig Venter Institute

09:00-09:40

Track Chair:

Priyasma BhoomikPD Research Scientist,
Novartis, Switzerland

Keynote Address:

**Topic: NGS-based
methodologies for studying
genetic variation - Title TBC****Emmanouil Dermitzakis**,
Professor, Department
of Genetic Medicine and
Development, University of
Geneva, Switzerland

09:00-09:40

HEALTHCARE CASE STUDIES

TOOLS, TECHNOLOGIES
& PLATFORMSINNOVATION, INVESTMENT
& START-UPSCASE STUDIES AND APPLICATIONS
IN MEDICAL RESEARCH

Solution Provider Presentation:

Title TBC**Senior Representative**, Bio-Rad Laboratories**BIO-RAD**

09:40-10:10

Solution Provider
Presentation:**Empowering computer-
aided biological design by
using in vivo characterized
Standard Biological Parts****Davide De Lucrezia**, Doulix


09:40-10:10

Solution Provider
PresentationFor sponsorship opportunities
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09:40-10:10

Solution Provider
Presentation:**Title TBC****Senior Representative**,
Fluigent

09:40-10:10

Solution Provider
PresentationFor sponsorship opportunities
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globalengage.co.uk

09:40-10:10

**Using DNA methylation dPCR for urine-based detection
of bladder****Guro Lind**, Professor, Oslo University Hospital, Norway

10:10-10:35

**Engineering cells and
genes based on whole cell
simulations for various
biotechnological objectives****Tamir Tuller**, Associate
Professor of Computational
Systems and Synthetic
Biology, Tel Aviv University

10:10-10:35

**Synthetic Biology and
Gene Editing - IP and
Commercialisation****Sarah Lau**, Partner, Kilburn
& Strode

10:10-10:35

**Disease models on-a-
Chip: Medical applications
of Organ-on-a-Chip
Technology****Peter Ertl**, Professor,
Vienna University of
Technology

10:10-10:35

**Microfluidic applications in
single cell RNA sequencing****Bart Deplancke**, Associate
Professor & Swiss Institute of
Bioinformatics Group Leader,
Institute of Bioengineering,
School of Life Sciences,
EPFL, Switzerland

10:10-10:35

10:35-11:25

Morning Refreshments / Odd Numbered Poster Presentation Sessions / One-to-One Partnering Meetings

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qPCR & DIGITAL PCR CONGRESS

Solution Provider Presentation:
Development of gene signatures as cancer biomarkers using Applied Biosystems™ TaqMan® Array Cards

Darren Roberts, Postdoctoral Research Associate - University of Manchester - Division of Cancer Sciences

11:25-11:55 **Multi-platform qPCR approaches to elucidating expression profiles in ageing**

Ben Lee, Research Technician & PhD Researcher - University of Exeter Medical School

ThermoFisher
SCIENTIFIC

The Power of Molecular Viral Diagnostics in Clinical Medicine

Suzan Pas, Clinical Molecular Microbiologist, Microvida

11:55-12:20

Early Career Researcher Presentation:
Digital PCR in health care and clinical diagnostics: data analysis challenges

Wim Trypsteen, PhD Researcher and Academic Staff Member, Ghent University, Belgium

12:20-12:35

Early Career Researcher Presentation:
Developing Ultra-sensitive PCR Assays and protocols for HIV Vaccine Research

Catherine Kibirige, Clinical Research Scientist, Imperial College London, UK

12:35-12:50

Analysis of viral integration events in single cells

Vincenzo Di Cerbo, Analytical Development Scientist, Cell Therapy Catapult, UK

12:50-13:15

SYNTHETIC BIOLOGY & GENE EDITING CONGRESS

Solution Provider Presentation:
Automating Analysis of CRISPR Genome Editing
Andy Higgs, UK Operations Manager, Advanced Analytical Technologies Ltd.

11:25-11:40

Solution Provider Presentation

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11:40-11:55

Hijacking Nature's Blueprints for Synthetic human Tissue Assembly

Kelly Stevens, Assistant Professor of Bioengineering, University of Washington

11:55-12:20

Early Career Researchers Presentation:
Simcells: A novel chassis for synthetic biology and drug delivery
Catherine Fan, DPhil Student, University of Oxford

12:20-12:45

Early Career Researchers Presentation:
Essential domains if unknown function in yeast
Norman Goodacre, Postdoctoral Fellow, Food and Drug Administration

12:45-13:00

Engineering of Mycoplasma pneumoniae as a tool to dissolve in vivo biofilms
Luis Serrano, CRG Director, CRG Barcelona

13:00-13:15

Solution Provider Presentation

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11:25-11:55

Start-up Showcase: Next-gen biotherapeutics for precise microbiome engineering and sequence-specific antimicrobials

Xavier Duportet, CEO, Eligo Bioscience

11:55-12:20

The Interface between Big Data, IPRs & Competition Law in SynBio and SysBio – From Big Data to Smart Data
Timo Minssen, Professor University of Copenhagen

12:20-12:45

Panel Discussion: The bioeconomy – commercialising synthetic biology research
Timo Minssen (Reserved), Professor, University of Copenhagen

12:45-13:15

x3 Senior Representatives

MICROFLUIDICS CONGRESS

Solution Provider Presentation:
Title TBC
Senior Representative, KLA-Tencor

11:25-11:40

Solution Provider Presentation

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11:40-11:55

Paper-based analysis for environmental and clinical applications

Nicole Pamme, Professor, University of Hull

11:55-12:20

Microfluidic solutions for cell and tissue studies
Winnie Svendsen, Associate Professor, Technical University of Denmark

12:20-12:45

Liquid biopsy to droplet biopsy: Combining microarrays with microfluidics for circulating tumor cell
Balaji Panchapakesan, Senior Associate Professor, Mechanical Engineering Department, Worcester Polytechnic Institute

12:45-13:15

CLINICAL DIAGNOSTICS & PERSONALISED MEDICINE

Exploiting NGS for clinical individualized neoantigen cancer vaccines

John Castle, CSO, Achilles Therapeutics, UK

11:25-11:55

Personalized detection of circulatory tumor DNA mutations for cancer recurrence monitoring

Bernhard Zimmermann, Vice President R&D, Molecular Research, Natera, Inc., USA

11:55-12:20

Roundtable Discussions:
Table 1: Interpreting Non-Coding Mutation

Jim Hughes, University of Oxford, UK

Table 2: Platform Comparison
Sean Kennedy, Institut Pasteur, France

Table 3: Nanopore Sequencing
Marija Drndic, University of Pennsylvania, USA

Table 4: Clinical Implementation
Philip Beer St James' Hospital, Leeds, UK; Visiting Scientist, Sanger Institute, Hinxton, UK

Table 5: Computational Biology
Raffaele Calogero, University of Torino, Italy

12:20-13:10

13:15-14:10

Lunch

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MICROFLUIDICS CONGRESS

NGS TECH & APPLICATIONS
CONGRESS**Evaluation of qPCR tools and assay for the analysis of cell-free DNA****Pamela Pinzani,**

Associate Professor, University of Florence, Italy

14:10-14:35

Molecular heterogeneity in haematological cancers addressed by qPCR**Charlotte Guldberg Nyvold,** Professor, Haematology-Pathology Research Laboratory, Odense University Hospital, Denmark

14:35-15:00

Digital PCR for monitoring minimal residual disease in hematological malignancies**Pontus Lundberg,** Head of Molecular Diagnostics, University of Basel, Switzerland

15:00-15:25

Leveraging CRISPR-Cas9 genome editing tools to engineer non-traditional yeasts for chemical biosynthesis**Ian Wheeldon,** Assistant Professor, University of California Riverside

14:10-14:35

Miniaturized laboratories for synthetic biology**Steve Shih,** Assistant Professor, Concordia University

14:35-15:00

Building and optimising multi-enzyme in vitro cascade reactions**Nicholas Harmer,** Senior lecturer in Structural Biochemistry, Living Systems Institute, University of Exeter

15:00-15:25

Round-Table Discussion: Challenges for the future of Synthetic Biology**Roundtable 1:** Ethics and Society**Roundtable 2:** IP and Regulation**Roundtable 3:**

Collaboration strategies

Kelly Stevens, Assistant Professor of Bioengineering, University of Washington

14:35-15:25

Spermatozoa selection and analysis on microfluidic chips**Loes Segerink,** Assistant professor, Institute of Nanotechnology, University of Twente

14:10-14:35

Fast antibiotics susceptibility testing using direct single cell imaging**Johan Elf,** Professor, Uppsala University

14:35-15:00

Development of a new generation personal bio-detection system**Chuck Henry,** Professor of Chemistry, Colorado State University, Bacterial and antimicrobial resistance detection

15:00-15:25

Track Chair:**Ahmad Khodr,** Researcher, International Microbiology Department, L'Oréal Research & Development, France

14:10-14:35

Challenges in using NGS as a clinical diagnostic tool**Christian Gloeckner,** Chief Technology Officer, NEO New Oncology GmbH, Germany

14:35-15:00

The clinical interface between precision medicine and the gastroenterologist**Ferga Gleeson MD,** Professor of Medicine, Mayo Clinic, Rochester, Minnesota, USA

15:00-15:25

Every rose has its thorn- barriers to the implementation of next-generation sequencing technologies in oncology clinical practice**Philip Beer,** Consultant Haematopathologist, HMDS, St James' Hospital, Leeds, UK; Visiting Scientist, Sanger Institute, Hinxton, UK

15:25-15:55

Afternoon Refreshments / Even Numbered Poster Presentations

Development and Clinical Validation of Liquid ddPCR Tests for Actionable Somatic Mutations for NSCLC**Gary Pestano,** Vice President, Development and Operations, Biosesix

15:55-16:20

Data-Driven Design of Cell Factories and Communities**Niko Sonnenschein,** Senior Researcher, Novo Nordisk Foundation Center for Biosustainability

15:55-16:20

Invitation Out

15:55-16:20

Self-powered programmable microfluidic platform for point-of-care diagnostics**Jeroen Lammertyn,** Professor, Head of the MeBioS Biosensors Group, KU Leuven

15:55-16:20

Title TBC**Victor Neduva,** Group Leader, GlaxoSmithKline, UK

15:55-16:20

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16:20-16:45	Title TBC Invitation Out	16:20-16:45	No Talk in this Track	16:20-16:45	16:20-16:35
			No Talk in this Track		
16:45		Chair's Closing Remarks / Conference Close			16:35-17:00
					17:00
					Chair's Closing Remarks / Conference Close

MICROFLUIDICS CONGRESS

Optical DNA mapping for characterization of plasmids coding for antibiotic resistance: principles and clinical applications

Fredrik Westerlund,
Associate Professor,
Chalmers University of
Technology

NGS TECH & APPLICATIONS CONGRESS

Early Career Researcher Presentation: Comparative metagenomic sequencing of 16S rRNA genes and transcripts reveals metabolic activity of commensal bacteria in mouse gut and lung

Matthias Hauptmann
Postdoctoral Scientist,
Department of Cellular
Microbiology, Research
Center Borstel, Germany

L'Oréal approach for the Skin Microbiome project: Scientific watch associated to best practices for sampling, sequencing and analysis

Ahmad Khodr Researcher,
International Microbiology
Department, L'Oréal
Research & Development,
France

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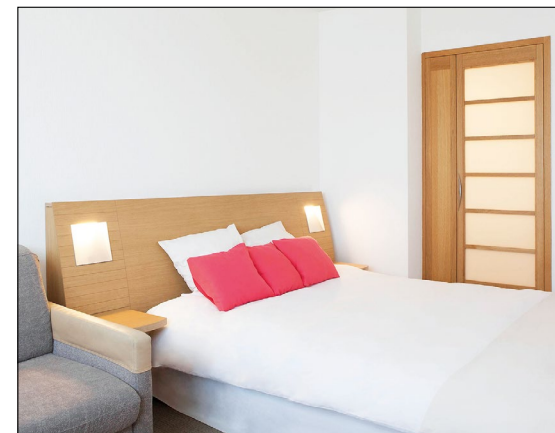
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Novotel London West,
1 Shortlands,
Hammersmith International Centre
London, W6 8DR, UK

The 4-star hotel Novotel London West hotel is conveniently located near the shopping area of Kensington and the famous Hammersmith Apollo Theatre. This London hotel has easy access to 3 tube lines, corporate offices and the capital's shopping areas. The Novotel London West has excellent meeting and event facilities, and is able to accommodate events from 1,000 person conventions to wedding banquets. The Novotel London West also boasts two international restaurants.



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Following on from last year's sell-out event, Global Engage is pleased to announce the **5th qPCR & Digital PCR Congress**, which will be held on 4th-5th December 2017 in London, United Kingdom. As part of the 4Bio Summit this conference will be co-located with our 4th Synthetic Biology Congress, 3rd Microfluidics Congress and Inaugural NGS Tech and Clinical Applications Congress.

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.

With increasing numbers of real-time PCR and qPCR 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 and real-time PCR.

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, expert led case study presentations and interactive Q&A sessions from a 30-strong speaker faculty examining topics on three separate tracks.

EXPERT SPEAKERS Include:**YIU-LIAN FONG**Global Diagnostic Innovation Lead,
Johnson and Johnson, UK**JONAS BLOMBERG**Emeritus Professor of Clinical Virology,
Uppsala University, Sweden**DANIEL WETTERSKOG**Senior Scientist,
Institute of Cancer Research, UK**VALERIE TALY**Group Leader,
University of Paris Descartes, France

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DAY 1 - STREAM 1

Digital PCR: Possibilities & Opportunities

- Introduction, benefits, and future development of dPCR
- Comparing digital PCR to qPCR and when to use each method
- Integrating dPCR with other systems like NGS
- Converting to dPCR and choosing your system
- Digital PCR workflow optimisation and current bottlenecks
- Bioinformatics and data analysis systems
- Multiplexing in digital PCR
- Validation of dPCR methods and how to bring this technology into the clinic
- Detection of rare/patient-specific mutations
- Applications for precision medicine

DAY 1 - STREAM 2

qPCR: Strategies & Developments

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

DAY 2 - STREAM 1

Healthcare Case Studies

- Clinical/Diagnostic applications
- Companion and Point-of-Care diagnostics development
- Single cell analysis
- Liquid Biopsies
- ctDNA, cfDNA, CTC, and miRNA applications
- Clinical test validation
- Oncology
 - ▶ Rare variant detection
 - ▶ Mutation detection
 - ▶ Monitoring therapy response
 - ▶ Early relapse detection
- Prenatal diagnostics
- Infectious diseases
- Using PCR-based technologies for protein analysis
- Biomarker discovery and target validation
- Gene expression and analysis
- Antimicrobial resistance marker identification and validation



CONFIRMED SPEAKERS

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YIU-LIAN FONG

Global Head of Diagnostic Innovation, Janssen and Johnson & Johnson Innovation, UK



ANDREAS WEINHAUSEL

Associate Professor, University of Natural Resources and Applied Life Sciences, and Senior Scientist, Austrian Institute of Technology, Austria



WARD DE SPIEGELAERE

Assistant Professor, Gent University, Belgium



HAKAN JONSSON

Assistant Professor, KTH Royal Institute of Technology, Sweden



NASRIN SARAFAN-VASSEUR

Liquid Biopsy Scientific Leader, Research Team on Oncology (IRON), INSERM and University of Rouen, France



PETER HORVATH

Distinguished Professor and Group Leader, Institute of Molecular Medicine Finland and Hungarian Academy of Sciences, Finland



SENIOR REPRESENTATIVE

Bio-Rad Laboratories



DANIEL WETTERSKOG

Senior Scientist, Institute of Cancer Research, UK



VALERIE TALY

Group Leader, University of Paris Descartes, France



CHARLOTTE PROUDHON

Circulating Biomarkers Team Leader, Institut Curie, France



JAN RUIJTER

Assistant Professor, University of Amsterdam, The Netherlands



JONAS BLOMBERG

Emeritus Professor of Clinical Virology, Uppsala University, Sweden



KUO-PING CHIU

Associate Professor, National Taiwan University, and Associate Research Fellow, Genomics Research Center, Academia Sinica, Taiwan



WILLIAM LEENDERS

Associate Professor of Tumor Targeting, Radboud UMC, The Netherlands



JEAN-CHRISTOPHE AVARRE

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



SUZAN PAS

Clinical Molecular Microbiologist, Microvida



LUCY BOCK

Senior Scientist/Project Team Leader, Technology Development Group, Public Health England, UK



MARIE KORABECNA (Track Chair)

Associate Professor, Charles University in Prague, Czech Republic



CHARLOTTE GULDBORG NYVOLD

Professor, Haematology-Pathology Research Laboratory, Odense University Hospital, Denmark



DARREN ROBERTS

Postdoctoral Research Associate - University of Manchester - Division of Cancer Sciences



BEN LEE

Research Technician & PhD Researcher - University of Exeter Medical School



PONTUS LUNDBERG

Head of Molecular Diagnostics, University of Basel, Switzerland



VINCENZO DI CERBO

Analytical Development Scientist, Cell Therapy Catapult, UK



ALEXANDRA MARTIN

Application Specialist, Stilla Technologies



SENIOR REPRESENTATIVE

JN Medsys



PAMELA PINZANI

Associate Professor, University of Florence, Italy



ANTHONY MAGLIOCCO

Chair of Anatomical Pathology, Moffitt Cancer Center, USA



GUORO LIND

Professor, Oslo University Hospital, Norway



JON JONSSON

Professor and Chair of Biochemistry and Molecular Biology, University of Iceland, and Medical Director, National University Hospital, Iceland



CATHERINE KIBIRIGE

Clinical Research Scientist, Imperial College London, UK



SENIOR REPRESENTATIVE

Fluorogenics



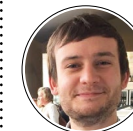
KERRY EMSLIE

Senior Research Scientist, National Measurement Institute, Australia



GERWYN JONES

Senior Researcher, LGC, UK



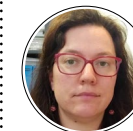
WIM TRYPSTEEN

PhD Researcher and Academic Staff Member, Ghent University, Belgium



GARY PESTANO

Vice President, Development and Operations, Bidesix



SARA MOUTAILLER

PhD. Researcher at ANSES, Animal Health Laboratory, JRU BIPAR, Vectoq Team

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8:00-8:50 Registration & Refreshments

8:50-9:00 TRACK CHAIR: **GARY PESTANO**, Vice President, Development and Operations, Biodesix

09:00-09:40

**KEYNOTE ADDRESS:****YIU-LIAN FONG**

Global Head of Diagnostic Innovation, Janssen and Johnson & Johnson Innovation, UK

Applying PCR methods for improved diagnostics - Title TBC

09:40-10:15

**KEYNOTE ADDRESS:****KERRY EMSLIE**

Senior Research Scientist, National Measurement Institute, Australia

Digital PCR for high accuracy measurement of DNA Reference Materials

- The principle of digital PCR as a direct counting approach
- Major strengths of digital PCR for nucleic acid quantification
- Factors affecting accuracy and reliability of digital PCR data
- Applying digital PCR as a high accuracy reference method for certification of nucleic acid reference materials

10:15-10:45

**SOLUTION PROVIDER PRESENTATION:****ALEXANDRA MARTIN**

Application Specialist, Stilla Technologies

Single Cell Analysis with the Naica System

The Naica System uniquely allows users to image droplets and their contents, both pre- and post-amplification, as well as recover droplets for downstream analysis. We have taken advantage of these features to develop exciting new applications for single cell analysis in mammalian cells and bacteria



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

DIGITAL PCR: POSSIBILITIES & OPPORTUNITIES

TRACK CHAIR: **GARY PESTANO**,

Vice President, Development and Operations, Biodesix

11:55-12:20

**WARD DE SPIEGELAERE**

Assistant Professor, Gent University, Belgium

Prospects for digital PCR in absolute quantification of DNA and RNA

- Using examples of virology I will talk about the possibilities and pitfalls of current digital PCR technology for absolute quantification of DNA and RNA
- I will expand on a tool we developed for data driven threshold setting in digital PCR
- I will discuss a method for normalization of RNA data in digital PCR

qPCR: STRATEGIES & DEVELOPMENTS

TRACK CHAIR: **MARIE KORABECNA**,

Associate Professor, Charles University, Czech Republic

11:55-12:20

**JONAS BLOMBERG**

Emeritus Professor of Clinical Virology, Uppsala University, Sweden

Optimized design of broadly detecting qPCR Primers and Probes using a conservation and hybridization prediction algorithm, 'ConSort'

Design of broadly detecting qPCRs is a challenge. It requires both an accurate analysis of sequence conservation and of how primers and probes interact with their targets. Hybridization prediction has gone from a simple reliance on GC content to more precise algorithms. Nearest neighbour analysis relies on short distance prediction. We developed an algorithm for longer nucleotide distances, NucZip. It allows design of long primers and probes, using wobble positions and inosine. A computer program which embodies both conservation analysis and hybridization prediction, ConSort, was developed. We used it for development of qPCRs for Orthomyxo-, Corona-, Entero-, Retro- and Noroviruses. Different aspects of the design process will be discussed.

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12:20-12:45

**GERWYN JONES**

Senior Researcher, LGC, UK

Application of digital PCR for quantification of minority targets in human disease and antimicrobial resistance monitoring

Digital PCR has shown growing utility as a higher order method for absolute quantification of nucleic acids. The ability to accurately quantify minority targets at lower fractional abundances achieved by qPCR, lends itself to the advancement of applications relying on nucleic acid metrology, including antimicrobial resistance monitoring, viral load measurement and quantification of drug resistance/ sensitivity mutations during cancer treatment. Albeit a powerful technology in its own right, the application of digital PCR to quantify control materials also provides potential benefits for current molecular diagnostics methods using qPCR. Here we discuss some dPCR studies our group has contributed to, with a particular focus on quantification of integrated viral targets and antimicrobial resistance genes.

12:45-13:15

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13:15-14:15

Lunch / Scheduled One-to-One Meetings

TRACK CHAIR: WARD DE SPIEGELAERE,

Assistant Professor, Gent University, Belgium

**HAKAN JONSSON**

Assistant Professor, KTH Royal Institute of Technology, Sweden

Droplet PCR for liquid biopsy analysis

14:15-14:40

12:20-12:45

**KUO-PING CHIU**

Associate Professor, National Taiwan University, and Associate Research Fellow, Genomics Research Center, Academia Sinica, Taiwan

T oligo-primed polymerase chain reaction (TOP-PCR) and its applications

We have developed T oligo-primed polymerase chain reaction (TOP-PCR) for full-length amplification of minute DNA fragments ranging between ~100 bp - ~1.5 Kb. TOP-PCR employs homogeneous half adaptor (HA), generated by annealing P oligo (carrying a phosphate group at the 5' end) and T oligo (carrying a T-tail at the 3' end), for efficient ligation and subsequent amplification using T oligo alone as the PCR primer. Data have shown that TOP-PCR outperforms Illumina's PCR method in a number of aspects. TOP-PCR has been successfully applied to detect cancer mutations in plasma cell-free DNA (cfDNA) for early-onset breast cancer (EOBC) patients and apoptosis using liquid biopsies. More results will be presented in the conference.

12:45-13:15

SOLUTION PROVIDER PRESENTATION:**MARTIN A LEE**

CEO, Fluorogenics Limited

Admix™: Custom lyophilised RT-PCR reagents for point-of-use applications

Fluorogenics is an ISO 13485 certified provider of lyophilized molecular reagents. Fluorogenics provides its custom product service "Admix™" to deliver ambient stable products using enzymes from almost any supplier. These products may include custom oligonucleotides and other reagents, available in custom packing, for a variety of analysers and workflows. In this presentation we describe the opportunities, technology and product development processes. The development process is exemplified for a commercially available point-of-use hand-held (sample-to-result) PCR system. This system can deliver rapid testing facilitated by an innovative developer's kit to accelerate the route to market for your assays.

**TRACK CHAIR: CATHERINE KIBIRIGE,**

Clinical Research Scientist, Imperial College London, UK

**JAN RUIJTER**

Assistant Professor, University of Amsterdam, The Netherlands

Discordance between replicate qPCR reactions

In the analysis of qPCR data, the Cq values of replicate reactions is required to differ no more than 0.5 cycles. However, the sampling error that occurs when pipetting a low number of target molecules into the PCR plate is governed by the Poisson distribution. For each Cq and PCR efficiency value we calculated this unavoidable range of Cq values. This range increases with higher Cq values (less target). A decision to exclude replicate reactions based on this expected sampling error avoids bias, prevents unwanted loss of data and increases the statistical power. For a dataset with replicate qPCR measurements of 12 miRNA targets in 834 patients (20,016 reactions) the fraction of excluded measurements decreased from 39% to 7%.

14:15-14:40

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14:40-15:05

**NASRIN SARAFAN-VASSEUR**

Liquid Biopsy Scientific Leader, Research Team on Oncology (IRON), INSERM and University of Rouen, France

Circulating tumor DNA detection from heparin plasma samples by droplet digital PCR

Heparin is often used as plasma anticoagulant for tumor marker analysis but corresponds also to an inhibitory of PCR not enabling circulating tumor DNA (ctDNA) detection, which has been highlighted as a potential "liquid biopsy". We evaluated the impact of heparinase addition on heparinized plasma samples to allow ctDNA analysis. Circulating ESR1 and KRAS mutations were quantified by digital PCR, in plasma collected in heparinized tubes (n=194) from hormone receptor-positive metastatic breast cancer (HR+MBC) and pancreatic adenocarcinoma (PA) patients. We improved significantly PCR efficiency in 91/144 HR+MBC and 26/50 PA plasma samples, enabling ctDNA detection in 22/91 and 13/26 patients. This new processing did not alter quantitatively and qualitatively ctDNA detection and could make the samples from heparinized blood-derived collections suitable for ctDNA analysis.

15:05-15:30

**CHARLOTTE PROUDHON**

Circulating Biomarkers Team Leader, Institut Curie, France

Multiple hotspot mutations scanning by single droplet digital PCR

- Progress in the field of 'liquid biopsy' combined to the development of droplet digital PCR (ddPCR) enables non-invasive monitoring of mutations with high detection accuracy
- However, current ddPCR assays detect a restricted number of mutations per reaction
- We established two ddPCR assays detecting all genomic alterations within KRAS exon 2 and EGFR exon 19 mutation hotspots, which are of clinical importance in colorectal and lung cancer, using a unique pair of TaqMan oligo-probes.

15:30-16:00

**SOLUTION PROVIDER PRESENTATION:
SENIOR REPRESENTATIVE**JN Medsys
Title TBC

jnmedsys

14:40-15:05

**JON JONSSON**

Professor and Chair of Biochemistry and Molecular Biology, University of Iceland, and Medical Director, National University Hospital, Iceland

Optimization of Molecular Procedures with Two-Dimensional Strandness-Dependent Electrophoresis

- Two-Dimensional Strandness-Dependent Electrophoresis (2D-SDE) in microgels is a fast technique of nucleic acid separation based on size, strandness, and conformation changes.
- A derived technique Northern Lights Assay (NLA) can be used for comprehensive detection of DNA damage in various samples including cells, cfDNA, FFPE and other biosamples. Lesions detected include single-stranded breaks, double-stranded breaks, interstrand and intrastrand DNA crosslinks, modified bases and denatured DNA.
- This technology has diverse applications ranging from testing integrity of samples to efficiency of nucleic acid amplifications including whether PCR products are double-stranded or single-stranded. 2D-SDE and NLA can be used to determine if sample repair is needed and whether it improved samples quality. Efficiency of cDNA synthesis can be measured including amount and length distribution of RNA-DNA hybrids and dsDNA.

15:05-15:30

**JEAN-CHRISTOPHE AVARRE**

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

High Resolution melting: a novel workflow for the automated identification of a large number of variants

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 method that enables the simultaneous discrimination of a large number of variants from their HRM profile. This method relies on the establishment of a melting profile library and offers a fully automated analysis workflow. Using this workflow, it was possible to discriminate 19 nontuberculous mycobacterial species from their HRM profile. It was also possible to design a multiplex diagnostic tool targeting five pathogens responsible for abortive diseases in cattle.

15:30-16:00

**SOLUTION PROVIDER PRESENTATION:
SARA MOUTAILLER**

PhD. Researcher at ANSES, Animal Health Laboratory, JRU BIPAR, Vectotiq Team

Screening of tick-borne pathogens in European ticks using High-throughput real-time PCR on the Biomark™ HD System

Due to increased travel, climatic, and environmental changes, the incidence of tick-borne disease in both humans and animals is increasing throughout Europe. To accurately screen tick-borne pathogens, a large scale epidemiological study was conducted on 19,474 Ixodes ricinus nymphs collected from five European countries using a powerful new high-throughput and cost-effective approach on the Fluidigm Biomark™ HD System. This advanced methodology permitted the simultaneous detection of 25 bacterial, 12 parasitic and 22 viral species across 94 samples. We successfully determined the prevalence of expected, unexpected and rare pathogens, some of them detected for the first time in the five countries. This surveillance method represents a major improvement in epidemiological studies, able to facilitate comprehensive testing of tick-borne pathogens in ticks, mammals and humans, and which can also be customized to monitor emerging diseases.

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16:00-16:50 Afternoon Refreshments / Poster Presentations

16:50-17:15

**PETER HORVATH**

Distinguished Professor and Group Leader, Institute of Molecular Medicine Finland and Hungarian Academy of Sciences, Finland

Life beyond the pixels: single-cell phenotyping using machine learning, dPCR, and image analysis methods

I will give an overview of the computational steps in the analysis of a single cell-based large-scale microscopy experiments. First, I will present a novel microscopic image correction method designed to eliminate vignetting and uneven background effects. Novel single-cell image segmentation methods will be presented using energy minimization methods. I will discuss the Advanced Cell Classifier (ACC) (www.cellclassifier.org), a machine learning software tool capable of identifying cellular phenotypes based on features extracted from the image. It provides an interface for a user to efficiently train machine learning methods to predict various phenotypes. Our recently developed single-cell isolation methods, based on laser-microcapturing and patch clamping, utilize the selection, extraction and molecular analysis (such as dPCR, sequencing) of specific cell(s) using the above machine learning models.

17:15-17:45

SOLUTION PROVIDER PRESENTATION

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17:45-18:10

**DANIEL WETTERSKOG**

Senior Scientist, Institute of Cancer Research, UK

Clinical utility of ddPCR in the management of patients with castration resistant prostate cancer

The Treatment Resistance Team at the Institute of Cancer Research has been using plasma to interrogate resistance in castration-resistant prostate cancer (CRPC) and develop biomarkers for selecting treatment. Using targeted next-generation sequencing and droplet digital PCR on cfDNA from sequential plasma samples AR mutations was found to emerge with resistance to abiraterone and enzalutamide. A strong association between plasma AR aberrations in the form of AR gain and mutations and resistance to abiraterone or enzalutamide in CRPC patients was also seen, supporting the clinical utility of cfDNA studies in metastatic prostate cancer.

18:10-18:35

**VALERIE TALY**

Group Leader, University of Paris Descartes, France

Droplet-based PCR for the clinical follow up of cancer patients

Droplet-based digital PCR has recently emerged as a tremendous tool for cancer research and cancer patient follow-up. It allows non-invasive highly sensitive and quantitative analysis of circulating tumor DNA within blood patient samples. We will demonstrate how picoliter droplet-based PCR can be used for the follow-up of cancer progression and tumor response to treatment in several cancer pathologies.

16:50-17:15

**ANDREAS WEINHAUSEL**

Associate Professor, University of Natural Resources and Applied Life Sciences, and Senior Scientist, Austrian Institute of Technology, Austria

High through-put DNA methylation analysis of LungCancer - plasma cfDNA for biomarker development

- Technology pipeline for methylation biomarker development
- High throughput DNA methylation-qPCR workflows
- Liquid biopsy – cfDNA methylation testing

17:15-17:45

SOLUTION PROVIDER PRESENTATION

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17:45-18:10

**WILLIAM LEENDERS**

Associate Professor of Tumor Targeting, Radboud UMC, The Netherlands

Targeted transcriptome profiling using single molecule Molecular Inversion Probes

Detection of disease-specific molecular aberrations is of great importance in this era of personalized medicine. Molecular aberrations may comprise overexpression of genes that cannot be inferred from genetic analysis, such as genes involved in metabolism. We here present a novel method of targeted RNA sequencing using single molecule Molecular Inversion Probes (smMIPs), allowing semiquantitative measurement of transcripts of (currently 200) genes that are of interest in cancer and carries potential predictive value for cancer treatment. We show that data that are obtained with this cost-effective technique are quantitatively and qualitatively similar to whole RNA next gen sequencing. Furthermore, the technique allows detection of specific splice variants.

18:10-18:35

**LUCY BOCK**

Senior Scientist/Project Team Leader, Technology Development Group, Public Health England, UK

Explaining biocide tolerance of Gram negative bacteria - using SyBr Green qPCR as a versatile tool to develop and support hypotheses

Working on multiple organisms and constantly changing gene-targets requires use of an easily optimisable and cheap qPCR method, which is why we use SyBr Green qPCR. We have investigated chlorhexidine resistance in *Klebsiella pneumoniae* and are about to publish on biocide resistance in *Acinetobacter baumannii* and *Pseudomonas aeruginosa*. I will explain our approach and our optimisation and robustness strategies, as well as an overview of the hypotheses we developed and confirmed using our qPCR approach.

18:35-19:35 Closing Remarks End of Day One / Networking Drinks

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08:30-08:55

Morning Refreshments

08:55-09:00

TRACK CHAIR: **LUCY BOCK**, Senior Scientist/Project Team Leader, Technology Development Group, Public Health England, UK

09:00-09:40

**KEYNOTE ADDRESS:**
ANTHONY MAGLIOCCO

Chair of Anatomical Pathology, Moffitt Cancer Center, USA

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

The Moffitt 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.

09:40-10:10

SOLUTION PROVIDER PRESENTATION:
SENIOR REPRESENTATIVE

Bio-Rad Laboratories

Title TBC

BIO-RAD

TRACK 1 - HEALTHCARE CASE STUDIES

10:10-10:35

**GURO LIND**

Professor, Oslo University Hospital, Norway

Using DNA methylation dPCR for urine-based detection of bladder cancer

- Bladder cancer is one of the most expensive cancer types to manage for the society due to the high recurrence rate and subsequent extensive monitoring by cystoscopy
- A non-invasive urine-based test for bladder cancer may replace parts of these cystoscopies. Suitable DNA methylation biomarkers for bladder cancer detection have been identified from methylome sequencing and is currently being validated in urine samples using digital PCR
- To increase the accuracy of dPCR DNA methylation analyses we have developed an internal control and accompanying algorithm for separating positive from negative droplets.

10:35-11:25

Morning Refreshments / Poster Presentations

11:25-11:55

**SOLUTION PROVIDER PRESENTATION:**
DARREN ROBERTS

Postdoctoral Research Associate - University of Manchester - Division of Cancer Sciences

Development of gene signatures as cancer biomarkers using Applied Biosystems™ TaqMan® Array Cards

- Development of gene signatures as biomarkers
- Selection of endogenous controls for clinical research samples
- Pros and cons of Applied Biosystems™ TaqMan® Array cards in biomarker studies

ThermoFisher
SCIENTIFIC**BEN LEE**

Research Technician & PhD Researcher - University of Exeter Medical School

Multi-platform qPCR approaches to elucidating expression profiles in ageing

- Age is the largest risk factor for many chronic diseases with some 80% of all illness, morbidity and mortality costs occurring after the age of 65. Our research focuses on the molecular system involved in ageing and longevity, specifically the effects of RNA processing and post-transcriptional mechanisms.
- Alternative mRNA splicing and expression of splicing regulatory factors are a key strand of our research. I will talk about our use of different qPCR formats in the work we have published and some of our current projects
- We also have an interest in post-transcriptional regulation of gene expression. I will describe how we have used multiple qPCR platforms to discover associations between microRNA expression and lifespan and how we are currently using these formats to look at links with age-associated disease.

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11:55-12:20

**SUZAN PAS**

Clinical Molecular Microbiologist, Microvida

The Power of Molecular Viral Diagnostics in Clinical Medicine

Molecular diagnostics is one of the major techniques used in clinical virology nowadays, including techniques like qPCR and sequencing. This lecture will focus on the challenges and power of molecular diagnostics used in the past two decades in a reference laboratory during peace time and outbreaks like Ebola and Zika virus.

12:20-12:35

**EARLY CAREER RESEARCHER PRESENTATION:****WIM TRYPSTEEN**

PhD Researcher and Academic Staff Member, Ghent University, Belgium

Digital PCR in health care and clinical diagnostics: data analysis challenges

- Status & challenges of digital PCR in health care and clinical diagnostics
- Data analysis solution: ddpcRquant
- Example in a HIV clinical trial study (HIV DNA quantification)

12:35-12:50

**EARLY CAREER RESEARCHER 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.

12:50-13:15

**VINCENZO DI CERBO**

Analytical Development Scientist, Cell Therapy Catapult, UK

Analysis of viral integration events in single cells

- Use GFP-expressing lentivirus and retrovirus models.
- Estimate the heterogeneity of infection in a population of transduced human T-cells.
- Employ digital PCR methods to quantify the viral copy number at single cell level.

13:15-14:10

Lunch

14:10-14:35

**PAMELA PINZANI**

Associate Professor, University of Florence, Italy

Evaluation of qPCR tools and assay for the analysis of cell-free DNA

Cell-free DNA (cfDNA) represents a promising biomarker in cancer. In cancer patients cfDNA amount is higher than in controls and bears tumor specific alterations. Our studies aim at investigating a panel of markers associated to cfDNA in solid tumors. To this purpose we optimized qPCR assays for assessing the quantity and quality (in terms of DNA integrity) of cfDNA and for detecting tumor-derived cell-free DNA. We evaluated cfDNA quantity, integrity, BRAFV600E mutation and RASSF1A promoter methylation in plasma from patients affected by melanoma and thyroid nodules, demonstrating that an approach based on cfDNA could improve the diagnosis of these diseases.

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4BIO Registration

14:35-15:00

**CHARLOTTE GULDBORG NYVOLD**

Professor, Haematology-Pathology Research Laboratory, Odense University Hospital, Denmark

Molecular heterogeneity in haematological cancers addressed by qPCR

- Haematological cancer is a heterogeneous enclave, with respect to presentation and prognosis and can to a wide extent be characterized by genetic alterations of the malignant cells defining subgroups of the disease.
- However, genetic signatures are still lacking for a substantial number of cases and progression of subclones may confuse the molecular surveillance of the disease and lead to progression and relapse of the disease.
- By using qPCR the heterogeneous expression of genes can be determined and new subgroups of the haematological cancers can be defined which might influence the choice of precision medicine in the future.

15:00-15:25

**PONTUS LUNDBERG**

Head of Molecular Diagnostics, University of Basel, Switzerland

Digital PCR for monitoring minimal residual disease in hematological malignancies

Monitoring of minimal residual disease (MRD) in haematological malignancies is an important prognostic tool, as well as a tool to find relapsing patients early. However, MRD analysis is often limited to a small number of molecular markers for which standardized assay exists. Since the introduction of next generation sequencing in routine diagnostics, there now exists a large number of molecular aberrations that can be used to monitor therapy response and find relapse at an early stage. I will discuss how digital PCR and next generation sequencing can be used for monitoring MRD in patients where standard MRD markers, such as NPM1, are unavailable.

15:25-15:55

Afternoon Refreshments / Poster Presentations

15:55-16:20

**GARY PESTANO**

Vice President, Development and Operations, Biodesix

Development and Clinical Validation of Liquid ddPCR Tests for Actionable Somatic Mutations for NSCLC

We have developed and validated blood-based variant specific ddPCR tests for EGFR, KRAS, BRAF, EML4-ALK, ROS1 and RET variants. These tests are intended for use in patients diagnosed with Non-Small Cell Lung Cancer (NSCLC). The tests have been on the market as "the GeneStrat® test" since 2015; and in that time, has been utilized to analyze over 80,000 individual variants. Greater than 90% of tests have been delivered in less than 72 hours from receipt at the testing Laboratory. We will report on factors critical to the development, validation and on-market support of these tests. In this talk we will cover:

- Learning how Droplet Digital™ PCR technology is being used for liquid biopsy testing in the clinical setting
- Reviewing development and validation case studies for cfDNA testing using ddPCR
- Reviewing performance data and quality metrics from on-market experiences

16:20-16:45

Invitation Out
Title TBC

16:45

Conference Close

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Building on the success of the 3rd Synthetic Biology Congress held in October last year, Global Engage is pleased to announce the **4th Synthetic Biology & Gene Editing Congress**, to be held on the 4th and 5th December at the Novotel in Hammersmith, central London. Part of Global Engage's 4Bio summit this conference will be co-located with the 5th qPCR and Digital PCR Congress, 3rd Microfluidics Congress: Europe and NGS Europe Congress. 4Bio will host over 100 expert speakers and is expected to attract over 550 attendees and 100 poster presentations.

Designed for experts working in genome engineering, gene editing technological developments, protein design, the Synthetic Biology & Gene Editing congress will examine the latest developments in tools and platforms for synthetic biology and its applications in healthcare and human sciences, and will look ahead to the future of the field. To this end the conference will include a number of early career researcher presentations to allow the audience to engage with some of the up-and-coming names in the field, as well as the opportunity for successful start-ups to showcase the commercial potential of synthetic biology.

As technologies and strategies continue to mature, synthetic biology continues to be an exciting and rapidly developing area in the life sciences with the potential to revolutionise many aspects of society. With a focus on healthcare and investment, this interactive meeting will allow you to keep up to date with cutting edge of research and tool development, access to case studies on drug discovery, therapeutics and technologies, and the opportunity to make connections with academics, entrepreneurs, investors and businesses in your field.

EXPERT SPEAKERS Include:



RICHARD KITNEY

Professor of BioMedical Systems Engineering,
Imperial College London



JOHN GLASS

Professor & Leader of the Synthetic Biology
and Bioenergy Group, J. Craig Venter Institute



XAVIER DUPORTET

CEO,
Eligo Bioscience



SAMIRA KIANI

Assistant Professor,
Arizona State University

CONFIRMED SPEAKERS

The latest scientific advances in novel methods, investment opportunities and applications of synthetic biology and gene editing in the healthcare sector.

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DAY 1 – STREAM 1

Genomic Engineering & Synthesis

- Keynote Presentations Future perspectives – collaborations, strategies and technologies Engineering bacteriophages
- Panel Discussion 1 Next steps in synthesis approaches – novel approaches, directed evolution, cell free systems
- Case studies Synthetic genetic circuits
- Case studies Synthetic protein secretion
- Case studies Cell factory behavioural programming
- Case studies New model host organisms
- Early career researchers

DAY 1 – STREAM 2

Applications of Synthetic Biology in healthcare

- Case studies Therapeutic production
- Case studies Synthetic immunology and immune-oncology
- Case studies Synthetic biology for the production of antibiotics
- Case studies Novel synthetic production of antibiotics
- Early career researchers

DAY 2 – STREAM 1

Building Synthetic Life & Tools, technologies and platforms

- Keynote presentation Minimal cell project
- Case studies CRISPR techniques in mammalian cells to develop gene therapy platforms
- Case studies Developing platforms for immunotherapy
- Case studies Computational interface for cells
- Case studies Modelling software for designing synthetic biology

DAY 2 TRACK 2

Innovation, investment, strategies and start-ups

- Start-up case study Antimicrobial production
- Start-up case study Therapeutics and synthetic vaccines
- Case studies IP and legal strategies
- Case studies The global supply chain: logistical concerns in synthetic biology
- Panel discussion The bioeconomy – commercializing synthetic biology research
- Round Tables Ethics, strategies and challenges in Synthetic Biology

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RICHARD KITNEY
Professor of BioMedical
Systems Engineering, Imperial
College London



THORSTEN STAFFORST
Group Leader, Institute for
Biochemistry, Universität
Tübingen



MALATHI RAMAN
European Product Manager,
Takara Bio Europe, St Germain
en Laye, 78100, France



GEORG FRITZ
Independent Group Leader,
LOEWE Center for Synthetic
Microbiology, Philipps-
University Marburg



MARK ISALAN
Reader in Gene Network
Engineering, Imperial College
London



CĂLIN GUET
Assistant Professor, IST Austria



MARK KOTTER
Clinical Lecturer, University of
Cambridge



JOHN GLASS
Professor & Leader of
the Synthetic Biology and
Bioenergy Group, J. Craig
Venter Institute



PAUL RACE
Senior Lecturer, University of
Bristol



HAO YUAN KUEH
Assistant Professor, University
of Washington



GÜNTER MAYER
Professor, University of Bonn



**JEAN-SEBASTIEN
HULOT**
Professor of Medicine,
Pharmacology, Institute of
Cardiometabolism & Nutrition,
UMRS Inserm



COLIN HARWOOD
Professor of Synthetic Biology,
Newcastle University



CHRIS WILLIS
Professor of Organic
Chemistry, University of Bristol



GARETH COOPER
Investigator, Biological
Technologies UK R&D, Advanced
Manufacturing Technologies,
GlaxoSmithKline



ALFONSO JARAMILLO
Professor of Synthetic Biology,
University of Warwick



PHILIPPE JAIS
President and Chief Scientific
Officer, Eukarys



ANTONELLA FIDANZA
University of Edinburgh
(Scottish Centre for
Regenerative medicine, UK)



**VICTOR RODRIGO
IBARRA CHAVEZ**
PhD Student, University of
Glasgow



MARIA LLUCH SENAR
Staff Scientist, Center for
Genomic Regulation



RALF TAKORS
Professor, Director of the
Institute of Biochemical
Engineering, University of
Stuttgart



JUMAI ABIOYE
PhD Student, University of
Glasgow



TAMIR TULLER
Head of the Laboratory of
Computational Systems and
Synthetic Biology, Tel Aviv
University



KELLY STEVENS
Assistant Professor of
Bioengineering, University of
Washington



LUIS SERRANO
CRG Director, CRG Barcelona



IAN WHEELDON
Assistant Professor, University
of California Riverside



NICHOLAS HARMER
Senior lecturer in Structural
Biochemistry, Living Systems
Institute, University of Exeter



STEVE SHIH
Assistant Professor, Concordia
University



SARAH LAU
Partner, Kilburn & Strode



XAVIER DUPORTET
CEO, Eligo Bioscience



TIMO MINSEN
Professor University of
Copenhagen



NIKO SONNENSCHN
Senior Researcher, Novo
Nordisk Foundation

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CONFIRMED SPEAKERS



LIONEL CLARKE
Co-Chair of the Synthetic
Biology Leadership Council



CATHERINE FAN
DPhil Student, University of
Oxford



NORMAN GOODACRE
Postdoctoral Fellow, FDA



DAVIDE DE LUCREZIA
Doulix



ANDY HIGGS
UK Operations Manager,
Advanced Analytical
Technologies Ltd

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08:00-08:50

Registration & Refreshments

08:50-09:00

Global Engage Welcome Address and Morning Chair's Opening Remarks

09:00-09:40


**KEYNOTE ADDRESS:
RICHARD KITNEY**

Professor of BioMedical Systems Engineering, Imperial College London

Improving Bio Design Reliability and Reproducibly through the use of Foundries

Synthetic biology is now seen as a key driver of the bio economy. Synthetic biology (or engineering biology) will achieve industrial translation by the implementation of a model that uses a range feedstocks and synthetic biology for new industrial processes and products. A key aspect of this process is reliable, reproducible bioparts and gene circuits. The paper will address how this can be achieved by the use of foundries, where is it possible to control the characterisation processes through automation and monitoring. This requires the use of information technology and process management systems - as well as optimisation methodology. The overall aim is to achieve the implementation of high level BioDesign that links directly to automated foundries.

09:40-10:15


**KEYNOTE ADDRESS:
LIONEL CLARK**

Co-chair of the Synthetic Biology Leadership Council

Strategies for the future: the research and commercial landscape - Title TBC

10:15-10:45


**SOLUTION PROVIDER PRESENTATION:
MALATHI RAMAN**

European Product Manager, Takara Bio Europe, St Germain en Laye, 78100, France

Discover Innovative Technologies to Rapidly Generate Synthetic Genes and Proteins

There is a constant need for faster and more efficient cloning and protein purification methods at all scales within the Synthetic Biology field. Scientists can accelerate the generation of synthetic gene expression constructs using our innovative Next-Gen In-Fusion® HD Cloning Plus technology which is fast (15 mins), highly efficient (>95% cloning efficiency), sequence independent (Any insert can be cloned into Any vector at Any locus), seamless (no extra bp), directional, HTP ready, and is ideal for the assembly of complex synthetic genes. After generation of the required expression construct and downstream expression of the target protein, Takara offers Next-Gen Capturem™ technology to allow fast (5-15 mins) and easy resin-free purification of high quality and concentrated His-tagged proteins or native untagged antibodies. Our revolutionary Capturem technology, available in miniprep, maxiprep and 96-well plate formats, consists of spin columns or plates containing high-capacity nylon membranes immobilized with either Ni²⁺ or Protein A, thus allowing His-tagged protein or antibody purification directly from even complex matrices, such as cell culture supernatants or serum, within minutes. This talk will review several applications of our technologies including the assembly of complex synthetic genes, HTP antibody cloning, simplified purification of membrane and secreted proteins, fast hybridoma screening, and rapid immunoprecipitation (IP)/co-immunoprecipitation (Co-IP). We will also introduce our new Capturem Trypsin technology that enables 1 min on-column tryptic digests.



10:45-11:55

Morning Refreshments / Poster Presentations / Scheduled One-to-One Meetings

GENOMIC ENGINEERING

APPLICATIONS OF SYNTHETIC BIOLOGY IN HEALTHCARE & RESEARCH

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11:55-12:20

**GEORG FRITZ**Independent Group Leader, LOEWE Center for Synthetic Microbiology,
Philipps-University Marburg**Engineering orthogonal synthetic timer circuits in bacteria**

- The rational design of synthetic circuits is often restricted by cross-reactions between circuit components and physiological processes within the heterologous host.
- Here, seek to overcome these restrictions by using extracytoplasmic function σ factors (ECFs), which represent ideal orthogonal regulators because of their high promoter specificity. After evaluating several heterologous ECF switches in *E. coli* and *B. subtilis*, computational modelling allows us to predict cascades with two and three ECFs. These "autonomous timer circuits" activate a series of target genes with defined time delays, which we find in excellent agreement with experimental data.
- These results not only serve as a proof of concept for the application of ECFs as organism-independent building blocks in synthetic biology, but could also be used in biotechnological applications, e.g. to introduce a timing hierarchy in the expression of biosynthetic pathway components.

12:20-12:45

**MARK ISALAN**

Reader in Gene Network Engineering, Imperial College London

Synthetic Biology via continuous directed evolution

Recent advances in the field of directed evolution for protein engineering could potentially revolutionize genetic circuit engineering. We are developing a low-cost plug-and-play methodology for the rapid de novo engineering of biomolecules and genetic logic gates through in vivo directed evolution. The system uses a programmable robot with a bioreactor that mixes bacteria and phage. This allows continuous selections and counterselections, thus evolving useful properties. We illustrate the system by evolving the first set of dual activator-repressor switches for orthogonal logic gates, based on bacteriophage λ ci variants and multi-input promoter architectures. Because the ci transcription factor is used in so many synthetic biology projects, the new set of variants will easily slot into the existing projects of other groups, greatly expanding current engineering capacities.

12:45-13:00

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13:15-14:15

Lunch / Poster Presentations / Scheduled One-to-One Meetings

14:15-14:40

**CĂLIN GUET**

Assistant Professor, IST Austria

The synthetic frontier - unravelling the complexity of biology

Biology has a long history of using powerful model systems that capture important aspects of the intrinsic complexity of living systems. The use of simple model systems in Synthetic Biology can unravel fundamental questions that Biology still keeps under lock from us.

11:55-12:20

**PAUL RACE**

Senior Lecturer, University of Bristol

Rational Design and Redesign of Natural Product Pharmaceuticals

Natural products have, and continue to be, a mainstay of pharmaceutical drug discovery. Many of these compounds are generated by sophisticated biosynthetic megaenzymes which may be rationally manipulated to deliver functionally optimised products. Here I summarise recent efforts in the rational engineering of such systems to deliver high potency 'non-natural' natural product pharmaceutical leads.

12:20-12:45

**HAO YUAN KUEH**

Assistant Professor, University of Washington

Control of the T-cell fate by a chromatin-based timing control switch

The decision to become a T-cell is controlled by a genetic switch involving activation of a key transcriptional regulator Bcl11b. Here, we studied the activation dynamics of Bcl11b at the single cell level, using a novel dual color reporter tagging strategy to separately follow the two genomic copies of Bcl11b in single progenitor cells. Our experiments show that Bcl11b activation and T-cell lineage commitment is controlled by a slow, all-or-none gene switch implemented directly on the Bcl11b chromatin environment. These results reveal a previously unappreciated role for chromatin-based mechanisms in controlling cell fate switching dynamics, and establish a strategy for studying chromatin-based gene expression control in living cells.

12:45-13:15

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12:45-13:15

**GÜNTER MAYER**

Professor, University of Bonn

Bacterial RNA structures as drug targets

- RNA elements in bacterial mRNA regulate gene expression
- These elements also regulate control the expression of essential genes
- Artificial compounds targeting these RNA elements represent candidates for developing novel antibiotics

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14:40-15:05

**MARK KOTTER**

Principal Investigator, University of Cambridge

Inducible and deterministic forward programming of human pluripotent stem cells into somatic cell types

- Recent advances in the field of stem cell research promise unprecedented opportunities for the study of human biology, and potentially the treatment of crippling diseases.
- However, the isolation or in vitro derivation of many human cell types remains challenging and inefficient. Direct conversion of human pluripotent stem cells (hPSCs) by forced expression of transcription factors provides a potential alternative.
- By optimising the way reprogramming cassettes are expressed in human stem cells, we have made cellular reprogramming deterministic. This allows the generation of functional human cells within very short time frames (3-4 days as compared to months), at purities approaching 100%.

**RALF TAKORS**

Professor, Director of the Institute of Biochemical Engineering, University of Stuttgart

Escherichia coli HGT: a novel high glucose throughput chassis, engineered for large scale production and derived from systems biology studies

ppGpp, the alarmone of stringent response, turned out to be protagonist of the observed regulation programs. Carefully engineering intracellular ppGpp levels resulted in E. coli HGT (Michalowski et al., Metabolic Engineering, 2017) with about 10 fold increased glucose uptake rates (compared to native maintenance demands) under resting or slow growth conditions. Ultimately, novel microbial producers should find their way into large scale bioreactors for commercializing the product. However, successful scale-up is often hampered by harsh production conditions which expose the strains to frequently changing substrate supply due to technical limits of mixing. Accordingly, metabolic and transcriptional responses of E. coli to large-scale conditions were studied unraveling short- and long-term consequences of changing glucose and nitrogen availabilities (Löffler et al., Metabolic Engineering, 2016; Simen et al. Microbial Biotechnology, 2017). About 600 genes were found to be frequently up- and down regulated. Consequently, cellular maintenance demands increased by 40 to 50%.

15:30-16:00

14:40-15:05

**JEAN-SEBASTIEN HULOT**

Professor of Medicine, Pharmacology, Institute of Cardiometabolism & Nutrition, UMRS Inserm

Genome and epigenome editing for cardiovascular disease

- Use of genome-editing techniques to target missense mutations causing genetic cardiomyopathies
- Use of epigenome-editing techniques to reprogram cell identity in the cardiovascular system
- Insight into CRISPR possibility to treat cardiovascular disorders

15:05-15:30

**CHRIS WILLIS**

Professor of Organic Chemistry, University of Bristol

Taking Inspiration from Nature for the Generation of Novel Antibiotics

Nature has provided the scientific community with a wealth of fascinating molecules which have served as leads for the development of new medicines and agrochemicals. By gaining an in-depth understanding of the biosynthetic pathways to natural products, we can now genetic modify these complex "assembly lines" to provide biologically active compounds which cannot be accessed efficiently using traditional chemical synthesis. Recent progress on the use of synthetic biology to prepare novel targets with antibiotic activity will be described

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16:00-16:50

Afternoon Refreshments / Poster Presentations

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16:50-17:15

**ALFONSO JARAMILLO**

Professor of Synthetic Biology, University of Warwick

Next-generation RNA circuits in living cells

We propose a general methodology based on biophysical principles to automatically design RNA components with complex features previously only found in transcription factors: non-linearity, feedback, signal transduction, multimeric riboregulation, "switchable" RNA cascades and anti-termination RNA switches. Furthermore, we are able to engineer regulatory RNAs able to self-circularize after undergoing a maturation step. Our RNAs are different to any known non-coding sequence and their predicted behavior is validated in *E. coli* at the population and single-cell levels. The RNA networks can also be used to regulate target genes in any living system where CRISPR is known to work. We also show that we can sense the transcript levels of a target gene in vivo, which we use to determine the cell-cycle phase in eukaryotic cells. Our RNAs can form complex interaction networks to provide novel synthetic gene networks working in prokaryotic and eukaryotic systems.

17:15-17:30

**EARLY CAREER RESEARCHERS PRESENTATION:
ANTONELLA FIDANZA**

University of Edinburgh (Scottish Centre for Regenerative medicine, UK)

Transcriptional activation of endogenous transcription factors using novel all-in-one dCas9-SAM system

1. We developed an all-in-one dCas9 SAM system – UniSAM – which activates endogenous gene expression of target loci with one gRNA in a single transfection, resulting in improved SAM system and simplified workflow.
2. The UniSAM successfully activates the transcription of target genes in different cell types including human pluripotent stem cells, on both mRNA and protein level.
3. The UniSAM results in significant higher cell viability when compared with the previous available multiplasmid system, this allows to exploit the system on sensitive cell types such as human pluripotent stem cells.

17:30-17:45

**EARLY CAREER RESEARCHERS PRESENTATION:
JUMAI ABIOYE**

PhD Student, University of Glasgow

Rational engineering of Tal-effector recombinases for genome editing

- Most genome editing approaches being developed as potential therapeutic strategies utilize nuclease-based systems such as CRISPR-Cas9.
- These systems have off-target activities which can lead to adverse effects in therapy and other bioapplications.
- We present the rational engineering of modular programmable tools called Tal-effector recombinases (TALERS) that are capable of specific excision and religation on non-cognate sequences.
- As a proof of concept, we have targeted a highly conserved region within the HIV-1 long terminal repeats (LTR) flanking the proviral DNA at both ends. Our engineered proteins target the sequence and excise in an in vitro system and an in vivo *E. coli* model system
- We are working to progress into testing TALERS in more complex eukaryotic systems. This research provides a novel tool and technique for optimizing precision and programmability in genome engineering.

16:50-17:15

**GARETH COOPER**

Investigator, Biological Technologies UK R&D, Advanced Manufacturing Technologies, GlaxoSmithKline

Using Synthetic Biology and CRISPR/Cas9 bacterial genome engineering for drug development

Using synthetic biology approaches to augment and modify bacterial genomes allows the exploration of synthetic enzyme cascades and pathways in vivo. From a pharmaceutical standpoint, if these technologies could be harnessed correctly it may allow the biological production of active pharmaceutical ingredients or important intermediates. This would give scope to reducing production costs, reducing solvent and water use and improving safety aspects of drug production. The design and application of a CRISPR/Cas9 genome editing system for a non-model bacterium was investigated as it produced a secondary metabolite of pharmaceutical interest. Development of this system has allowed directed genome edits to be performed with examples of gene knockout, larger knockouts of chromosomal regions and knock-ins of synthetic expression cassettes.

17:15-17:30

**EARLY CAREER RESEARCHERS PRESENTATION:
VICTOR RODRIGO IBARRA CHAVEZ**

PhD Student, University of Glasgow

Synthetic Phage Biosensors for Pathogen Detection and Eradication

Diagnosis and treatment of infectious diseases is one of the major challenges we face. This, coupled with the emerging global threat of antimicrobial resistance, requires that we consider new paradigms in therapy. As innovative and affordable alternatives emerge that allow us to rapidly detect bacteria at the point-of-care, we use synthetic biology to combine the two concepts of diagnostics and therapy to "seek & destroy" specific bacteria. To achieve this, we have created a synbio toolbox to develop sensing systems able to identify the presence of pathogens at the point-of-care. These novel biosensors will be able to detect and eliminate the pathogen by using the pathogen itself to modify its genome specifically to produce a reporter (seek) and/or a killing switch (destroy).

17:30-17:45

**EARLY CAREER RESEARCHERS PRESENTATION:
MARIA LLUCH SENAR**

Staff Scientist, Center for Genomic Regulation

Engineering of minimal chassis as delivery system to dissolve biofilms

Engineering bacteria to deliver therapeutic agents has been proposed for different applications. Currently, the main bottleneck towards applying them in human therapy is our inability to predict their behavior in the host. Thus, bacteria with minimal genomes could facilitate their comprehensive characterization by Systems biology approaches to become predictable. The small genome of *Mycoplasma pneumoniae* (816 kb) makes this human lung pathogen, a well-suited model for Systems biology and Synthetic biology. By combining a comprehensive Systems Biology analysis and recent implemented genetic tools, we have rationally engineered *M. pneumoniae* as chassis to dissolve biofilms formed by *Staphylococcus aureus*. We envisage that this delivery system could be used to treat human lung diseases opening new perspectives in synthetic biology applications.

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17:45-18:10

**THORSTEN STAFFORST**

Group Leader, Institute for Biochemistry, Universität Tübingen

Site-directed RNA with ADARs and engineered riboproteins

- In contrast to DNA editing, RNA editing allows to manipulate gene expression in a tunable and reversible fashion thus allowing to introduce potentially lethal or readily compensable mutations.
- For therapeutic applications the harnessing of endogenous ADARs is most attractive. We will present antisense oligonucleotides that allow for recruitment of human ADARs and demonstrate their application in the restoration of mitophagy signaling.
- For tool development, we have engineered SNAP-deaminases that apply the SNAP-tag to assemble artificial RNA-guided editases inside cells and living organisms. Highly efficient editing of several sites in distinct transcripts is feasible. Due to chemical modification of the guideRNA, editing specificity is highly controllable and photoactivation can be readily implemented.

18:10-18:35

**PHILIPPE JAIS**

President and Chief Scientific Officer, Eukarys

Artificial C3P3 transcriptional engine for synthetic gene therapy

Transcription and post-transcription are processes of exquisite complexity, which has impeded the development of artificial systems able to generate mature messenger RNA (mRNA) in eukaryotic cells. We present the so-called C3P3 technology, which is the first artificial system ever able to autonomously synthesize mature mRNA in the cytoplasm of eukaryotic cells. This enzymatic system, now in its second generation for mammals, relies on a single monomeric enzyme developed by synthetic biology. Once expressed, this enzyme transcribes specific DNA templates, and then performs the key modifications of the transcripts required for their translation. Among the different applications of the C3P3 system, we will present the results for a novel approach of gene compensation of monogenic and multifactorial human disorders, called synthetic gene therapy. Its potential will be illustrated by the results of EUK-LPR, our first synthetic gene therapy that is a liver pro-regenerative treatment with demonstrated efficacy in animal models.

18:35-19:35

Closing Remarks End of Day One / Drinks Reception

17:45-18:10

**COLIN HARWOOD**

Professor of Synthetic Biology, Newcastle University

Secretion of heterologous proteins from *Bacillus subtilis*: from the cradle to the grave

- *Bacillus subtilis* is widely used for the production of industrial products including enzymes, vitamins, amino acids, antimicrobial peptides and surface-active agents
- Importantly, *B. subtilis* efficiently secretes native proteins and those from related bacteria into the culture medium at concentrations in excess of 20 g/L. However, yields of foreign proteins, such as mammalian therapeutic proteins, is much more variable (μ – mg/L).
- With a view to addressing the issue of why *Bacillus* species are generally poor secretors of foreign proteins, we have used a combination of synthetic biology and gene editing technology to systematically identify bottlenecks in the secretion pathway. In part, the answer lies in the folding characteristics and structure of the target proteins and what we refer to as the cell's Quality Control Machinery

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08:00-08:35 Refreshments & Networking Meetings

08:35-08:40 Morning Chair's Opening Remarks

09:00-09:40

**KEYNOTE ADDRESS:
JOHN GLASS**

Professor & Leader of the Synthetic Biology and Bioenergy Group, J. Craig Venter Institute

Design, Construction, and Analysis of a Minimal Bacterial Cell

- Synthetic genome containing only the 474 genes needed for rapid growth in laboratory media designed and built
- One third of the genes have no known function and most of those unknowns are widely conserved in prokaryotes and eukaryotes
- We are constructing a whole cell computational model that accurately embodies minimal cell biology

TOOLS, TECHNOLOGIES AND PLATFORMS

09:40-10:10

**SOLUTION PROVIDER
PRESENTATION:
DAVIDE DE LUCREZIA**

Doulix

**Empowering computer-aided biological design by using in vivo
characterized Standard Biological Parts**

The SB has already revolutionized production paradigms in many different fields. These remarkable achievements have largely been 'one-offs' since each one is a special case and though they must be regarded as milestones in the respective field they do not provide a comprehensive and coherent engineering framework. We advocate that the main barriers that prevent SB full exploitation are: i) lack of biochemical characterization of biological parts and ii) lack of a multi-scale modeling platform. We will present the latest results of our ongoing efforts to develop a comprehensive and highly integrated toolkit based on i) comprehensive in vivo characterization of BioBricks and ii) development of a computer aided design tools (CAD).



10:10-10:35

**TAMIR TULLER**

Associate Professor of Computational Systems and Synthetic Biology, Tel Aviv University

**Engineering cells and genes based on whole cell simulations for
various biotechnological objectives.**

Some recent studies have demonstrated how the competition for the finite pool of available gene expression factors has an important effect on fundamental gene expression aspects. Thus, accurate gene expression models that also consider such competitions should provide important advantages for designing synthetic genes and organisms.

INNOVATION, INVESTMENT AND START-UPS

09:40-10:10

SOLUTION PROVIDER PRESENTATION

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

10:10-10:35

**SARAH LAU**

Partner, Kilburn & Strode

Synthetic Biology and Gene Editing - IP and Commercialisation

- The evolution of synthetic biology - from the lab to commercialisation
- Case studies on synthetic biology and gene editing commercialisation
- The latest on the CRISPR patent battles in the US

10:35-11:25 Morning Refreshments / Poster Presentations

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4BIO Registration

11:25-11:40

**SOLUTION PROVIDER PRESENTATION:****ANDY HIGGS**

UK Operations Manager, Advanced Analytical Technologies Ltd.

Automating Analysis of CRISPR Genome Editing

Advanced Analytical Technologies has developed optimized screening protocols and QC analysis solutions for CRISPR workflows. An optimized heteroduplex cleavage assay uses T7 Endonuclease I to address the challenges associated with other screening protocols including zygosity determination and scalability. Similarly, understanding the quality of CRISPR reagents to be used in a genome editing workflow – namely single guide RNA (sgRNA) and gauging polyadenylation of Cas9 mRNA – is of paramount importance to success.



11:40-11:55

SOLUTION PROVIDER PRESENTATION

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

11:55-12:20

**KELLY STEVENS**

Assistant Professor of Bioengineering, University of Washington

Hijacking Nature's Blueprints for Synthetic human Tissue Assembly

Human development – the process by which a single celled zygote transforms into a human being – involves the incredibly complex and self-orchestrated specification, differentiation, and assembly of trillions of cells. Despite nature's power during development, the adult body cannot always reassemble or repair itself after injury, such as after a heart attack or liver cirrhosis. My lab's research seeks to hijack and rewire aspects of nature's developmental programs to control the processes by which cells assemble to form human systems. Here I will highlight some of our work in both constructing and controlling artificial heart and liver tissue using both nature's blueprints and new bioprinting technologies.

12:20-12:45

**EARLY CAREER RESEARCHERS PRESENTATION:****CATHERINE FAN**

DPhil Student, University of Oxford

SimCells: A novel chassis for synthetic biology and drug delivery

The rapidly growing field of synthetic biology involves the manipulation of biological systems for valuable purposes. However, many challenges arise as living systems cannot be engineered without interference from their native metabolic networks and genetically modified organisms are not trusted by the public. To address these issues, a novel technology called "SimCells" has been created as an alternative, organic chassis to living organisms. SimCells are essentially bacterial cells lacking genomes (i.e. they cannot replicate) but which remain fully equipped with the cellular resources to produce proteins or small molecules from introduced DNA carried by plasmids. This new chassis will allow researchers to study basic cellular processes more robustly and allow cells to be more efficient chemical factories. The safe application of a bacterial chassis in mammalian cell therapy and regenerative medicine will open new avenues for synthetic biology.

11:25-11:55

SOLUTION PROVIDER PRESENTATION

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11:55-12:20

**START-UP SHOWCASE:****XAVIER DUPORTET**

CEO, Eligo Bioscience

Next-gen biotherapeutics for precise microbiome engineering and sequence-specific antimicrobials

- Increasing number of high unmet medical needs associated with microbiome
- CRISPR-Cas based antimicrobials: a new tool to elucidate causality relationships between bacteria and diseases
- New tool for targeted eradication of pathogenic and antibiotic-resistance bacteria

12:20-12:45

**TIMO MINSEN**

Professor, University of Copenhagen

The Interface between Big Data, IPRs & Competition Law in SynBio and SysBio – From Big Data to Smart Data

The vast prospects of Big Data and the shift to more "personalized", "open" and "transparent" innovation models highlight the importance of an effective governance, regulation and stimulation of high-quality data-uses in the health and life sciences. Intellectual Property Rights (IPRs) and related rights come into play when research is translated into safe and efficient "real world" uses. While the need of recalibrating IPRs to fully support Big Data advances is being intensely debated among multiple stakeholders, there seems to be much confusion about the availability of IPRs and their legal effects. This presentation provides an overview on the most relevant IPRs for data-based research in Synthetic Biology and Systems Biology. It will discuss selected areas that demonstrate emerging tensions and potential solutions at the interface of Big Data, Standardization and Intellectual Property Rights.

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12:45-13:00

**EARLY CAREER RESEARCHERS PRESENTATION:
NORMAN GOODACRE**

Postdoctoral Fellow, FDA

Essential domains of unknown function in yeast

- Single-gene-knockout data for both *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* was taken from the Database of Essential Genes (DEG), and gene-protein-domain mapping was performed using Uniprot
- Essential domains underpinning essentiality of DEG genes was inferred using both rule-based and statistical approaches (expectation maximization)
- 68 inferred essential domains had no known function in the Protein Families (Pfam) database and were termed "yeDUFs" (yeast essential domains of unknown function)
- Gene Ontology (GO) terms associated with proteins wherein these 68 yeDUFs were found indicate roles in alternative carbohydrate metabolism, mitochondrial transport, nuclear pore complex, mRNA processing, initiation of translation, protein complex assembly, and membrane-binding.
- ~25% of these yeDUFs are broadly conserved across all kingdoms of life (including Bacteria), while a small number are found in large numbers of proteins in mammals.

13:00-13:15

**LUIS SERRANO**

CRG Director, CRG Barcelona

Engineering of *Mycoplasma pneumoniae* as a tool to dissolve in vivo biofilms

Mycoplasma pneumoniae is one of the best known bacteria with complete -OMICS sets as well as a whole cell model. Taking advantage of its unique characteristics (gliding motility, lack of cell wall, no LPS and a genetic code that uses a stop codon for Trp) we have created a non-pathogenic chassis. By developing new genetic tools, we have developed a new delivery chassis that can express peptides targeting *S. aureus* biofilms. In vitro, ex-vivo and in vivo experiments show its efficacy in catheter assays. We plan to extend its biofilm dispersion activity against other common human lung infections

13:15-14:10

Lunch / Poster Presentations / Scheduled One-to-One Meetings

14:10-14:35

**IAN WHEELDON**

Assistant Professor, University of California Riverside

Leveraging CRISPR-Cas9 genome editing tools to engineer non-traditional yeasts for chemical biosynthesis

A valuable approach to synthetic biology is identifying desirable phenotypes in microorganisms and developing genome engineering tools to control and enhance these properties. The widespread adoption of CRISPR-Cas9 systems for genome editing has enabled this approach by making less genetically tractable organisms more accessible. In this context, we have designed new synthetic RNA polymerase III promoters for CRISPR-Cas9 guide RNA expression in non-*Saccharomyces* yeasts. The genome editing systems can efficiently create gene disruptions and insertions as well as regulate the expression of arbitrary genes. We targeted *Yarrowia lipolytica* for its high capacity to convert sugars to oleochemicals, and our newly developed tools have allowed us to rapidly engineer strains that produce high titers of carotenoids. We targeted *Kluyveromyces marxianus* because of its thermotolerance and native capacity to produce ethyl acetate and ethanol at high rates. Application of CRISPR-Cas9 genome editing and gene regulation has enabled the identification of novel ester biosynthesis pathways and the engineering of new high producing strains.

12:45-13:15

PANEL DISCUSSION:**Challenges in the commercialization of synthetic biology research****Reserved:****Timo Minssen**, Professor, University of Copenhagen**Invitations to:**

3x Senior Representatives

14:10-15:25

ROUNDTABLE DISCUSSIONS:**Challenges for the future of Synthetic Biology**

- **Roundtable 1:** Ethics and society
- **Roundtable 2:** IP and Regulation
- **Roundtable 3:** Collaboration strategies

**KELLY STEVENS**

Assistant Professor of Bioengineering, University of Washington

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14:35-15:00

**STEVE SHIH**

Assistant Professor, Concordia University

Miniaturized laboratories for synthetic biology

Miniaturizing and automating laboratories has been a way to automate synthetic biology – speeding up the cycle of design-build-test. Digital microfluidics (DMF) is a means of miniaturizing laboratories that enables the control of individual droplets on an array of electrodes with the advantages of automation and integration. In this talk, I plan to discuss two projects that are harnessing the power of DMF in making synthetic biology quick and easy. In the first project, we are automating gene editing processes and to search for genes suspected to be involved in various cancer pathways. In the second project, we developed a rapid prototyping process that will be capable of creating DMF devices using off-the-shelf equipment for automating DNA assembly and transformation.

14:10-15:25

Continued

15:00-15:25

**NICHOLAS HARMER**

Senior lecturer in Structural Biochemistry, Living Systems Institute, University of Exeter

Building and optimising multi-enzyme in vitro cascade reactions

- Biocatalysis and synthetic biology are increasingly attractive as routes for green chemistry.
- Developing robust pathways requires good modelling.
- This presentation will show the development and optimisation of a seven enzyme cascade in vitro as a model for a synthetic biology pathway.
- Developing this pathway in vitro highlights the benefit of understanding the pathway thoroughly before progressing to a cellular model.

15:25-15:55

Afternoon Refreshments / Poster Presentations

15:55-16:20

**NIKO SONNENSCHN**

Senior Researcher, Novo Nordisk Foundation

Data-Driven Design of Cell Factories and Communities

With ultra-precise genome editing tools at our disposal, the life sciences will shift from one-factor-at-a-time type of experiments to an ever increasing need to design complex non-intuitive manipulations involving simultaneous changes at multiple loci. In principle, integration of omics data and systems biology models would provide the means for optimizing knowledge gain through rational target selection and experimental design. They are not leveraged effectively, however, due to a lack of readily available tools to rapidly access and analyze public and private data. With this project we aim to make a broad spectrum of omics data useful to biotechnology and life science research by integrating systems biology with design in a one-stop platform that will serve a variety of application areas, ranging from industrial biotechnology to agriculture and human health. All research efforts will be integrated in an interactive, web-based platform available to both industrial and academic research. A first iteration of the platform is already available at <http://dd-decaf.eu>.

15:55-16:20

Invitation Out

16:45

Closing Remarks Conference Close

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Building on the success of our 2016 Microfluidics Congress in London, Global Engage is pleased to announce the **3rd Microfluidics Congress: Europe** which will be held on the 4th and 5th December at the Novotel London West in central London. As part of Global Engage's 4Bio summit this conference will be co-located with the 5th qPCR & Digital PCR Congress, 4th Global Synthetic Biology & Gene Editing Congress, and NGS Europe Congress. 4Bio will host over 100 expert speakers and is expected to attract over 550 attendees and 100 poster presentations.

With a continually expanding range of applications, microfluidics is proving itself a vital field in the advancement of human health. At the intersection of engineering, physics, chemistry, nanotechnology and biotechnology, microfluidics is revolutionising the way patients are diagnosed, monitored and treated.

This congress brings together experts working in the development and application of microfluidic devices, and will showcase case studies examining the latest advancements in point-of-care diagnostics, single cell analysis, lab-on-a chip applications including organs-on-chips, droplet microfluidics and next generation microfluidics. This interactive meeting will allow you to keep up to date with the cutting edge of research and the opportunity to make connections with academics, entrepreneurs and businesses in your field.

EXPERT SPEAKERS Include:



ANDREW DE MELLO

Professor of Biochemical Engineering &
Chairman, ETH Zurich



EUGENIA KUMACHEVA

Professor,
University of Toronto



CHUCK HENRY

Professor of Chemistry,
Colorado State University



WINNIE SVENDSEN

Associate Professor,
Technical University of Denmark

CONFERENCE SYNOPSIS

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DAY 1

Strategy and Technology in Microfluidics

- Keynote Presentations Optical tweezers in microfluidic devices
- Case Studies Centrifugal microfluidics
- Case Studies Acoustic and opto-fluidics
- Case Studies Microfluidic device fabrication
- Case Studies Integration of spectroscopy and microfluidic devices

DAY 2

Case Studies and Applications in Medical Research

- Keynote presentation Detecting antimicrobial resistance
- Case Studies Organ on a chip
- Case Studies Point of care diagnostics
- Case Studies Biological and Environmental sensors
- Case Studies Using microfluidic devices for particle synthesis
- Case Studies Microfluidics for assisted reproductive technologies

CONFIRMED SPEAKERS

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ANDREW DE MELLO
Professor of Biochemical
Engineering & Chairman,
ETH Zurich



EUGENIA KUMACHEVA
Professor, University of Toronto



NILS PAUST
Head of Division of Microfluidic
Platforms, Hahn Schickard



PER AUGUSTSSON
Assistant Professor in
Biomedical Engineering,
University of Lund



**WOUTER METSOLA
VAN DER WIJNGAART**
Professor of micro- and
nanofluidic systems, KTH



ANDERS KRISTENSEN
Professor, Technical University
of Denmark



ELAINE FU
Assistant Professor in Bio
Engineering, Oregon State
University



**NIRVEEK
BHATTACHARJEE**
Postdoctoral Fellow, Folch Lab,
University of Washington



DANIEL MCCLUSKEY
Chief Engineer, Applied R&D:
Biodetection, University of
Hertfordshire



CHUCK HENRY
Professor of Chemistry,
Colorado State University



PETER ERTL
Professor, Vienna University of
Technology



NICOLE PAMME
Professor, University of Hull



MONICA BRIVIO
Strategic R&D Manager,
Micronit Microtechnologies



WINNIE SVENDSEN
Associate Professor, Technical
University of Denmark



**BALAJI
PANCHAPAKESAN**
Senior Associate Professor,
Mechanical Engineering
Department, Worcester
Polytechnic Institute



LOES SEGERINK
Assistant professor, Institute
of Nanotechnology, University
of Twente



JOHAN ELF
Professor, Uppsala University



JEROEN LAMMERTYN
Professor, Head of the MeBioS
Biosensors Group, KU Leuven



**FREDRIK
WESTERLUND**
Associate Professor, Chalmers
University of Technology



DAVE WEITZ
Mallinckrodt Professor of
Physics and Applied Physics,
Harvard University

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08:00-08:50 Registration & Refreshments

08:50-09:00 Global Engage Welcome Address and Morning Chair's Opening Remarks

09:00-09:40

**KEYNOTE ADDRESS:****ANDREW DE MELLO**

Professor of Biochemical Engineering & Chairman, ETH Zurich

Optical Tools for Ultra High-Throughput Cellular Analysis

The considerable advantages that are afforded through the use of microfluidic systems are in large part made possible by system downscaling and the associated improvements in mass and thermal transfer. Nonetheless, handling and processing fluids with instantaneous volumes on the fL-nL scale represents a critical challenge for molecular detection, and still defines one of the key limitations in the use of a microfluidic system in a given application. I will present recent studies focused on the development of novel imaging flow cytometry platform that leverages the integration of inertial microfluidics with stroboscopic illumination to allow for high-resolution imaging of cells at throughputs excess of 100,000 cells/second. Additionally, I will describe how vibrational and photothermal techniques can be used for high sensitivity molecular fingerprinting within microfluidic environments. Such "label-free" techniques are of particular significance to chemical and biological systems, since they directly engender the high-throughput and sensitive analysis of non-fluorescent species.

09:40-10:15

**KEYNOTE ADDRESS:****EUGENIA KUMACHEVA**

Professor, University of Toronto

Microfluidic platforms to study gas-liquid interactions

Over the past decade, microfluidics has emerged as an efficient tool in fundamental and applied studies of gas-liquid processes. In my talk, I will highlight our progress in studies of chemical reactions and physical processes involving carbon dioxide (CO₂), one of the most important green house gases. To synthesize efficient catalysts and optimize chemical formulations, fundamental knowledge has to be developed on the mechanisms, kinetics and thermodynamics of gas-liquid reactions, as well as physical CO₂-mediated processes, e.g., extraction and phase separation. We have developed several microfluidic platforms to study CO₂ reactions in two exemplary systems: "switchable solvents" and Frustrated Lewis pairs. The platforms provided unique information on thermodynamic properties, equilibrium constants, conversion, and completeness of CO₂-mediated phase separation, separation of gas mixtures, screening of the efficiency of chemical reagents, and the recovery of CO₂, all achieved in a time- and labour-efficient manner.

10:15-10:45

**SOLUTION PROVIDER PRESENTATION:****HOLGER BECKER**

Co-founder and CSO, microfluidic ChipShop GmbH

True lab-on-a-chip devices: Complexity and Manufacturing challenges

With the advent of highly integrated microfluidic devices, the original concept of a lab-on-a-chip is becoming a reality in many life science or diagnostic applications. For the development and industrial manufacturing of such devices however, significant challenges exists during development and in the selection of suitable manufacturing technologies. The talk will explore solutions to such challenges in order to not only end up with a functional but also a commercially viable device. Examples from diagnostics, analytical and biotech applications will be presented.



10:45-11:55 Morning Refreshments / Poster Presentations

STRATEGY AND TECHNOLOGY IN MICROFLUIDICS

11:55-12:20

**DAVE WEITZ**

Mallinckrodt Professor of Physics and Applied Physics, Harvard University

Droplet based microfluidic applications in biotechnology - Title TBC

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12:20-12:45

**NILS PAUST**

Head of Division of Microfluidic Platforms, Hahn Schickard

Centrifugal Microfluidics: Recent developments

Forces in rotating disks are used to pump liquids, load pneumatic chambers, mix liquids, generate droplets etc. The idea is not new but nevertheless, new functionalities and the implementations of new applications are being introduced at high pace. Centrifugal microfluidics for miniaturization, automation and parallelization of biochemical workflows is attractive because no interfaces to pumps and valves are required, the artificial gravity field eliminates bubble problems and surface forces can be overcome for volumes down to the nanoliter range. In this talk I will give an overview on recently developed methods for efficient and robust layout of centrifugal microfluidics systems and I will discuss new implementations such as integrated nucleic acid analysis based on digital PCR.

12:45-13:15

SOLUTION PROVIDER PRESENTATION:**SENIOR REPRESENTATIVE**

Elveflow

Title - TBC



13:15-14:15

Lunch

14:15-14:40

**PER AUGUSTSSON**

Assistant Professor in Biomedical Engineering, University of Lund

Iso-acoustic focusing organizes cells and liquids based on their acoustic properties

In iso-acoustic focusing cells are separated in continuous flow based on their acoustic properties and independent of their size. We apply acoustic fields on complex mixtures of cells and liquids of inhomogeneous acoustic properties and study how they re-organize according to their relative density and compressibility. This new equilibrium modality of acoustophoresis opens the route to process cells from particle rich suspensions and also enables precise separation of sub-micron particles due to a much reduced acoustic streaming. The fundamentals of iso-acoustic focusing will be outlined and recent results relating to cell mechano-phenotyping and separation will be presented. Application areas that are under current investigation will be discussed.

14:40-15:05

**WOUTER METSOLA VAN DER WIJNGAART**

Professor of micro- and nanofluidic systems, KTH

OSTEMERS - new opportunities for micro- and nanofluidics

Off-stoichiometry thiol-ene polymers, in short OSTEMERS, are the first polymer system specifically designed for lab-on-a-chip applications. The polymers unique properties stem from the fact that they feature reactive groups on their surface, which allows straightforward covalent surface modification and bonding of the material. The presentation will introduce the material system, as well as a number of novel diagnostic and therapeutic applications enabled by this material.

15:05-15:30

**ELAIN FU**

Assistant Professor in Bio Engineering, Oregon State University

Porous Microfluidic Sensors for Field Use Applications

Porous microfluidic sensors are well suited to field use applications. Advantages of the use of porous materials include a relatively low cost, capillary flow for fluid transport, and rapid and cost-effective device fabrication methods. This presentation will highlight the development of porous microfluidic systems in the context of health-related applications for human disease diagnosis and therapy monitoring.

15:30-16:00

**SOLUTION PROVIDER PRESENTATION:****MONICA BRIVIO**

Strategic R&D Manager, Micronit Microtechnologies

Microfluidic functionalities and microfabrication technologies for Point-of-Care testing and Cell Culturing

Micronit Microtechnologies has developed over the years a portfolio of microfluidic and microfabrication platform technologies that, through design customization and integration of functionalities, support the transfer of multistep laboratory protocols to a microfluidic format. This presentation focuses on recent advances in flow control, including membrane-based valves realized via adhesive-free techniques, combining a range of thermoplastic and elastomeric materials, as well as electrostatic triggered capillary burst valve enabling sequential capillary flow in fully autonomous Point-of-Care devices. Integration techniques particularly relevant to the Organ-on-Chip field, integrating membranes and sensing elements, for TEER (transepithelial electrical resistance) and oxygen sensing will also be illustrated. Commercially and scientifically relevant examples will also be presented to illustrate the applicability of the developed technologies



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16:00-16:50 Afternoon Refreshments / Poster Presentations

16:50-17:15

**JON COOPER**

Professor, University of Glasgow

Multiplexed DNA Malaria Sensing using Origami Paper Folding in Uganda

We have been developing our first generation of very low-cost tests in a paper-based format, enabling us to determine the species causing the infectious disease, from a finger-prick of blood. The design of the device means that testing can be done by a non-expert – using folding of the paper in a manner similar to origami- to process the sample. Importantly, we integrated the sample preparation into a multiplexed lateral flow device – akin to a conventional pregnancy test - so that untrained staff could easily read the result visually. We tested our devices in rural Uganda working with the Ministry of Health on species specific malaria detection. In other studies, we have also demonstrated the potential of multiplexed 'sample-to-answer' origami DNA tests for infections caused by trematodes, protozoa, bacteria and viruses, from a variety of samples including blood, sperm and faeces in both humans and animals.

17:15-17:45

**NIRVEEK BHATTACHARJEE**

Postdoctoral Fellow, Folch Lab, University of Washington

3D-Printed Bio-Microfluidics

The miniaturization of biomedical assays is of paramount importance for expanding healthcare access, for reducing healthcare costs, and for expediting biological research. However, biologists and clinicians typically do not have access to microfluidic technology because they do not have the engineering expertise or equipment required to fabricate and/or operate microfluidic devices. Furthermore, the present commercialization path for microfluidic devices is usually restricted to high-volume applications in order to recover the large investment needed to develop the plastic molding processes. We are developing microfluidic devices through stereolithography, a form of 3D printing, in order to make microfluidic technology readily available via the web to biomedical scientists. Most available SL resins do not have all the favorable physicochemical properties of the above-named plastics (e.g., biocompatibility, transparency, elasticity, and gas permeability), so the performance of SL-printed devices is still inferior to that of equivalent PDMS devices. Inspired by the success of hydrogel PEG-DA biocompatibility, we have developed microfluidic devices by SL in resins that share all the advantageous attributes of PDMS and thermoplastics so that we can 3D-print designs with comparable performance and biocompatibility to those that are presently molded.

17:45-18:10

**ANDERS KRISTENSEN**

Professor, Technical University of Denmark

Laser printed flat optics metasurfaces for microfluidics integration

Optical metasurfaces are defined by upscalable nanoimprinting and Si deposition. The Metasurfaces are post-processed by high resolution (127,000 DPI) laser printing to generate flat optical components. This enables definition and precise alignment of lenses embedded in optofluidic chips.

18:10-18:35

**DANIEL MCCLUSKEY**

Chief Engineer, Applied R&D: Biodetection, University of Hertfordshire

Development of a new generation personal bio-detection system

The University of Hertfordshire MEMS Group has developed an integrated system comprising an Electrostatic Precipitation (ESP) personal sampler and laboratory-grade Electrowetting on Dielectric (EWOD) sample recovery platform. This integrated system delivers a high concentration sample for downstream bio-analysis. Developed for military or civilian applications this approach provides wide area biological monitoring of an individual's biological agent (BA) exposure. With a focus on the complexities inherent in incorporating emerging research into field-deployable prototypes and Proof-of-Principle instrumentation here we present this concept seeking to address the challenge of low airborne BA toxic-thresholds and large BA concentration dynamic ranges. This integrated system is a significant step forward in addressing the limitations of existing equipment's capabilities.

18:35-19:35 Closing Remarks End of Day One / Networking Drinks

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08:00-08:35 Morning Refreshments

08:35-08:40 Morning Chair's Opening Remarks

09:00-09:40
Invitation Out09:40-10:10
SOLUTION PROVIDER PRESENTATION:
SENIOR REPRESENTATIVE
Fluigent
Title TBC

CASE STUDIES AND APPLICATIONS IN MEDICAL RESEARCH

**PETER ERTL**

Professor, Vienna University of Technology

Disease models on-a-Chip: Medical applications of Organ-on-a-Chip Technology

Microfluidics is vital for cell analysis because it is the only technology capable of simulating the physiological environment of cells and cell assemblies to investigate cellular transport mechanisms and cell proliferation events in the presence of test reagents, temperature or shear force gradients. In light of the benefits of microfluidics, my research group at TUW is developing lab-on-a-chip systems containing integrated fluid handling, degassing and biosensing systems to non-invasively monitor dynamic cell population responses.

In course of the presentation various components including microvalves, micropumps, degassers and sensing systems for lab-on-a-chip will be presented as well as the application of various organ-on-a-chip technologies in placenta research, rheumatic arthritis and osteoarthritis studies as well as Parkinson's diseases progression.

10:35-11:25 Morning Refreshments / Poster Presentations

11:25-11:40
SOLUTION PROVIDER PRESENTATION:
SENIOR REPRESENTATIVE
KLA-Tencor
Title TBC

11:40-11:55

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sponsorship@globalengage.co.uk

**NICOLE PAMME**

Professor, University of Hull

Paper-based analysis for environmental and clinical applications

- Micro analytical paper devices (uPADs)
- Analysis of watch list chemicals in river water and sediments
- Pathogen analysis in veterinary applications

**WINNIE SVENDSEN**

Associate Professor, Technical University of Denmark

Microfluidic solutions for cell and tissue studies

Cell and tissue culturing are normally performed in vials or flask in a static medium. This does not mimic the in vivo situation very well, where nutrients and waste products are highly controlled by the body through fluid flow. In this talk I will discuss various microfluidic solutions for more in-vivo like cell and tissues cultures. The platform is highly versatile and has been optimized using numerical simulations to control the concentration of nutrients or other molecules at the culturing site by simply changing the flow rate. Acute neuronal cells, hippocampal brain slices, bacteria and white blood cells have successfully been cultured. Moreover, the platform has integrated custom made sensor for real time monitoring of e.g. dopamine or glucose and TEER values.

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12:45-13:15

**BALAJI PANCHAPAKESAN**

Senior Associate Professor, Mechanical Engineering Department, Worcester Polytechnic Institute

Liquid biopsy to droplet biopsy: Combining microarrays with microfluidics for circulating tumor cell capture

In this talk, I will be presenting a future vision for circulating tumor cell capture based on an approach that combines microarrays and microfluidics. Liquids fractionated into droplets on microarrays can result in cell capture using multiple antibodies simultaneously and can be more effective compared to using simple microfluidics alone. We have established this proof of principle recently using our "Nanotube-CTC-Chip" and the future of this technology will be discussed.

13:15-14:10

Lunch

14:10-14:35

**LOES SEGERINK**

Assistant professor, Institute of Nanotechnology, University of Twente

Spermatozoa selection and analysis on microfluidic chips

Our aim is to improve the diagnosis and treatment of the (sub)fertile man by developing a microfluidic platform for single spermatozoa analysis and selection for assisted reproductive technologies. We showed that specific variables of a semen analysis, such as concentration and motility can be assessed using a microfluidic system. Furthermore microfluidic techniques can be used to assess and select single spermatozoa for assisted reproductive technologies, such as in vitro fertilization (IVF) or intracytoplasmic sperm injection (ICSI).

14:35-15:00

**JOHAN ELF**

Professor, Uppsala University

Fast antibiotics susceptibility testing using direct single cell imaging

We capture bacterial cells directly from dilute cultures using a novel microfluidic chip and monitor their individual growth rates using microscopy. Our results show that it is possible to detect changes in growth rate in response to clinically relevant antibiotics in minutes. In a small text clinical UPEC isolates, all of them were correctly classified as susceptible or resistant to ciprofloxacin in <10min.

15:00-15:25

**CHUCK HENRY**

Professor of Chemistry, Colorado State University

Bacterial and antimicrobial resistance detection

15:25-15:55

Afternoon Refreshments / Poster Presentations

15:55-16:20

**JEROEN LAMMERTYN**

Professor, Head of the MeBioS Biosensors Group, KU Leuven

Self-powered programmable microfluidic platform for point-of-care

We present in this paper a new concept of a self-powered infusion microfluidic pump for lab on a chip (LOC) applications, called (i)SIMPLE. By combining infusion and withdraw mode of pumping a whole new world for designing and implementing complex multi-step bio-assay protocols on a lab on a chip opens up. The pumping system is robust, easy to fabricate, inexpensive, user-friendly, and suited for mass replication technologies addressing most of the LOC requirements. Here we present the implementation of a bio-assay for the detection of creatinine in serum samples of patients with chronic kidney disease.

16:20-16:45

**FREDRIK WESTERLUND**

Associate Professor, Chalmers University of Technology

Optical DNA mapping for characterization of plasmids coding for antibiotic resistance: principles and clinical applications

I will present our work on optical DNA mapping of bacterial plasmids in nanochannels for identifying and characterizing bacterial plasmids. We have developed a method where single plasmids are confined in nanofluidic channels and imaged using fluorescence microscopy. In a single experiment, we obtain the number of different plasmids in a sample and their size, the presence of specific resistance genes as well as a plasmid barcode that can be used for identification and characterization. We have shown that we can identify sequenced plasmids as well as trace plasmids during resistance outbreaks. Current efforts are devoted to moving closer to the clinic as well as multiplexing and automating the process.

16:45

Conference Close

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qPCR & Digital PCR
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Synthetic Biology
& Gene Editing
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Microfluidics
Congress

NGS Tech &
Applications Congress

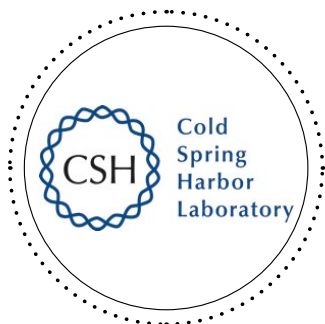
4BIO Registration

Global Engage is pleased to announce the **2017 NGS Tech & Applications Congress**, which will be held on 4-5 December in London, as part of the 4Bio Summit. The event will be co-located with the 5th qPCR & Digital PCR Congress, the 4th Synthetic Biology Congress and the 3rd Microfluidics Congress.

Over the past decade, advances in sequencing technology and significant cost reductions have been instrumental to medical research. Scientists are continuing to develop new sequencing techniques, tools and methods of analysis, and subsequently discovering new applications in medical 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.

Attracting experts working in all areas of genomic sequencing, the conference will examine the latest developments in the technologies and techniques being used for progressing medical research, the clinical applications of sequencing, as well as the challenges and future of the field. Should you be an expert in developing sequencing technologies, or a scientists using NGS to further medical research, the conference will be an excellent opportunity to learn, share, discuss and engage with the most current NGS-based research and technology. During the two-day conference, there will be networking breaks to promote interaction with your peers, expert led case study presentations, roundtable discussions for in-depth exploration of key issues, and a dynamic exhibition room filled with technology providers showcasing their technologies and solutions.

EXPERT SPEAKERS Include:



RICHARD MCCOMBIE

Professor, Cold Spring Harbor Laboratory,
USA



JASON BETLEY

Senior Director, Technology Development,
Illumina



MARIJA DRNDIC

Fay R. and Eugene L. Langberg Professor of
Physics, University of Pennsylvania, USA



ADRIAN W. BRIGGS

Head of Molecular Biology, Receptor
Discovery, Juno Therapeutics, USA

CONFERENCE SYNOPSIS

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STRATEGY, TECHNOLOGY AND ANALYSIS METHODS

- Prior to sequencing: strategies for library & sample preparation, DNA amplification
- Novel sequencing methods such as Drop-seq & SMILE-seq
- Updates to older methods such as ChIP-seq
- Platform comparison
- When to do whole genome, targeted or exome sequencing
- Overview of data analysis methodology
- The possibilities of single-cell sequencing

MEDICAL APPLICATIONS OF NGS

Using NGS to further research and medicine in the areas of:

- Personalized medicine
- Clinical diagnostics
- Targeted therapy
- Genetic screening
- Genotyping
- Biomarker discovery
- Gene expression profiling

ROUNDTABLE DISCUSSIONS

- Sample/Library Prep
- Sequencing Workflow
- Platform Comparison
- Nanopore Sequencing
- Single-Cell Genomics
- Clinical Implementation
- Computational Biology

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CONFIRMED SPEAKERS



RICHARD MCCOMBIE
Professor, Cold Spring Harbor
Laboratory, USA



JASON BETLEY
Senior Director, Technology
Development, Illumina



MARIJA DRNDIC
Fay R. and Eugene L. Langberg
Professor of Physics, University
of Pennsylvania, USA



JOAKIM LUNDEBERG
Professor in Gene Technology,
KTH Royal Institute of
Technology; Director of the
Genomics Platform, Science for
Life Laboratory, Sweden



MARTA GRZELAK
Senior Scientific Associate,
CRUK Cambridge Institute
Genomics Core, UK



ADRIAN W. BRIGGS
Head of Molecular Biology,
Receptor Discovery, Juno
Therapeutics, USA



KUO PING CHIU
Associate Research Fellow,
Genomics Research Center,
Academia Sinica, Taiwan



IWANKA KOZAREWA
Senior Scientist - Translational
Science, IMED Oncology,
AstraZeneca, UK



SAULIUS KLIMASAUSKAS
Director and Chief Scientist,
Institute of Biotechnology,
Vilnius University, Lithuania



JULIEN MARQUIS
Genomics Associate Specialist,
Nestlé Institute of Health
Sciences, Switzerland



SIMON FISHILEVICH
Senior Data Scientist,
Department of Molecular
Genetics, Weizmann Institute
of Science, Rehovot, Israel



RAYMOND DALGLEISH
Professor of Human Genetics,
University of Leicester, UK



EMMANOUIL DERMITZAKIS
Professor, Department
of Genetic Medicine and
Development, University of
Geneva, Switzerland



XIANGYU RAO
NGS Field Application
Manager, Europe, Integrated
DNA Technologies



BART DEPLANCKE
Associate Professor & Swiss
Institute of Bioinformatics
Group Leader, Institute of
Bioengineering, School of Life
Sciences, EPFL, Switzerland



JOHN CASTLE
CSO, Achilles Therapeutics, UK



FERGA GLEESON MD
Professor of Medicine, Mayo
Clinic, Rochester, Minnesota,
USA



BERNHARD ZIMMERMANN
Vice President R&D, Molecular
Research, Natera, Inc., USA



CHRISTIAN GLOECKNER
Chief Technology Officer,
NEO New Oncology GmbH,
Germany



VICTOR NEDUVA
Group Leader,
GlaxoSmithKline, UK



MATTHIAS HAUPTMANN
Postdoctoral Scientist,
Department of Cellular
Microbiology, Research Center
Borstel, Germany



PRIYASMA BHOUMIK
(Track Chair)
PD Research Scientist,
Novartis, Switzerland



AHMAD KHODR
Researcher, International
Microbiology Department,
L'Oréal Research &
Development, France



SEAN KENNEDY
Director of the Biomix Pole,
Institut Pasteur, France



SENIOR REPRESENTATIVE
Perkin Elmer



RAFFAELE CALOGERO
Associate Professor,
Department of Biotechnology
and Health Sciences,
University of Torino, Italy



VINZENZ LANGE
Chief Technology Officer,
DKMS Life Science Lab



JIM HUGHES
Associate Professor of
Genome Biology, Weatherall
Institute of Molecular Medicine,
University of Oxford, UK



PHILIP BEER
Consultant Haematopathologist,
HMDS, St James' Hospital,
Leeds, UK; Visiting Scientist,
Sanger Institute, Hinxton, UK

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4BIO Registration

08:00-09:00 Registration & Refreshments

09:00-09:05 Global Engage Welcome Address and Morning Chair's Opening Remarks

09:05-09:40



KEYNOTE ADDRESS:
RICHARD MCCOMBIE

Professor, Cold Spring Harbor Laboratory, USA

Title TBC

09:40-10:15



KEYNOTE ADDRESS:
JASON BETLEY

Senior Director, Technology Development, Illumina

Recent progress in genomics

- Review of recent technologies
- Emerging applications in genomics
- Future direction

10:15-10:45

SOLUTION PROVIDER PRESENTATION:

XIANGYU RAO

NGS Field Application Manager, Europe, Integrated DNA Technologies

Improving exome sequencing, targeted sequencing, and low frequency variant detection with better coverage uniformity, higher on-target rates, and unique molecular identifiers

Learn about:

- The influence of variables such as coverage uniformity, on-target rate, and capture efficiency on the integrity of targeted sequencing data
- The independent benchmark study that shows how the xGen® Exome Research Panel provides an effective solution to the challenges of exome capture
- The IDT and Illumina partnership for exome sequencing
- Unique molecular identifiers and other NGS product development at IDT



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

11:55-12:20



MARIJA DRNDIC

Fay R. and Eugene L. Langberg Professor of Physics, University of Pennsylvania, USA

Bioelectronics applications with nanostructures

I will describe experiments that push the limits of nanoelectronics device size to atomic scale in thin materials and expand their function and precision. Experiments include fabrication of nanoribbons and field-effect-transistors from novel two-dimensional materials down to sub-nm widths and the ultrafast, all-electronic detection and analysis of biomolecules with nanopores. As molecules are driven through nanopores in solution, they block the ion current flow resulting in current reductions from which molecule's physical and chemical properties are inferred. DNA, proteins and other biomolecules can be analyzed. The temporal, spatial resolution and sensitivity in these experiments have been improved over the last few years thanks to advanced materials, device designs and new electronics.

12:20-12:45



IWANKA KOZAREWA

Senior Scientist - Translational Science, IMED Oncology, AstraZeneca, UK

Pushing the limits of mutation detection in circulating tumour DNA

- ctDNA is quickly becoming the material of choice for genomic profiling of cancer patients. It is available throughout treatment allowing patient monitoring at different time-points. However, its use for sequencing comes with its specific challenges: limited amount, small size, and dilution with non-tumour DNA.
- We have evaluated the use of unique molecular indices (UMIs) in our targeted NGS workflow and their effects on sensitivity and specificity of variants identified, noise reduction and amount of sequencing required.
- In this talk, I will advise on best practices to utilise UMIs in the library preparation workflow and to analyse data produced using UMIs. I will also showcase how the use of UMIs is helping us to understand why certain patients respond to therapy and mechanisms of resistance.

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12:45-13:00



EARLY CAREER RESEARCHER PRESENTATION:

MARTA GRZELAK

Senior Scientific Associate, CRUK Cambridge Institute Genomics Core, UK

Topic: Sample & library prep; single-cell RNA-seq - Title TBC

13:00-13:15



SOLUTION PROVIDER PRESENTATION:

VINZENZ LANGE

Chief Technology Officer, DKMS Life Science Lab

Population scale sequencing by cost-efficient targeted NGS

NGS has revolutionized the costs for whole genome sequencing. However, targeted applications can also benefit from the high volume of data delivered by current NGS instruments if samples are tagged by molecular identifiers. Taking advantage of more than 9000 distinct identifiers, we have built a highly cost efficient workflow for high-throughput genotyping. We applied our workflow to characterize more than 4 million samples with excellent accuracy. Originally restricted to HLA genotyping, we have meanwhile extended the scope to include blood groups, MICA/B and high resolution KIR analysis. After mastering the complexity of the HLA and KIR regions, we are now offering high-volume genotyping services for custom panels on demand.

DKMS
Life Science Lab

13:15-14:15

Lunch

14:15-14:40



JOAKIM LUNDEBERG

Professor in Gene Technology, KTH Royal Institute of Technology; Director of the Genomics Platform, Science for Life Laboratory, Sweden

Spatial maps of cancer transcriptomes reveal an unexplored landscape of heterogeneity

- Spatial transcriptomics - spatially resolved transcriptomics
- RNA sequencing in a tissue context
- Cancer and its microenvironment

14:40-15:05



ADRIAN W. BRIGGS

Head of Molecular Biology, Receptor Discovery, Juno Therapeutics, USA

Massively parallel single cell immune sequencing for immunotherapy discovery

Lymphocytes are the source of antibodies and T-cell receptors used in adaptive immune responses. Our single cell sequencing technology allows deep and unbiased immune receptor recovery directly from lymphocytes in blood and tumor tissue, together with phenotypic information from each cell. This platform has widespread potential for basic and applied research into the patient immune response to cancer and immunotherapy discovery.

15:05-15:30



KUO PING CHIU

Associate Research Fellow, Genomics Research Center, Academia Sinica, Taiwan

How TOP-PCR can help NGS

Since Jonathan Rothberg kicked off the first NGS platform, 454, in 2005, NGS has experienced a turbulent period of evolution which selects Illumina as the winner to dominate the NGS market. The right choice of using DNA polymerase and well-designed sequencing methods and adaptors targeting genomic DNA and DNA samples readily available secured the success. However, as biological investigation inches towards previously untouchable territories, such as cell-free DNA (cfDNA) in body fluids, the chance of facing insufficient amount of DNA for making a representative sequencing library increases substantially, forcing current NGS to deal with new challenges. To overcome such obstacles, we have invented T Oligo-Primed Polymerase Chain Reaction (TOP-PCR), which uses half adaptor (HA) to lift the efficiencies of adaptor ligation and PCR amplification, making it suitable for the amplification of minute DNA. We have empirically demonstrated that TOP-PCR is able to make a sequencing library from 0.01 pg cfDNA input, which is only 1/50,000 of the minimal DNA requirement (0.5 ng) for current NGS, dramatically narrowing down the gap between PCR and NGS. Taken together, TOP-PCR is a robust technology aiming to amplify low abundance, low copy number and even partially degraded DNA samples more efficiently and more comprehensively. It can help NGS to explore new territories, such as liquid biopsy, for the detection of disease-associated mutations, prenatal genetic defects and infectious agents.

15:30-16:00

SOLUTION PROVIDER PRESENTATION:

SENIOR REPRESENTATIVE

Perkin Elmer

Title TBC

For the Better

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16:00-16:50

Afternoon Refreshments / Odd Numbered Poster Presentations

16:50-17:15

**SAULIUS KLIMASAUSKAS**

Director and Chief Scientist, Institute of Biotechnology, Vilnius University, Lithuania

Methylation-sensitive profiling of genomic CpG sites using TOP-seq

Modification of CpG dinucleotides in DNA is part of epigenetic regulation of gene function in vertebrates and is associated with complex human disease. Here, we describe a novel epigenome profiling approach, named TOP-seq, which relies on covalent tagging of individual unmodified CpG sites followed by non-homologous priming of the DNA polymerase action at these sites to directly produce adjoining regions for their sequencing and precise genomic mapping. Pilot analyses showed a better agreement of TOP-seq with published bisulfite sequencing maps as compared to widely used enrichment-based techniques and permitted identification of long-range and gene-level differential methylation among human tissues and neuroblastoma cell types. The proposed approach avoids whole-genome sequencing and is well suited for large-scale high-resolution studies.

17:15-17:45

**JULIEN MARQUIS**

Genomics Associate Specialist, Nestlé Institute of Health Sciences, Switzerland

MitoRS, a method for high throughput, sensitive, and accurate detection of mitochondrial DNA variants

Mitochondrial dysfunction has been linked with many pathologies. In several instances, this could be associated with polymorphism in one of the > 1'000 nuclear DNA encoded genes involved mitochondrial function. However, it is still technologically challenging to perform large scale analysis of the mitochondrial DNA (mtDNA) itself, and the contribution of mtDNA encoded variants is still poorly understood. We have developed MitoRS, a method tackling these challenges by applying next generation sequencing for universal, high throughput, robust, sensitive and accurate detection of mtDNA variants. Fine-tuned parameters are applied in the analysis to allow detection of variants even of low frequency heteroplasmy. We anticipate this method will promote the systematic analysis of mtDNA polymorphisms and may help assessing the impact of mtDNA heteroplasmy on disease or pathological conditions.

17:45-18:10

**SIMON FISHILEVICH**

Senior Data Scientist, Department of Molecular Genetics, Weizmann Institute of Science, Rehovot, Israel

GeneHancer and VarElect: disease interpretation of whole genome sequence variants

- The emergence of whole genome sequencing (WGS) poses considerable challenges to variant disease interpretation, whereby much of the WGS "variant avalanche" resides within developmentally important transcription regulatory elements - promoters and enhancers,.
- GeneHancer, a novel comprehensive regulatory element database in the framework of the GeneCards suite (www.genecards.org), integrates four enhancer data sources - ENCODE, Ensembl regulatory build, FANTOM and VISTA enhancer browser, with target genes obtained via the GTEx expression quantitative trait loci, Capture Hi-C, FANTOM eRNA expression correlations, transcription factor expression correlations and genomic distance scores.
- GeneHancer, embedded within the GeneCards Suite, fortifies its disease interpretation tools VarElect and TGex, mapping non-coding variants onto enhancers, then assigning target genes to variants, thus providing a facile, automatable route to discovering the genic roots of diseases.

18:10-18:35

**RAYMOND DALGLEISH**

Professor of Human Genetics, University of Leicester, UK

VariantValidator: a web application to accurately validate and convert between HGVS nomenclature and Variant Call Format

The Human Genome Variation Society (HGVS) variant nomenclature is widely used to describe sequence variants in scientific publications, clinical reports and databases. However, the nomenclature is complex and inaccurate variant descriptions are often reported. VariantValidator (<https://variantvalidator.org/>) is a web-based tool which utilizes the open-source hgvs Python library and assists users who wish to accurately describe and report HGVS-compliant sequence-level variations. VariantValidator was designed to ensure that users are guided through the intricacies of the HGVS nomenclature; e.g. if the user makes a mistake, VariantValidator automatically corrects the mistake if it can or provides helpful guidance if it cannot. In addition, VariantValidator can interconvert genomic variant descriptions in HGVS and Variant Call Format (VCF) with a degree of accuracy which surpasses the majority of competing solutions.

18:35

Chair's Closing Remarks and End of Day One

18:35-19:35

Networking Drinks Reception

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08:20-09:00

Refreshments

08:40

MORNING CHAIR: PRIYASMA BHOUMIK, PD Research Scientist, Novartis, Switzerland

09:00-09:40

**KEYNOTE ADDRESS:****EMMANOUIL DERMITZAKIS**

Professor, Department of Genetic Medicine and Development, University of Geneva, Switzerland

Topic: NGS-based methodologies for studying genetic variation - Title TBC

09:40-10:10

SOLUTION PROVIDER PRESENTATION

For sponsorship opportunities please contact Nick Best/Gavin Hambrook at:

sponsorship@globalengage.co.uk

10:10-10:35

**BART DEPLANCKE**

Associate Professor & Swiss Institute of Bioinformatics Group Leader, Institute of Bioengineering, School of Life Sciences, EPFL, Switzerland

Microfluidic applications in single cell RNA sequencing

- Single cell RNA-seq is revolutionizing our ability to uncover the cellular composition of individual tissues or specific developmental patterns, as evidenced by recent work of my lab to reveal the heterogeneity among adipose-embedded mesenchymal stem cells.
- Microfluidic technologies such as drop-seq or 10X Genomics enable the processing of thousands of cells in a short and inexpensive manner. Yet, these technologies feature a relatively poor cell capturing efficiency, making them less amenable to identify rare cell types or to handle samples with a low number of cells
- Here, I will present a new microfluidic technology developed by our lab involving two layer lithography, which allows us to capture and profile single cells with very high efficiency (>80%). I will illustrate the potential of this technology by discussing our recent results on individual embryos and organoids.

10:35-11:25

Morning Refreshments / Odd Numbered Poster Presentations / One-to-One Partnering Meetings

CLINICAL DIAGNOSTICS & PERSONALISED MEDICINE

11:25-11:55

**JOHN CASTLE**

CSO, Achilles Therapeutics, UK

Exploiting NGS for clinical individualized neoantigen cancer vaccines

We are treating cancer patients with individualized vaccines manufactured on-demand based on a NGS-profile of the patient tumor. We exploit NGS, bioinformatics, and computational immunology to generate the patient-specific vaccine blueprint. Our second-generation neoantigen vaccine platform, AutoSynVax™ (ASV™), entered the clinic in April and encodes mutation-containing peptides in a proprietary formulation and clinically tested adjuvant.

11:55-12:20

**BERNHARD ZIMMERMANN**

Vice President R&D, Molecular Research, Natera, Inc., USA

Personalized detection of circulatory tumor DNA mutations for cancer recurrence monitoring

The detection of tumor mutations in circulating cell-free DNA holds promise for the non-invasive detection of therapeutically relevant mutations, detection of minimal residual disease after curative-intent treatment, and the early detection of relapse before clinical manifestation. We have developed an approach to detect cancer signatures in plasma by ultra-deep sequencing of personalized, multiplex PCR assays that are specifically designed to detect mutations found in a patient's tumor. We demonstrate the ability to detect clonal and subclonal mutations in patients with treatment-naïve lung cancer. Also, we detect tumor DNA in plasma up to one year before clinical relapse, and are able to identify emerging subclones. In addition to characterizing the subclonal dynamics of relapsing NSCLC, bespoke circulatory DNA profiling can identify resistance to adjuvant chemotherapy. These findings indicate that it is now feasible to perform drug development guided by ctDNA platforms to identify residual disease.

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12:20-13:10

ROUNDTABLE DISCUSSIONS:

**TABLE 1: Interpreting Non-Coding Mutation**
JIM HUGHES

Associate Professor of Genome Biology, Weatherall Institute Of Molecular Medicine, University of Oxford, UK

**TABLE 2: Platform Comparison**
SEAN KENNEDY

Director of the Biomix Pole, Institut Pasteur, France

- Oxford Nanopore versus PacBio, Data quality, analysis, advantages and disadvantages of each system
- Illumina Roadmap (HiSeq, NovaSeq and what might be next)
- A future for Ion Proton?
- Maintaining and testing multiple technology platforms at your institute; finding the right balance.

**TABLE 3: Nanopore Sequencing**
MARIJA DRNDIC

Fay R. and Eugene L. Langberg Professor of Physics, University of Pennsylvania, USA

- Outlining nanopore applications
- Potential advantages and markets for nanopores
- Outlining challenges and what has to be still achieved/demonstrated (in the context of specific applications)

**TABLE 4: Clinical Implementation**
PHILIP BEER

Consultant Haematopathologist, HMDS, St James' Hospital, Leeds, UK; Visiting Scientist, Sanger Institute, Hinxton, UK

Moving next-generation sequencing into routine clinical practice.

- What are the main issues facing the NHS? Are these issues different in the rest of the EU? In the US?
- Who are the best agencies to oversee the validation of clinical NGS platforms? What can we learn from the FDA LDT stand-off?
- What needs to be done to empower physicians/oncologists to make the best use of cancer genomic data?

**TABLE 5: Computational Biology**
RAFFAELE CALOGERO

Associate Professor, Department of Biotechnology and Health Sciences, University of Torino, Italy

Analysis processes in computational biology are complex, multi-staged,

heterogeneous, these characteristics rise multiple questions:

- Is reproducibility possible in computational biology?
- Which technology might help in providing reproducibility? (docker, cloud, etc.)
- Big data massive reanalysis, e.g. hundreds of whole genomes, is feasible?
- Multi-omics integration is possible?

13:10-14:10

Lunch

TRACK CHAIR: AHMAD KHODR, Researcher, International Microbiology Department, L'Oréal Research & Development, France

14:10-14:35

**CHRISTIAN GLOECKNER**

Chief Technology Officer, NEO New Oncology GmbH, Germany

Challenges in using NGS as a clinical diagnostic tool

14:35-15:00

**FERGA GLEESON MD**

Professor of Medicine, Mayo Clinic, Rochester, Minnesota, USA

The clinical interface between precision medicine and the gastroenterologist

- A new paradigm: the bench has reached the bedside
- Molecular cytology genotyping
- Theranostic possibilities and triaging for clinical trials

15:00-15:25

**PHILIP BEER**

Philip Beer, Consultant Haematopathologist, HMDS, St James' Hospital, Leeds, UK; Visiting Scientist, Sanger Institute, Hinxton, UK

Every rose has its thorn- barriers to the implementation of next-generation sequencing technologies in oncology clinical practice

- Platform selection: is whole genome sequencing the answer to everything?
- Regulatory perspectives: approaches to validation and laboratory standards.
- Clinical interpretation: sorting the wood from the trees (and the cancer drivers from the passengers).

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15:25-15:55

Afternoon Refreshments / Even Numbered Poster Presentations

SEQUENCING MICROBES

15:55-16:20

**VICTOR NEDUVA**

Group Leader, GlaxoSmithKline, UK

Title TBC

16:20-16:35

**EARLY CAREER RESEARCHER PRESENTATION:****MATTHIAS HAUPTMANN**

Postdoctoral Scientist, Department of Cellular Microbiology, Research Center Borstel, Germany

Comparative metagenomic sequencing of 16S rRNA genes and transcripts reveals metabolic activity of commensal bacteria in mouse gut and lung

Antibiotic treatment disturbs microbiota in mouse gut and lung. Intranasal application of 4 bacterial mouse lung isolates reestablishes the pretreatment microbiota.

We perform metagenomic 16S rRNA amplicon sequencing on the gene and transcript levels. By that, we investigate the commensal bacteria compositions and their metabolic activities in mouse gut and lung samples. Comparative gene and transcript sequencing offers the possibility to compare activity-related 16S rRNA metagenomic data.

16:35-17:00

**AHMAD KHODR**

Researcher, International Microbiology Department, L'Oréal Research & Development, France

L'Oréal approach for the Skin Microbiome project: Scientific watch associated to best practices for sampling, sequencing and analysis

Study design for skin microbiome research is multifaceted and integral to all downstream steps. Many published studies examined the biases introduced by the skin sampling methods and sample storage, controls and contamination sources, sequencing biases, and possible quantitation. Thus, standardization and validation of the protocols, bio-informatic pipelines and sequencing platforms is a crucial step for a successful skin microbiome analysis. During my talk, I would review the different biases influencing skin Microbiome metagenomic studies. I

would present the validation and harmonization approach that is of vital importance for L'Oréal RI where we have developed a complete validation process for our international sequencing platforms network and a harmonization of the methods used for skin microbiome studies.

17:00

Conference Close

WORKSHOP



Sunday, 3rd December 2017 – 15:00pm-17:00pm

Cost for all Attendees: £100.00

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



Sunday 3rd December 2017 – 17:30pm-19:30pm
Cost for all Attendees: £100.00

Innovations in Digital Nucleic Acid Amplification

In its first part, this workshop will provide an introduction to digital PCR including its principle, related statistics, methods for sample partitioning and commercially available digital PCR systems.

The second part of the workshop will treat technological innovations comprising the microfluidic integration of droplet generation as well as amplification and detection within one single cavity. Furthermore, strategies for the integration of digital sample to answer nucleic acid analysis will be discussed.

Thirdly, in a live lab we will demonstrate how digital nucleic acid amplification can be performed using standard laboratory devices only (i.e. mini-centrifuge, incubator, fluorescence reader), enabled by a novel microfluidic chip.

AGENDA

Introduction

- 17:30 Welcome, introduction of tutors and participants (Nils Paust)
- 17:35 Basics, statistics, and microfluidic principles of commercial systems for digital nucleic acid amplification (Nils Paust)

Innovation

- 18:10 Microfluidic integration of droplet generation, amplification and detection (Nils Paust)
- 18:30 Digital sample-to-answer nucleic acid analysis (Nadine Borst)

Innovation

- 19:00 Demonstration of digital nucleic acid analysis using standard laboratory devices (Nadine Borst)
- 19:20 Concluding remarks & feedback (tutors and participants)
- 19:30 End

Nils Paust

Dr Nils Paust studied energy and process engineering at the Technical University of Berlin with a focus on fluid mechanics, thermodynamics and control engineering (degree: diploma). He received his Ph.D. with the dissertation entitled "Passive and self-regulating fuel supply in direct methanol fuel cells" at the University of Freiburg in 2010. Since 2010 Nils works for Hahn-Schickard, first as a group leader and nowadays as the head of the division "Microfluidics Platforms". Main research interest of Nils Paust is the centrifugal microfluidic system integration. This comprises new microfluidic functionalities, the interface between fluidics and scalable cost-efficient mass fabrication and the implementation of complete laboratory workflows on centrifugal microfluidic cartridges.

Nadine Borst

Studied biochemistry at the University of Regensburg, Germany with a focus on molecular biology and protein biochemistry. Her PhD at the Technical University of Munich, Germany, was done in cooperation with the Fraunhofer Institute for Interfacial Engineering and Biotechnology. There, she worked in the field of enzyme engineering to provide novel protein variants for the application of renewable resources in the chemical industry. In 2016, Nadine Borst joined Hahn-Schickard and since February 2017 she is heading the Nucleic Acid Analysis group. Her current research is concentrated on digital assays, isothermal amplification and single cell analysis.

Conference Summary

Agenda Overview

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Venue

qPCR & Digital PCR
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Congress

Microfluidics
Congress

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