Global Engage

4BIO SUMMIT

--- London, UK ---

4-5 December 2017

www.global-engage.com

4BIO SUMMIT: 2017

#GEPCR17 #GESBC17 #GEMFC17 #GENGS17
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, UK
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, UK
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.
### Agenda Overview

**qPCR & Digital PCR Congress**

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

- **Solution Provider Presentation:** Single Cell Analysis with the Naica System  
  Alexandra Martin, Application Specialist, Stilla Technologies

**Synthetic Biology & Gene Editing Congress**

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

- **Solution Provider Presentation:** Title TBC  
  Senior Representative, Takara

**Microfluidics Congress**

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

**NGS Tech & Applications Congress**

- **Keynote Address:** Recent progress in genomics  
  Mostafa Ronaghi, Senior Vice President & Chief Technology Officer, Illumina

### Conference Schedule

#### MONDAY 4TH DECEMBER 2017

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>08:00</td>
<td>Registration / Refreshments / Global Engage Welcome Address and Morning Chair’s Opening Remarks</td>
</tr>
</tbody>
</table>
| 09:00 | Keynote Address: Digital PCR for high accuracy measurement of DNA Reference Materials  
  Kerry Emmsie, Senior Research Scientist, National Measurement Institute, Australia |
| 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 |
| 11:55 | Keynote Address: 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 |
| 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 |
| 10:45 | Solution Provider Presentation: True lab-on-a-chip devices: Complexity and Manufacturing Challenges  
  Holger Becker, Co-founder and CSO, microfluidic ChipShop GmbH |
| 09:05 | Keynote Address: Applications of Synthetic Biology in Healthcare & Research  
  Prof. R. McCombie, Cold Spring Harbor Laboratory, USA |
| 10:15 | Keynote Address: Mostafa Ronaghi, Senior Vice President & Chief Technology Officer, Illumina |
| 09:40 | Keynote Address: Challenges and Opportunities in Microfluidics  
  Prof. D. Weitz, Harvard University, USA |
| 10:45 | Keynote Address: The Future of Microfluidics: From benchtop to real-time  
  Prof. A. de Mello, ETH Zurich, Switzerland |
| 09:00 | Solution Provider Presentation: Roland Richter, Co-founder and CEO, ChipShop GmbH |
| 10:15 | Solution Provider Presentation: Roland Richter, Co-founder and CEO, ChipShop GmbH |
| 09:40 | Solution Provider Presentation: Roland Richter, Co-founder and CEO, ChipShop GmbH |
| 10:45 | Solution Provider Presentation: Roland Richter, Co-founder and CEO, ChipShop GmbH |
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| 09:40 | Solution Provider Presentation: Roland Richter, Co-founder and CEO, ChipShop GmbH |
| 10:45 | Solution Provider Presentation: Roland Richter, Co-founder and CEO, ChipShop GmbH |

### DAY 1

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

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| 11:55 | Keynote Address: The Future of Microfluidics: From benchtop to real-time  
  Prof. A. de Mello, ETH Zurich, Switzerland |

### 4BIO Registration

**qPCR & Digital PCR Congress**

- **Track Chair:** Gary Pestano  
  Vice President, Development and Operations, Biodexis

- **Prospects for digital PCR in absolute quantification of DNA and RNA**  
  Ward De Spiegelaere, Assistant Professor, Gent University, Belgium

- **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

**Synthetic Biology & Gene Editing Congress**

- **Track Chair:** Marie Korabecna  
  Associate Professor, Charles University, Czech Republic

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

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

**Microfluidics Congress**

- **Track Chair:** Georg Fritz  
  Group Leader, LOEWE Center for Synthetic Microbiology, Philipps-University Marburg

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

**NGS Tech & Applications Congress**

- **Keynote Address:** 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

**VENUE**

- **Agenda Overview**
- **Conference Summary**
- **Sponsors**
- **Venue**
- **NGS Tech & Applications Congress**
- **4BIO Registration**

**Venue**

- **Agenda Overview**
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<tbody>
<tr>
<td>11:20</td>
<td>Lunch</td>
<td>Lunch / One-to-One Partnering Meetings</td>
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<tr>
<td>12:45</td>
<td>Solution Provider Presentation</td>
<td>Admix™: Custom lyophilised RT-PCR reagents for point-of-use applications</td>
<td>Martin A Lee, CEO, Fluorogenics Limited</td>
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<td>Title TBC</td>
<td>Senior Representative, Elveflow</td>
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**Conference Schedule**

- **Consortium Overview**
- **Venue**
- **Synthetic Biology & Gene Editing Congress**
  - Application of digital PCR for quantification of minority targets in human disease and antimicrobial resistance monitoring
  - Speaker: Gerwyn Jones, Senior Researcher, LGC, UK
  - 11:30-11:45

- **qPCR & Digital PCR Congress**
  - T oligo-primed polymerase chain reaction (TOP-PCR) and its applications
  - Speaker: Kuo-Ping Chiu, Associate Professor, National Taiwan University, and Associate Research Fellow, Genomics Research Center, Academia Sinica, Taiwan
  - 11:45-12:00

- **Synthetic Biology via continuous directed evolution**
  - Speaker: Mark Isalan, Reader in Gene Network Engineering, Imperial College London
  - 12:00-12:15

- **Control of the T-cell fate by a chromatin-based timing control switch**
  - Speaker: Hao Yuan Kueh, Assistant Professor, University of Washington
  - 12:15-12:30

- **Centrifugal Microfluidics: Recent developments**
  - Speaker: Nils Paust, Head of Division of Microfluidic Platforms, Hahn Schickard
  - 12:30-12:45

- **Early Career Researcher Presentation:**
  - Topic: Sample & library prep; single-cell RNA-seq – Title TBC
  - Speaker: Marta Grzelak, Senior Scientific Associate, CRUK Cambridge Institute Genomics Core, UK
  - 12:45-13:00

- **Synthetic Biology via continuous directed evolution**
  - Speaker: Călin Guet, Assistant Professor, IST Austria
  - 13:00-13:15

- **Bacterial RNA structures as drug targets**
  - Speaker: Günter Mayer, Professor, University of Bonn
  - 13:15-13:30

- **Pushing the limits of mutation detection in circulating tumour DNA**
  - Speaker: Iwanka Kozarewa, Senior Scientific Associate, CRUK Cambridge Institute Genomics Core, UK
  - 13:30-13:45

- **Solution Provider Presentation:**
  - Title: Admix™: Custom lyophilised RT-PCR reagents for point-of-use applications
  - Speaker: Martin A Lee, CEO, Fluorogenics Limited
  - 12:45-13:00

- **Solution Provider Presentation:**
  - Title: Title TBC
  - Speaker: Senior Representative, Elveflow
  - 12:45-13:00

- **Track Chair:**
  - Ward De Spiegelaere, Assistant Professor, Gent University, Belgium
  - Catherine Kibirige, Clinical Research Scientist, Imperial College London, UK

- **Droplet PCR for liquid biopsy analysis**
  - Speaker: Hakan Jonsson, Assistant Professor, KTH Royal Institute of Technology, Sweden
  - 14:15-14:30

- **Discordance between replicate qPCR reactions**
  - Speaker: Jan Ruijter, Assistant Professor, University of Amsterdam, The Netherlands
  - 14:30-14:45

- **The synthetic frontier – unravelling the complexity of biology**
  - Speaker: Călin Guet, Assistant Professor, IST Austria
  - 14:45-14:50

- **Bacterial RNA structures as drug targets**
  - Speaker: Günter Mayer, Professor, University of Bonn
  - 14:50-14:55

- **Iso-acoustic focusing organizes cells and liquids based on their acoustic properties**
  - Speaker: Per Augustsson, Assistant Professor in Biomedical Engineering, University of Lund
  - 14:55-15:10

- **Spatial maps of cancer transcriptomes reveal an unexplored landscape of heterogeneity**
  - Speaker: Joakim Lundeberg, Professor in Gene Technology, KTH Royal Institute of Technology; Director of the Genomics Platform, Science for Life Laboratory, Sweden
  - 15:10-15:25
<table>
<thead>
<tr>
<th>Time</th>
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<th>Speaker/Details</th>
</tr>
</thead>
<tbody>
<tr>
<td>17:15-17:45</td>
<td>Clinical utility of ddPCR in the management of patients with castration resistant prostate cancer</td>
<td>Daniel Wetterskog, Senior Scientist, Institute of Cancer Research, UK</td>
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<tr>
<td>17:45-18:10</td>
<td>Targeted transcriptome profiling using single molecule Molecular Inversion Probes</td>
<td>William Leenders, Associate Professor of Tumor Targeting, Radboud UMC, The Netherlands</td>
</tr>
<tr>
<td>18:10-18:35</td>
<td>Explaining biocide tolerance of Gram negative bacteria – using SyBr Green qPCR as a versatile tool to</td>
<td>Lucy Bock, Senior Scientist/Project Team Leader, Technology Development Group, Public Health England, UK</td>
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<tr>
<td></td>
<td>develop and support hypotheses</td>
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<tr>
<td>18:35-19:35</td>
<td>Chair’s Closing Remarks / End of Day 1</td>
<td></td>
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</tbody>
</table>

**Networkig Drinks**
### Conference Schedule

#### qPCR & Digital PCR Congress

- **Track Chair:** Lucy Bock  
  Senior 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

#### Synthetic Biology & Gene Editing Congress

- **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

#### Microfluidics Congress

- **Track Chair:** Priyasma Bhoumik  
  PD 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

#### NGS Tech & Applications Congress

- **Track Chair:** Priyasma Bhoumik  
  PD Research Scientist, Novartis, Switzerland

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

#### Conference Summary

- **CONGRESS SCHEDULE**
- **08:00-08:40**
  - Refreshments / Morning Chair’s Opening Remarks
  - 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

  - Solution Provider Presentation: Title TBC  
    Senior Representative, Bio-Rad Laboratories

- **09:00-09:40**
  - 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

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

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

  - Solution Provider Presentation: Title TBC  
    Senior Representative, Fluigent

- **10:10-10:35**
  - 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

  - Solution Provider Presentation: Disease models on-a-Chip: Medical applications of Organ-on-a-Chip Technology  
    Sarah Lau, Partner, Kilburn & Strode

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

  - Solution Provider Presentation: Title TBC  
    Senior Representative, Fluigent

- **10:40-10:55**
  - Morning Refreshments / Odd Numbered Poster Presentation Sessions / One-to-One Partnering Meetings

### 4BIO Registration

- **Venue**
- **Sponsors**
- **qPCR & Digital PCR Congress**
- **Synthetic Biology & Gene Editing Congress**
- **Microfluidics Congress**
- **NGS Tech & Applications Congress**

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**4BIO SUMMIT: 2017**
### 4BIO SUMMIT: 2017

#### DAY 2 TUESDAY 5TH DECEMBER 2017

<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker/Institution</th>
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<tbody>
<tr>
<td>09:45-10</td>
<td>SYNTHETIC BIOLOGY &amp; GENE EDITING CONGRESS</td>
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<tr>
<td>10:20-10:35</td>
<td>Presentation:</td>
<td>Wim Trypsteen, PhD Researcher, Academic Staff Member, Ghent University, Belgium</td>
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<tr>
<td>10:40-10:55</td>
<td>Early Career Researchers Presentation:</td>
<td>Catherine Fan, DPhil, University of Oxford</td>
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<tr>
<td>11:00-11:15</td>
<td>Early Career Researchers Presentation:</td>
<td>Norman Goodacre, Postdoctoral Fellow, Food and Drug Administration</td>
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<td>11:20-11:35</td>
<td>Early Career Researchers Presentation:</td>
<td>Maria Diacinga, Assistant Professor, BioEngineering, University of Washington</td>
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<td>11:40-11:55</td>
<td>Early Career Researchers Presentation:</td>
<td>Bollywood Hubby, Chief Technology Officer, Agenovir</td>
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<td>12:00-12:15</td>
<td>Early Career Researchers Presentation:</td>
<td>Timo Minssen, CEO, Eligo Bioscience</td>
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<td>Early Career Researchers Presentation:</td>
<td>Winnie Svendsen, Technical University of Copenhagen</td>
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<td>Bernhard Zimmermann, Eligo Therapeutics</td>
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<td>15:00-15:15</td>
<td>Early Career Researchers Presentation:</td>
<td>Xuan Wang, CSO, Eligo Bioscience</td>
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<td>15:20-15:35</td>
<td>Early Career Researchers Presentation:</td>
<td>Joseph Yang, CSO, Eligo Bioscience</td>
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<td>Early Career Researchers Presentation:</td>
<td>Gaetan Pons, CSO, Eligo Bioscience</td>
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<td>Marija Drndic, University of Brussels</td>
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### Conference Summary

- **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
  - Multi-platform qPCR approaches to elucidating expression profiles in ageing
    - Ben Lee, Research Technician & PhD Researcher - University of Exeter Medical School

- **Synthetic Biology & Gene Editing Congress**
  - Solution Provider Presentation: Automating Analysis of CRISPR Genome Editing
    - Andy Higgs, UK Operations Manager, Advanced Analytical Technologies Ltd.
  - Start-up Showcase: Next-gen biotherapeutics for precise microbiome engineering and sequence-specific antimicrobials
    - Xavier Duportet, CEO, Eligo Bioscience

- **Microfluidics Congress**
  - Solution Provider Presentation: Title TBC
    - Senior Representative, KLA-Tencor
  - Paper-based analysis for environmental and clinical applications
    - Nicole Pamme, Professor, University of Hull
  - Microfluidic solutions for cell and tissue studies
    - Winnie Svendsen, Associate Professor, Technical University of Denmark

### Venue

- **Agenda Overview**
- **Venue**
- **Sponsors**
- **NGS Tech & Applications Congress**
- **Microfluidics Congress**
- **qPCR & Digital PCR Congress**
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<td>16:45 Chair’s Closing Remarks / Conference Close</td>
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####qPCR & Digital PCR Congress
- **Title TBC**
- **Invitation Out**

####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

####Synthetic Biology & Gene Editing 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

- **No Talk in this Track**

- **Optical DNA mapping for characterization of plasmids coding for antibiotic resistance: principles and clinical applications**
  - Fredrik Westerlund,
  - Associate Professor,
  - Chalmers University of Technology

- **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

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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 1000 person conventions to wedding banquets. The Novotel London West also boasts two international restaurants.
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.
**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

**4BIO REGISTRATION**

**qPCR & Digital PCR Congress**

**NGS Tech & Applications Congress**

**Microfluidics Congress**

**Synthetic Biology & Gene Editing Congress**

**Venue**

**Sponsors**

**Agenda Overview**

**Conference Summary**

**Conference Summary**

**Applications Congress**

**4BIO Registration**

**NGS Tech & Applications Congress**

**Microfluidics Congress**

**Synthetic Biology & Gene Editing Congress**

**qPCR & Digital PCR Congress**

**Venue**

**Sponsors**

**Agenda Overview**

**CONFIRMED SPEAKERS**

**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

**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

**VINCENTO DI CERBO**
Analytical Development Scientist, Cell Therapy Catapult, UK

**ALEXANDRA MARTIN**
Application Specialist, Stilla Technologies

**SENIOR REPRESENTATIVE**
JN Medsys

**GURO 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

**KERRY EMLSLIE**
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, Biodesix

**SARA MOUTAILLER**
PhD, Researcher at ANSES, Animal Health Laboratory, JRU BIPAR, Vectotiq Team

4BIO SUMMIT: 2017
DAY 1 MONDAY 4TH DECEMBER 2017

REGISTERATION & REFRESHMENTS
8:00-8:50

KEYNOTE ADDRESS:
YIU-LIEN FONG
Global Head of Diagnostic Innovation, Janssen and Johnson & Johnson Innovation, UK
Applying PCR methods for improved diagnostics – Title TBC

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

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

TRACK CHAIR: GARY PESTANO,
Associate Professor, Charles University, Czech Republic

TRACK CHAIR: MARIE KORABECNA,
Associate Professor, Charles University, Czech Republic

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

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.
HAKAN JONSSON  
Assistant Professor, KTH Royal Institute of Technology, Sweden  
Droplet PCR for liquid biopsy analysis

AGENDA OVERVIEW

qPCR & Digital PCR Congress

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SOLUTION PROVIDER PRESENTATION

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.

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

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.

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.

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SOLUTION PROVIDER PRESENTATION:

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%.

TRACK CHAIR: WARD DE SPIEGELAERE,  
Assistant Professor, Gent University, Belgium

SOLUTION PROVIDER PRESENTATION:

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FOR SPONSORSHIP OPPORTUNITIES PLEASE CONTACT NICK BEST/GAVIN HAMBrook AT sponsorship@GLOBALENGAGE.CO.UK
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 inhibitor 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 quantifyed 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 cfDNA detection and could make the samples from heparinized blood-derived collections suitable for ctDNA analysis.

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.

SOLUTION PROVIDER PRESENTATION:
SOLUTION PROVIDER PRESENTATION:
SOLUTION PROVIDER PRESENTATION:
SOLUTION PROVIDER PRESENTATION:

FLUIDIGM

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

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.

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
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.
**KEYNOTE ADDRESS:**

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

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

**TRACK 1 – HEALTHCARE CASE STUDIES**

**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.

**SOLUTION PROVIDER PRESENTATION:**

**SENIOR REPRESENTATIVE**  
Bio-Rad Laboratories  
**Title TBC**

**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

**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.
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.

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)

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.

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.

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.
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.

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.

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

DAY 1 – STREAM 1

Genomic Engineering & Synthesis
- Keynote Presentations: Future perspectives – collaborations, strategies and technologies
- Panel Discussion 1: Engineering bacteriophages
- 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: New model host organisms
- 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
CONFIRMED SPEAKERS

RICHARD KITNEY
Professor of BioMedical Systems Engineering, Imperial College London

THORSTEN STAFFORST
Group Leader, Institute for Biochemistry, Universität Tübingen

SENIOR REPRESENTATIVE
Takara

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, UMR5 Inserm

CHRIS WILLIS
Professor of Organic Chemistry, University of Bristol

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 ABOYE
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 MINSSEN
Professor University of Copenhagen

NIKO SONNENSCHEIN
Senior Researcher, Novo Nordisk Foundation
CONFIRMED SPEAKERS

LIONEL CLARKE
Co-Chair of the Synthetic Biology Leadership Council

BOLYN HUBBY
Chief Technology Officer, Agenovir

CATHERINE FAN
DPhil Student, University of Oxford

NORMAN GOODACRE
Postdoctoral Fellow, FDA

PRASHANT YADAV
Visiting Scholar in Global Health and Social Medicine, Harvard Medical School

DAVIDE DE LUCREZIA
Doulix

ANDY HIGGS
UK Operations Manager, Advanced Analytical Technologies Ltd

CONFIRMED SPEAKERS
Global Engage Welcome Address and Morning Chair’s Opening Remarks

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.

SOLUTION PROVIDER PRESENTATION:

SENIOR REPRESENTATIVE
Takara
Title – TBC

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.

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.
### Agenda Overview

#### Venue

- **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.

- **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.

###qPCR & Digital PCR Congress

#### Synthetic Biology & Gene Editing Congress

- **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.

- **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%.

###Microfluidics Congress

#### NGS Tech & Applications Congress

- **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.

- **Jean-Sebastien Hulot**
  - Professor of Medicine, Pharmacology, Institute of Cardiometabolism & Nutrition, UMR5 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.

###4BIO Registration

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

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.

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.

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 has 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.

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 significantly 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.

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 synthetic 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).
EARLY CAREER RESEARCHERS PRESENTATION:  
JUMAI ABIJOYE  
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.

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 restauration 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.

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.

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.

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

**MONDAY 4TH DECEMBER 2017**
TUESDAY 5TH DECEMBER 2017

08:00-08:35 Refreshments & Networking Meetings

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

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

08:40-10:10 Tools, Technologies and Platforms

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 Morning Refreshments / Poster Presentations

10:35-11:25 Innovation, Investment and Start-ups

SOLUTION PROVIDER PRESENTATION

SARAH LAU
Partner, Kilburn & Strod
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
### Agenda Overview

**4BIO SUMMIT: 2017**

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<td>UK Operations Manager, Advanced Analytical Technologies Ltd.</td>
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<td><strong>CRISPR-Cas9 solutions for HPV and other persistent human infections</strong></td>
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<td><strong>KELLY STEVENS</strong></td>
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<td>Assistant Professor of Bioengineering, University of Washington</td>
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<td><strong>Hijacking Nature’s Blueprints for Synthetic human Tissue Assembly</strong></td>
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<td>Human development – the process by which a single celled zygote</td>
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<td>adult body cannot always reassemble or repair itself after injury,</td>
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<td>human systems. Here I will highlight some of our work in both</td>
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<td>constructing and controlling artificial heart and liver tissue using</td>
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<td>both nature’s blueprints and new bioprinting technologies.</td>
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<td><strong>CATHERINE FAN</strong></td>
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<td>DPhil Student, University of Oxford</td>
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<td><strong>Simcells: A novel chassis for synthetic biology and drug delivery</strong></td>
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<td>The rapidly growing field of synthetic biology involves the</td>
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<td>manipulation of biological systems for valuable purposes. However,</td>
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<td>many challenges arise as living systems cannot be engineered</td>
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<td>without interference from their native metabolic networks and</td>
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<td>genetically modified organisms are not trusted by the public. To</td>
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<td>address these issues, a novel technology called “SimCells” has</td>
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<td>been created as an alternative, organic chassis to living</td>
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<td>organisms. SimCells are essentially bacterial cells lacking genomes</td>
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<td>(i.e. they cannot replicate) but which remain fully equipped with</td>
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<td>the cellular resources to produce proteins or small molecules from</td>
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<td>introduced DNA carried by plasmids. This new chassis will allow</td>
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<td>regenerative medicine will open new avenues for synthetic biology.</td>
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**Day 2 Tuesday 5th December 2017**

**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.

### Start-Up Showcase: Xavier Dupontet

**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

### 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.
**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 (Pfm) 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.

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**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 develop 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.

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**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.

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**Timo Minssen**
Professor, University of Copenhagen

**The Interface between Big Data, IPRs & Competition Law in SynBio – 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.
### DAY 2 TUESDAY 5TH DECEMBER 2017

#### 14:35-16:20

**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.  
- 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.

#### 15:00-15:25

**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.

#### 14:35-15:00

**NIKO SONNENSCHEIN**  
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.

#### 15:25-15:55

**PRASHANT YADAV**  
Visiting Scholar in Global Health and Social Medicine, Harvard Medical School  
**The “self driving” supply chains for biologics and gene therapies**  
- New manufacturing technologies and digital technologies can enable high end biologics manufacturing to become interconnected webs of materials, goods and machines  
- This trend is most likely to start in gene therapy manufacturing  
- This talk focusses on what trends are enabling this and what can innovation leaders do to stay ahead

#### 16:20-16:45

**KELLY STEVENS**  
Assistant Professor of Bioengineering, University of Washington  
**Roundtable 3: Collaboration strategies**

#### Roundtable DISCUSSIONS:

**Challenges for the future of Synthetic Biology**
- **Roundtable 1: Ethics and society**
- **Roundtable 2: IP and Regulation**
- **Roundtable 3: Collaboration strategies**

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**Conference Summary**

**CONGRESS SCHEDULE**

**qPCR & Digital PCR Congress**

**Synthetic Biology & Gene Editing Congress**

**Microfluidics Congress**

**NGS Tech & Applications Congress**

**4BIO Registration**
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
**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

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

ELAIN 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 Ertl  
Professor of Physical Biology, 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
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 downsampling 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.

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 greenhouse 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.

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.

DAVE WEITZ
Malinckrodt Professor of Physics and Applied Physics, Harvard University
Droplet based microfluidic applications in biotechnology – Title TBC
**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.

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**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.

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**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.

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**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.

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**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.
**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.

**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.

**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.
## Conference Summary

### DAY 2 TUESDAY 5TH DECEMBER 2017

### CONGRESS SCHEDULE

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<td>CASE STUDIES AND APPLICATIONS IN MEDICAL RESEARCH</td>
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### SOLUTIO PROVIDER PRESENTATION:

- **SENIOR REPRESENTATIVE**
- **Fluent**

### FOR SPONSORSHIP OPPORTUNITIES

- **Fluent**
- **Title TBC**

### SOLUTIO PROVIDER PRESENTATION:

- **SENIOR REPRESENTATIVE**
- **KLA-Tencor**

### FOR SPONSORSHIP OPPORTUNITIES

- **KLA-Tencor**
- **Title TBC**

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**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.

**NICOLE PAMME**
Professor, University of Hull

**Paper-based analysis for environmental and clinical applications**

- Micro analytical paper devices (µPADs)
- 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.
## Day 2: Tuesday 5th December 2017

### Lunch

**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.

### Afternoon Refreshments / Poster Presentations

**13:15-13:45**

**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).

### 14:10-14:35

**Johan Elf**  
Senior Associate Professor, Mechanical Engineering Department, Worcester Polytechnic Institute  
**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 test clinical UPEC isolates, all of them were correctly classified as susceptible or resistant to ciprofloxacin in <10min.

### 14:35-15:00

**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.

### 14:45-15:00

**Chuck Henry**  
Professor of Chemistry, Colorado State University  
**Bacterial and antimicrobial resistance detection**

**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.

### Conference Close

**16:45**

**Conference Close**
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 scientist 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

- **MOSTAFA RONAGHI**
  Senior Vice President & Chief Technology Officer, 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
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
CONFIRMED SPEAKERS

**RICHARD MCCOMBIE**
Professor, Cold Spring Harbor Laboratory, USA

**MOSTAFA RONAGHI**
Senior Vice President & Chief Technology Officer, 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 KLIIMASIAUSKAS**
Chief Scientist and Head of Department, 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

**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 Biomics Pole, Institut Pasteur, France

**RICHARD MCCOMBIE**
Professor, Cold Spring Harbor Laboratory, USA

**MOSTAFA RONAGHI**
Senior Vice President & Chief Technology Officer, 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 KLIIMASIAUSKAS**
Chief Scientist and Head of Department, 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

**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

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4BIO SUMMIT: 2017
### KEYNOTE ADDRESS: RICHARD MCCOMBIE
Professor, Cold Spring Harbor Laboratory, USA
Title TBC

### KEYNOTE ADDRESS: MOSTAFA RONAGHI
Senior Vice President & Chief Technology Officer, Illumina
Recent progress in genomics
- Review of recent technologies
- Emerging applications in genomics
- Future direction

### 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

### 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.

### 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.
**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

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**SOLUTION PROVIDER PRESENTATION:**

**VINZENZ LANGE**  
Chief Technology Officer, DKMS Life Science Lab GmbH  
**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.

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**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

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**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.

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**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.
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 >1000 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.

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.

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 hgs 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.
08:20-09:00 Refreshments

09:00-09:40 MORNINGS CHAIR: PRIYASMA BHOUMIK, PD Research Scientist, Novartis, Switzerland

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 MORNINGS REFRESHMENTS / ODD NUMBERED POSTER PRESENTATIONS / ONE-TO-ONE PARTNERING MEETINGS

10:10-10:35 For sponsorship opportunities please contact Nick Best/Gavin Hambrook at: sponsorship@globalengage.co.uk

SOLUTION PROVIDER PRESENTATION

10:35-11:25 DAY 2 TUESDAY 5TH DECEMBER 2017

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 circulating 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.
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 Biomics 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 5: Single-Cell Genomics

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?

12:20-13:10
Lunch

13:10-14:10
TRACK CHAIR: AHMAD KHODR, Researcher, International Microbiology Department, L’Oréal Research & Development, France
CHRISTIAN GLOECKNER
Chief Technology Officer, NEO New Oncology GmbH, Germany
Challenges in using NGS as a clinical diagnostic tool

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

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).
15:25-15:55  Afternoon Refreshments / Even Numbered Poster Presentations

15:55-16:20  SEQUENCING MICROBES

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.

15:55-16:20  VICTOR NEDUVA
Group Leader, GlaxoSmithKline, UK
Title TBC

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.

15:55-16:20  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

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

16:35-17:00  SEQUENCING MICROBES

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Researcher, International Microbiology Department, L’Oréal Research & Development, France
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17:00  Conference Close
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

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.
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.