NGS GENERAL TALKS
Day 1 Stream 1 & Day 2 Stream 1 – Exploring Emerging Trends in NGS Data Analysis & NGS Application Strategies
- Overcoming challenges and solutions for data storage and management
- Processing and integrating NGS data
- Utilising novel methods and tools for NGS data analysis
- Updates in interpreting NGS data
- Reproducibility of NGS data analysis results
- New software and hardware analysis tools
- Advances in antibody repertoire sequencing
- Therapeutic case studies from the areas of:
  - Oncology
  - Inflammatory diseases
  - Neurodegenerative diseases
- Analysis of liquid biopsies by NGS

NGS PHARMA TALKS
Day 1 – NGS for Pharma: Data Analysis, Biomarker Development, Precision Medicine and Clinical Diagnostics
- Utilising precision medicine strategies in pharma
- Advances in checkpoint immunotherapy
- Biomarker discovery using proteomics and transcriptomics
- Utilising NGS for molecular diagnostics development
- NGS in biomarker development

NGS HEALTHCARE TALKS
Day 2 – NGS, Genomics and Clinical Diagnostics in Healthcare
- Updates in the clinical applications on NGS
- Using NGS for clinical diagnostics development
- Utilising whole genome sequencing in healthcare
- Latest updates in clinical metagenomics & microbiome research

SINGLE CELL GENERAL TALKS
5th Annual Single Cell Analysis Congress
Day 1 Stream 3 – Single Cell ‘Omics Analysis: Current and Emerging Tools
- Single cell ‘omics case studies and therapeutic applications:
  - Genomics & epigenomics
  - Transcriptomics
  - Proteomics
  - Metabolomics
- Using single cell analysis in clinical & diagnostic development
- Recent advancements in circulating tumour cells research
- Single cell genomics for understanding tumour heterogeneity
- Single cell RNA sequencing technologies and applications
Day 2 Stream 2 – Translation to Diagnostic and Therapeutic Applications
- Methods for single cell isolation, capture & purification
- Single cell analysis tools including PCR analysis technologies
- High throughput in-situ sequencing approaches
- The potential applications of single cell manipulation
- Case studies: infectious diseases
- Single cell imaging updates
Day 2 Stream 3 – Single Cell Data Analysis & Advances in Microfluidic Technologies
- Challenge 1: sample preparation for single cell analysis
- Challenge 2: bioinformatics:
  - Single cell data analysis
  - Single cell data handling
  - Identifying mutated genes in tumour samples
  - Improving the accuracy of quantitative analysis of transcripts
- Microfluidics technologies and advances in applications
- Statistical analysis of single cell data
- New technologies and instrumentation for high content flow and image cytometry

2017 Speakers Include:
- Ana Leite
  GlaxoSmithKline
- Etienne Ruppe
  Paris Diderot University
- Ken Chang
  Daiichi Sankyo
- Balázs Győrffy
  Semmelweis University
- Satu Nahkuri
  F. Hoffmann-La Roche
- Susann Mueller
  Helmholtz Centre
- Sarah Ennis
  University of Southampton
- Thomas Kroneis
  Medical University of Graz

For booking details & registration fees please refer to the last page or visit:
http://www.nextgenerationsequencing-congress.com/marketing/
Benefits to Attending

- **New to 2017! Learn more about NGS in pharma: biomarker development, precision medicine and clinical diagnostics.** Case studies include: linking NGS to clinical trials, biomarkers for precision therapies and innovative biology
- **New to 2017! NGS, genomics and clinical diagnostics in healthcare:** discuss the latest microbiome research results, updates in the clinical applications of NGS in healthcare and clinical metagenomics updates
- **Hear from and meet with the key innovators in pharma and academic next generation sequencing and single cell analysis.** Attendees include: Executive Director, Diagnostic Strategy, Novartis; Professor of Medical Genetics, University Medical Centre Utrecht; Professor of Cell Biology, Paris Descartes University; Professor, Tel Aviv University
- **Discover collaborative solutions to next generation sequencing and clinical diagnostics.** This prestigious congress brings together key opinion leaders to discuss topic areas ranging from novel methods to NGS data analysis, reproducibility of data analysis results and updates in interpreting NGS data
- **Find out about the latest advancement in single cell ‘omics analysis.** This prestigious event will cover updates in circulating tumor cells, novel updates in single cell analysis technologies and case studies from therapeutic areas such as infectious diseases
- **Unparalleled networking opportunities.** The two-day congress offers ample networking opportunities creating an interactive platform for high-level scientific and business discussions. Participate in formal or informal discussions during our networking breaks and pre-organised 1-2-1 meetings
- **A high quality programme devised with the help of our esteemed advisory board.** Presentations will cover areas including advances in immunotherapy, whole genome sequencing in healthcare and overcoming data storage challenges
  - **Co-located with 3rd Annual Genome Editing Congress**

Do not miss out on our free webinars:
- Advances in NGS Data Analysis: 13th September 2017. Register [here](#).
- Next Generation Sequencing for Liquid Biopsies: 26th September 2017. Register [here](#).
- Single Cell Protein Analysis: 20th September 2017. Register [here](#).

2017 Next Generation Sequencing & Clinical Diagnostics and Single Cell Analysis

**Confirmed Speakers Include:**

**Pharma:**
- Ken Chang, Director of Clinical Biomarkers, Daiichi Sankyo
- Holger Klein, Head of Computational Biology Expert Function, Boehringer Ingelheim
- Marc Sultan, Group Head, Human Genetics and Genomics, Novartis Institutes for BioMedical Research
- Miika Ahdesmäki, Associate Director Bioinformatics, AstraZeneca
- Satu Nahkuri, Principal Data Scientist, F. Hoffmann-La Roche
- Harpreet Saini, Associate Director, Bioinformatics, Astex Pharmaceuticals
- Eric Sarcey, Senior Scientist in Analytical Microbiology, Sanofi
- Ana Leite, Computational Biologist, GlaxoSmithKline

**Healthcare:**
- Balázs Győrffy, Scientific Advisor, Semmelweis University and Hungarian Academy of Sciences
- Dag Erik Undlien, Professor and Group Leader, Oslo University Hospital and University of Oslo
- Nine Knoers, Professor Clinical Genetics, Chair Department of Genetics, University Medical Centre Utrecht, The Netherlands
- Matthew Edwards, Senior Clinical Scientist, Royal Brompton Hospital
- Etienne Ruppe, MCU-PH/Associate Professor, Paris Diderot University and Bichat Hospital
- Saheer Gharbia, Professor and Head of Genomic Research, Public Health England
- Michael Pfaffl, Professor of Molecular Physiology, Technical University of Munich
- Susann Müller, Professor and Group Leader Flow Cytometry, Helmholtz Centre
- Jürgen Eils, Head of Data Management and Genomics IT, German Cancer Research Centre
- Michael Huber, Junior Group Leader and Deputy Head of Diagnostics and Development, University of Zurich
- Estee Torok, Senior Research Associate, University of Cambridge and Honorary Consultant in Infectious Diseases & Microbiology, Addenbrooke’s Hospital
- David Litt, Clinical Scientist, Public Health England
- Julia van Campen, Development Specialist, Sheffield Diagnostic Genetics Service

**Academic:**
- Eli Eisenberg, Professor, Tel Aviv University
- Jonathan Strefford, Professor of Cancer Molecular Genetics, University of Southampton
- Stefano Ceri, Professor, Politecnico di Milano
- Jan Komorowski, Professor and Chair of Bioinformatics, Uppsala University
- Winston Hide, Chair of Computational Biology, Center for Genome Translation, Sheffield Institute for Translational Neuroscience, University of Sheffield
- Sarah Ennis, Professor of Genomics, University of Southampton
- Stephan Lorenz, Head, Single Cell Genomics Core Facility, Wellcome Trust Sanger Institute
- Marina Granovskaya, Adjunct Associate Professor, University College Dublin

For more information please contact [marketing@oxfordglobal.co.uk](mailto:marketing@oxfordglobal.co.uk)
2017 Confirmed Speakers Continued:

- David R. Westhead, Head of the School of Molecular and Cellular Biology, Professor of Bioinformatics, University of Leeds
- Holger Heyn, Head, Single Cell Genomics Group, National Centre for Genomic Analysis
- James Hadfield, Head of Genomics, Cancer Research UK Cambridge Institute
- Jernej Ule, Group Leader and Professor of Molecular Neuroscience, The Francis Crick Institute
- Tom Freeman, Professor, Roslin Institute
- Akos Vertes, Professor of Chemistry, George Washington University
- Dafna Benayahu, Professor and Chair, Department of Cell and Developmental Biology, Tel Aviv University
- Patrizia Paternini-Bréchot, Professor of Cell Biology, Paris Descartes University
- Evi Lianidou, Professor of Analytical Chemistry and Clinical Chemistry, University of Athens
- Graziano Pesole, Professor of Molecular Biology, Head of the Italian Node of ELIXIR, University of Bari Aldi Moro
- Michael Rieger, Professor, Goethe University of Frankfurt
- Richard Festenstein, Clinical Professor of Molecular Medicine, Imperial College London
- Mark Lindsay, Professor in Molecular Pharmacology, University of Bath
- David Klug, Professor of Chemical Biophysics, Imperial College, Department of Chemistry
- Simon Amee-Beg, Group Leader and Principal Investigator, King’s College London
- Thomas Kroneis, Head of Research Unit for Single Cell Analysis and Senior Scientist, Medical University of Graz
- Mike Stubbington, Principal Staff Scientist, Wellcome Trust Sanger Institute
- Pamela Pinzani, Associate Professor, University of Florence
- Thierry Voet, Associate Professor and Group Leader, University of Leuven and Wellcome Trust Sanger Institute
- Colin Logie, Associate Professor, Radboud Institute for Molecular Life Sciences
- Ilan Tsafaty, Principal Investigator, Tel Aviv University
- Tomer Kalisky, Assistant Professor of Bioengineering, Bar-Ilan University
- Marcus Tindall, Associate Professor of Mathematical Biology, University of Reading
- Jari Louhelainen, Associate Professor of Biochemistry, University of Helsinki / Liverpool John Moores University
- Graeme Whyte, Associate Professor, Herriot-Watt University
- Christopher Yau, Associate Professor and Reader in Computational Biology, University of Birmingham and University of Oxford
- Marisa Martin-Fernandez, Functional Biosystems Imaging Group Leader, Science and Technology Facilities Council
- Antoine-Emmanuel Saliba, Group Leader, Helmholtz Centre for Infection Research
- Liming Ying, Senior Lecturer, Imperial College London
- Yannick Wurm, Senior Lecturer in Bioinformatics, Queen Mary University of London
- Louisa James, Lecturer in Immunology, Queen Mary University of London

2017 NGS & Clinical Diagnostics, Single Cell Analysis and Genome Editing Sponsor Speakers Include:

- Mark Behlke, Chief Scientific Officer, Integrated DNA Technologies, Inc.
- Guilhem Tourniaire, Founder and Scientific Director, Cellenion
- Anja Smith, Director, Research and Development, Dharmacon
- Chris Wetzel, Director Sales and Marketing, MMI
- Kevin Holden, Head of Synthetic Biology, Synthego
- Guillaume Pavlović, Department Head - Genetic Engineering and Model Validation Department, Phenomin-iCS
- Lukas Paul, Senior Manager of Scientific Affairs, Lexogen
- Xiangyu Rao, NGS Field Application Manager, Europe, Integrated DNA Technologies
- Cornelia Hampe, PhD, Scientific Support Specialist, Takara Bio Europe
- Elly Sinkala, Application Scientist, cytena
- Weng Hua, Khoo, PhD, student at The Garvan Institute, Bone Biology Division

If you’re on Twitter, make sure to follow us @xgenseq and join the Congress conversation on #xgenseq17
2017 Next Generation Sequencing, Single Cell Analysis and Genome Editing Congress Sponsors Include:

Silver Sponsors:

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For more information please contact marketing@oxfordglobal.co.uk
9th Annual Next Generation Sequencing and Clinical Diagnostics Congress & 5th Annual Single Cell Analysis Congress
Day One – 9 November 2017

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<tr>
<td>07.30 – 08.20</td>
<td>Registration</td>
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<tr>
<td>08.20 – 08.25</td>
<td>Oxford Global's Welcome Address</td>
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<tr>
<td>08.25 – 08.30</td>
<td>Chairperson’s Opening Address</td>
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</table>
| 08.30 – 09.00 | Keynote Address: A Novel Validation Strategy For NGS Mutation Profiling In FFPE Tissues
We have recently developed a “Concordance Calculator” and a novel replicate approach to eliminate technical artifacts including post tissue collection modifications (PTCM) such as deamination and oxidation artifacts. Use of the Concordance Calculator to quantify reproducibility of multi-variant calls among Next Generation Sequencing replicates and to eliminate technical artifacts including PTCM also allowed us to develop an unconventional validation strategy. We call this validation approach “in situ analytical validation and evaluation (iSAVE)”. This novel validation strategy and background information will be presented. |
| 09.00 – 09.30 | Stream Keynote Address: Molecular Information Application Strategy For Drug Development
• Challenges of omics analyses include prohibitively large size and scattered distribution of NGS data sets, as well as reproducibility of the applied bioinformatics methods
• As a solution, we are building Roche Data Commons, a modular scientific computation systems supporting data provenance and bringing compute to data
• We present a case study on how to use such a federated system for the benefit of drug development |

Ken Chang, Director of Clinical Biomarkers, Daiichi Sankyo

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<tr>
<th>Time</th>
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| 09.00 – 09.30 | Stream Keynote Address: Discovery Of Potential Biomarkers Using Combined Proteomics And Transcriptomics
A phosphoproteomics study using quantitative mass-spectrometry was carried out to demonstrate the feasibility of this approach for elucidating drug mechanism and broad changes in the cellular phosphoproteome as a measure of target modulation. Significant differences in the phosphorylation status of proteins from different classes were identified upon drug treatment in the A375 BRAFmut cancer cell line. Further, integrated analysis of proteomics & transcriptomics data using network-based approaches is providing insights into signaling pathways, biological processes and regulatory factors associated with the target and drug mechanism of action. |

Harpreet Saini, Associate Director, Bioinformatics, Astex Pharmaceuticals

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<tr>
<td>09.30 – 10.00</td>
<td><strong>Title To Be Confirmed</strong></td>
<td>Neil Ward, Regional Marketing Director, Illumina</td>
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<tr>
<td>10.00 – 11.20</td>
<td><strong>Morning Coffee &amp; Refreshments, Poster Presentation Sessions, One to One Meetings x3</strong></td>
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<tr>
<td>11.20 – 11.50</td>
<td><strong>Advanced Network Analytical Approaches For The Interpretation Of NGS Data</strong></td>
<td>Tom Freeman, Professor, Roslin Institute</td>
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<td>11.50 – 12.20</td>
<td><strong>Rule Networks – Discovering Molecular Interactions From High-Throughput Data</strong></td>
<td>Jan Komorowski, Professor and Chair of Bioinformatics, Uppsala University</td>
</tr>
<tr>
<td>11.20 – 11.50</td>
<td><strong>Quantifying Low-Frequency Revertants In Oral Poliovirus Vaccine Using Next Generation Sequencing</strong></td>
<td>Eric Sarcey, Senior Scientist in Analytical Microbiology, Sanofi</td>
</tr>
<tr>
<td>11.50 – 12.20</td>
<td><strong>Challenges Of NGS In Clinical Trials</strong></td>
<td>Marc Sultan, Group Head, Human Genetics and Genomics, Novartis Institutes for BioMedical Research</td>
</tr>
<tr>
<td>11.20 – 11.50</td>
<td><strong>Leveraging Single-Cell Genomics For Target Discovery</strong></td>
<td>Ana Leite, Computational Biologist, GlaxoSmithKline</td>
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<tr>
<td>11.50 – 12.20</td>
<td><strong>Small Molecules In Dividing Cells And Single Neurons Of Known Function</strong></td>
<td>Akos Vertes, Professor of Chemistry, George Washington University</td>
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<th><strong>Pharma Talks</strong></th>
<th><strong>Single Cell Analysis General Talks</strong></th>
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<td><strong>Precision Medicine, Biomarker Development And Clinical Diagnostics</strong></td>
<td><strong>Single Cell ‘Omics Analysis: Current And Emerging Tools</strong></td>
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<td>12.20 – 12.50</td>
<td>Solution Provider Presentation</td>
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<td><strong>Roche</strong></td>
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<tr>
<td>12.50 – 13.50</td>
<td>Lunch, Poster Presentation Sessions</td>
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<td>13.50 – 14.20</td>
<td>Solution Provider Presentation</td>
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<td><strong>QIAGEN</strong></td>
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<tr>
<td>14.20 – 14.50</td>
<td>Data-Driven Genomic Computing: Making Sense Of The Signals From The Genome</td>
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<td>• Motivation/focus of the talk on tertiary data analysis: integration of heterogeneous genomic datasets for supporting queries and data analysis over both private and public repositories</td>
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<td>• Presentation of GDM (Genomic Data Model) and GMQL (GenoMetric Query Language) with description of available prototypes and implementations</td>
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<td>• Scenarios of use of GMQL in order to respond to biological questions</td>
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<td>Stefano Ceri, Professor, Politecnico di Milano</td>
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<tr>
<td>14.50 – 15.00</td>
<td>Application Of Academic Knowledge To Clinical Diagnostics &amp; Enhancing Collaborations Between Pharma &amp; Academics</td>
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<td>Marina Granovskaya, Adjunct Associate Professor, University College Dublin</td>
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<td><strong>The Human Cell Atlas</strong></td>
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<td>• The Human Cell Atlas is a new international initiative that aims to define all human cell types in terms of their gene expression and other distinctive molecular characteristics</td>
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<td>• To achieve this, disparate fields of expertise in biology, medicine, genomics, technology development, and computation (including data analysis, software engineering, and visualization) will need to come together in a coherent, concerted way</td>
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<td>• I will introduce this nascent initiative and discuss how it will be achieved by groups working together throughout the world</td>
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<td>Mike Stubbington, Principal Staff Scientist, Wellcome Trust Sanger Institute</td>
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<th>Single Cell Analysis General Talks</th>
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<tr>
<td>14.50 – 15.20</td>
<td>Exploring Emerging Trends In NGS Data Analysis &amp; NGS Application Strategies</td>
<td>Precision Medicine, Biomarker Development And Clinical Diagnostics</td>
<td>Single-Cell RNA-Seq Analysis With Partek Flow Software</td>
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</table>
|           | Solution Provider Presentation                           |                                                   | Next generation sequencing analysis of single cell RNA-Seq data has emerged as one of the most propulsive topics in life sciences. However, data analysis can be quite challenging, especially for scientists new to the field. This talk will introduce Partek® Flow®, an intuitive and easy-to-use, graphical user interface-based tool package for analysis of next generation sequencing data. The topics include:  
• QA/QC of the single cell data  
• Visualisation of single cell data  
• Detection and characterisation of cell populations |

Ivan K. Lukić, Senior Field Application Scientist, Partek

| 15.20 – 15.40 | Technology Spotlight Presentation                       | Technology Spotlight Presentation                   |                                                   |

| 15.40 – 16.30 | Afternoon Coffee & Refreshments, Poster Presentation Sessions, One to One Meetings x2 |                                                   |                                                   |

| 16.30 – 17.00 | SLAMseq Kit – A New Method For Metabolic RNA Sequencing | Isolating Adherent Single Cells – The Taming Of The Shrew |
|              | • Analyze transcriptome-wide kinetics of RNA synthesis and turnover  
• Measure nascent RNA expression and transcript stability  
• Just two steps are added to an RNA-seq workflow | • Applications: Why analyse a single cell  
• Tools: How to precisely isolate a single cell  
• Case study: Isolating adherent single cells selectively |

Lukas Paul, Senior Manager of Scientific Affairs, Lexogen

Chris Wetzel, Microscopic Single Cell Isolation, MMI

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<th>Single Cell Analysis General Talks</th>
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<tr>
<td>17.00 – 17.30</td>
<td><strong>Utilizing RNA-Seq To Assess RNA Editing Levels, As A Diagnostic Tool In Cancer</strong>&lt;br&gt;• Level of A-to-I RNA editing by AΔR Enzymes is altered in various cancer types&lt;br&gt;• Extensive editing in cancer introduces RNA diversity or RNA mutations in mRNAs and micro-RNAs&lt;br&gt;• RNA modification events in tumours are as abundant as genomic DNA mutations&lt;br&gt;• Altered editing activity is associated with poor prognosis</td>
<td><strong>Integrating ‘Omnics Application In Complex Disease: Applications To Paediatric Inflammatory Bowel Disease (IBD)</strong>&lt;br&gt;Multiple contemporary sequencing approaches support better understanding of pathoetiologny in complex diseases. While ascertaining patients with early onset disease selects for the highest genetic burden, environmental factors and in particular gut microbiome dysbiosis can also impact clinical manifestation in IBD. We apply whole exome sequencing, gut epithelial transcriptomics and microbiome analyses alongside clinical, metabolomic and immun0-Profiling to inform on individual risk factors and their interpretation.</td>
<td><strong>Application Of Single-Cell RNA Sequencing In Diseased Tissues</strong>&lt;br&gt;• Single-cell RNA sequencing elucidates composition and dynamics of complex tissues&lt;br&gt;• Cell type deconvolution of diseased tissues pinpoints driving mechanisms&lt;br&gt;• Understanding genome activity through single-cell resolution screenings</td>
<td><strong>Holger Heyn, Head, Single Cell Genomics Group, National Centre For Genomic Analysis</strong></td>
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<td>Eli Eisenberg, Professor, Tel Aviv University</td>
<td><strong>Sarah Ennis, Professor of Genomics, University of Southampton</strong></td>
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<td>17.30 – 18.00</td>
<td><strong>Computational Tools For Studies Of RNA Regulation In Neurologic Diseases With iCLIP And RNA-Seq</strong>&lt;br&gt;• An interactive online platform for processing, management and secure storage of iCLIP and RNA-seq data&lt;br&gt;• Use of the platform for collaborative analysis, visualization and distribution of processed transcriptomic data&lt;br&gt;• RNA maps: integrating multiple types of NGS data to unravel the position-dependent RNA regulatory principles</td>
<td><strong>Aggressive Lymphomas: Taking Genome Scale Data And Bioinformatics To The Clinic</strong>&lt;br&gt;• The practical and biological challenges of applying large scale data in clinical trials and real populations&lt;br&gt;• Building prognostic and individual models and dealing with disease heterogeneity&lt;br&gt;• Precision medicine for lymphoma</td>
<td><strong>Clinical Impact Of Molecular Analysis Of Circulating Rare Cells</strong>&lt;br&gt;• Circulating rare cells represent a new field of medicine with potential clinical impact&lt;br&gt;• Their immunomolecular characterization is meant to improve personalized medicine&lt;br&gt;• Technical challenges have limited this field in the past but recent developments open new pathways for their analysis</td>
<td><strong>Patrizia Paterlini-Bréchot, Professor of Cell Biology, Paris Descartes University</strong></td>
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<td>Jernej Ule, Group Leader and Professor of Molecular Neuroscience, The Francis Crick Institute</td>
<td><strong>David Westhead, Head of the School of Molecular and Cellular Biology, Professor of Bioinformatics, University of Leeds</strong></td>
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<td>18.00 – 18.30</td>
<td><strong>Cheap Sequencing Is Disrupting Research On Emerging Model Organisms</strong>&lt;br&gt;• In particular, this has led to major discoveries regarding the genes responsible for social behaviour in ants, and created new approaches for diagnosing health of pollinators including bees&lt;br&gt;• I additionally highlight particular challenges of genome data science in small teams and present some of the tools and approaches we use to increase our productivity while reducing risks</td>
<td><strong>Single-Cell Multi-Omics To Understand The Biology Of Cellular Heterogeneity In Health And Disease</strong>&lt;br&gt;• Single-cell multi-omics technologies&lt;br&gt;• Single-cell genome analysis&lt;br&gt;• Somatic genetic variation</td>
<td><strong>Liquid Biopsies: The Potential Of Single Cell Analysis On CTCs</strong>&lt;br&gt;• “Liquid biopsy”, is based on minimally invasive blood-based tests that can be serially repeated&lt;br&gt;• “Liquid biopsy” has the potential to characterize the evolution of a solid tumor in real time, by extracting molecular information from circulating tumor cells (CTCs), circulating tumor DNA (ctDNA), circulating mRNA or exosomes&lt;br&gt;• Molecular characterization of CTCs at the single cell level holds considerable promise for the elucidation of the role of tumor heterogeneity in resistance mechanisms and on the efficacy of systemic therapies</td>
<td><strong>Thierry Voet, Associate Professor and Group Leader, University of Leuven and Wellcome Trust Sanger Institute</strong>&lt;br&gt;<strong>Evi Lianidou, Professor of Analytical Chemistry and Clinical Chemistry, University of Athens</strong></td>
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| 18.30 – 19.00 | **Single Cell Transcriptomics Reveals Specific RNA Editing Signatures In The Human Brain**  
- A-to-I RNA editing in humans is carried out by members of ADAR family of enzymes that act on double strand RNAs and can alter codon identity, splicing sites or base-pairing interactions within higher-order RNA structures  
- We have recently released a comprehensive human inosinome Atlas including more than 4.6 millions of A-to-I events (PMID: 26449202) and found that genes undergoing RNA editing were consistently enriched in genes involved in neurological disorders and cancer, confirming the relevant biological role of RNA editing in human (PMID: 27587585)  
- To characterize the complexity of A-to-I RNA editing at single cell resolution we analyzed RNA-seq data from 466 cortex cells (PMID: 26060301). RNA editing was cell-specific and bimodally distributed with an all or nothing pattern  
- The RNA editing profile clearly discriminated major brain cell types as neurons, astrocytes and oligodendrocytes remarking its primary role in modulating brain functions through key modifications in neurotransmitter receptors  

Graziano Pesole, Professor of Molecular Biology, Head of the Italian Node of ELIXIR, University of Bari Aldi Moro |
| 19.00 – 19.30 | **Single-Cell Analysis Of Kidney Development And Tumorigenesis**  
- A major challenge in stem cell biology is to identify and molecularly characterize tissue-specific stem cells in tissues and tumors  
- We use single cell technologies to measure gene expression from hundreds of individual cells in order to identify and molecularly characterize the cell subpopulation repertoire of a developing fetal kidney and Wilms’ tumor - a pediatric kidney tumor thought to originate from faulty differentiation of fetal developing tissues  
- We find that Wilms’ tumor is composed of cells resembling the most immature cell types in the developing fetal kidney  
- We find that not one – but two populations are required for the regeneration of this tumor  

Tomer Kalisky, Assistant Professor of Bioengineering, Bar-Ilan University |
| 19.30 | **Networking Drinks & End of Day One** |
### 9th Annual Next Generation Sequencing and Clinical Diagnostics Congress & 5th Annual Single Cell Analysis Congress

**Day Two – 10 November 2017**

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| 08.20 – 08.50 | **Keynote Address:** Improved Single Cell Full-Length Transcriptome Sequencing Protocol Enables Long-Term Storage And RNAse Protection  
Stephan Lorenz, Head, Single Cell Genomics Core Facility, Wellcome Trust Sanger Institute |
| 08.50 – 09.20 | **Stream Keynote Address:** Maximising The Signal To Noise Ratio In NGS Of Tumour FFPE And Liquid Biopsy Samples To Better Identify And Track Cancer Drivers  
Miika Ahdesmäki, Associate Director Bioinformatics, AstraZeneca |
| 08.50 – 09.20 | **Stream Keynote Address:** Cell Dispersal – A Source Of Bias In The Clinical Utilization Of Next Generation Sequencing  
Balázs Győrffy, Scientific Advisor, Semmelweis University and Hungarian Academy of Sciences |
| 08.50 – 09.20 | **Stream Keynote Address:** Sex, Disease, Stochastic Gene Silencing And The Epigenetic Code  
Richard Festenstein, Clinical Professor of Molecular Medicine, Imperial College London |
| 08.50 – 09.20 | **Stream Keynote Address:** The Role Of Mathematical Modelling In Informing Single Cell Studies  
Marcus Tindall, Associate Professor of Mathematical Biology, University of Reading |

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<td>09.20 – 09.50</td>
<td>Solution Provider Presentation</td>
<td>CRISPR/Cas9 Knockins – Get Better Specificity With Single-Stranded DNA Knockout mutations can usually be obtained with high efficiency, but knocking in longer sequences (&gt;200 bp) via homology directed repair is more difficult to achieve. Although single-stranded DNA (ssDNA) donor templates have recently been shown to have several advantages over double-stranded DNA, the usefulness of long ssDNA templates is limited due to the difficulty and high cost of producing them. Takara Bio has recently developed a simple and economical method for generating long ssDNA donor templates up to 5 kb. We will explain the features of our Guide-it Long ssDNA Production System as well as the benefits of using long ssDNA repair templates for knockin experiments. Cornelia Hampe, PhD, Scientific Support Specialist, Takara Bio Europe</td>
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| 09.50 – 10.20 | 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 Xiangyu Rao, NGS Field Application Manager, Europe, Integrated DNA Technologies | CellenONE®: A Revolutionary System For Single-Cell Isolation And Dispensing Of Rare Cell Samples  
- Piezo acoustic-based single cell isolation and dispensing system  
- Allow unseen automated single cell precision and recovery  
- Applied to single cell isolation from CSF samples prior to ultra-volume sample prep Guilhem Tourniaire, Founder and Scientific Director, Cellenion |
<p>| 10.20 – 10.50 | Morning Coffee &amp; Refreshments, Poster Presentation Sessions, One to One Meetings x2 | |</p>
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<tr>
<th>NGS General Talks</th>
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<th>Single Cell Analysis General Talks</th>
<th>Single Cell Data Analysis &amp; Advances In Microfluidic Technologies</th>
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<td><strong>Exploring Emerging Trends In NGS Data Analysis &amp; NGS Application Strategies</strong></td>
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<td><strong>Personalised Breast And Ovary Cancer Therapy Based On Single Cell Motility</strong></td>
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<td><strong>10.50 – 11.20</strong></td>
<td><strong>Analysis Of The Liquid Biopsy By Next Generation Sequencing</strong></td>
<td><strong>Exosomal Biomarkers In Clinical Diagnostics – Micro-Vesicle Purification And microRNA Sequencing In Sepsis Patients</strong></td>
<td><strong>The effect of targeted and chemo therapy on single cell morpho-kinetic parameters as predictor for response to therapy.</strong></td>
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<td>• Circulating tumors cells (CTCs) and cell-free DNA (cfDNA) are two key elements within the so-called liquid biopsy to be used as cancer biomarkers</td>
<td>• Why using exosomes in biomarker research</td>
<td>Michael Pfaffl, Professor of Molecular Physiology, Technical University of Munich</td>
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<td>• Here we report the feasibility of NGS analysis in single CTCs and cfDNA</td>
<td>• Optimization of exosome extraction patients</td>
<td>Michael Rieger, Professor, Goethe University of Frankfurt</td>
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<td>• Results will be compared in order to evidence pre-analytical and analytical problems as well as data analysis issues</td>
<td>• Characterization of exosomes (size, surface proteins, nucleic acids, etc.)</td>
<td>Ilan Tsarfaty, Principal Investigator, Tel Aviv University</td>
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<td>• The importance of analyzing both cfDNA and CTCs as complementary aspects of the liquid biopsy will be discussed</td>
<td>• Next generation sequencing of small RNAs</td>
<td><strong>Single Cell Chemical Imaging And Activity Analyses</strong></td>
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<td>Pamela Pinzani, Associate Professor, University of Florence</td>
<td>Michael Pfaffl, Professor of Molecular Physiology, Technical University of Munich</td>
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<td><strong>Solution Provider Presentation</strong></td>
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<td><strong>11.20 – 11.50</strong></td>
<td><strong>Solution Provider Presentation</strong></td>
<td><strong>Single Cell RNA Sequencing Of Dormant Myeloma Cells Identifies Therapeutic Targets</strong></td>
<td><strong>Personalised Breast And Ovary Cancer Therapy Based On Single Cell Motility</strong></td>
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<td><strong>LABCYTE</strong></td>
<td>Multiple myeloma is a neoplasm of plasma cells which develops in the skeleton. The bone microenvironment supports myeloma growth and long-term survival of dormant myeloma cells. Despite advances in treatments, survival is poor and patient typically relapse, suggesting a need for understanding the role of dormant cell and drug resistance. We developed single cell RNA sequencing approaches to isolate single dormant myeloma cells in vivo and define the transcriptome profile of these cells in order to identify pathways that control dormancy. This knowledge can be used to identify new targets that alter the behaviour of myeloma disease in the skeleton.</td>
<td><strong>The effect of targeted and chemo therapy on single cell morpho-kinetic parameters as predictor for response to therapy.</strong></td>
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<td><strong>PerkinElmer</strong></td>
<td>Weng Hua, Khoo – PhD student at The Garvan Institute, Bone Biology Division</td>
<td><strong>For more information please contact <a href="mailto:marketing@oxfordglobal.co.uk">marketing@oxfordglobal.co.uk</a></strong></td>
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<td>11.50 – 12.20</td>
<td><strong>Solution Provider Presentation</strong>&lt;br&gt;<strong>Qiagen</strong>&lt;br&gt;<strong>cytena’s patented single-cell printing technology enables fully automated isolation of single cells into standard microwell and PCR plate formats</strong>&lt;br&gt;<strong>This presentation will describe the single-cell printer and its technology. The talk will highlight how key features including image confirmation of single cell isolation, precise cell deposition, and minimal sample volume readily interfaces with downstream single cell applications</strong>&lt;br&gt;Elly Sinkala, Application Scientist, cytena</td>
<td><strong>Advances In Automated Cell Isolation For Single-Cell Analysis</strong>&lt;br&gt;<strong>Cell isolation is critical first step in single-cell analysis. It is essential that the isolation technique preserves the cell’s integrity and ensures only a single cell is isolated for accurate, high quality data</strong>&lt;br&gt;<strong>cytena’s patented single-cell printing technology enables fully automated isolation of single cells into standard microwell and PCR plate formats</strong>&lt;br&gt;<strong>This presentation will describe the single-cell printer and its technology. The talk will highlight how key features including image confirmation of single cell isolation, precise cell deposition, and minimal sample volume readily interfaces with downstream single cell applications</strong>&lt;br&gt;Elly Sinkala, Application Scientist, cytena</td>
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<td>12.20 – 12.50</td>
<td><strong>A Systems Approach For Drug/Target Discovery And Prioritization In Alzheimer’s Disease</strong>&lt;br&gt;<strong>With the goal of using integrative genetic and functional models as a powerful approach to defining therapeutic targets for interventions, we have developed a series of functional maps for relationships between pathways</strong>&lt;br&gt;<strong>A pathway correlation network (PCxN.org) reveals co-activity between gene sets for integrative whole genome sequencing genomic variant and functional models for experiment or genome association study</strong>&lt;br&gt;<strong>We expose key functional dynamics of disease progression in close correlation with plaque density, neurofibrillary tangles in post-mortem brains, and degradation in cognitive function</strong>&lt;br&gt;<strong>We are developing a framework to predict those drugs that appear to most specifically interact to correct these perturbations that result in disease</strong>&lt;br&gt;Winston Hide, Chair of Computational Biology, Center for Genome Translation, Sheffield Institute for Translational Neuroscience, University of Sheffield</td>
<td><strong>Implementation Of NGS In Healthcare With A Particular Focus On Rare Disease</strong>&lt;br&gt;<strong>Standardization and benchmarking in the Nordic countries</strong>&lt;br&gt;<strong>Ongoing initiatives for national as well as cross country data sharing</strong>&lt;br&gt;<strong>Development and sharing of ICT Tools</strong>&lt;br&gt;Dag Erik Undlien, Professor and Group Leader, Oslo University Hospital and University of Oslo</td>
<td><strong>Advanced Microscopy Solutions For Functional Imaging From Single Molecules To Humans</strong>&lt;br&gt;<strong>Novel imaging methodologies for protein interaction monitoring</strong>&lt;br&gt;<strong>Measuring FRET at the cellular interface with fluorescence anisotropy and fluorescence lifetime imaging</strong>&lt;br&gt;<strong>High content screening applications</strong>&lt;br&gt;<strong>Towards Super-resolved functional imaging - seeing more by imaging less</strong>&lt;br&gt;Simon Ameer-Beg, Group Leader and Principal Investigator, King’s College London</td>
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12.50 – 13.30 Lunch

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<td>Next Generation Sequencing (NGS) In Rare Disorders: Scientific Impact And Clinical Utility</td>
<td>Global Preamplification: Linking Single-Cell RT-qPCR And RNA-Sequencing</td>
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<td>• NGS</td>
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<td>• What we have learnt through the application of NGS technologies</td>
<td>• Whole exome sequencing (WES)</td>
<td>Thomas Kroneis, Head of Research Unit for Single Cell Analysis and Senior Scientist, Medical University of Graz</td>
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<td>• Clinical application and the future challenges</td>
<td>• Whole genome sequencing (WGS)</td>
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<td>Jonathan Strefford, Professor of Cancer Molecular Genetics, University of Southampton</td>
<td>• Diagnostic yield</td>
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<td>• Ethical and legal issues</td>
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<td>13.30 – 14.00</td>
<td>Nine Knoers, Professor Clinical Genetics, Chair Department of Genetics, University Medical Centre Utrecht, The Netherlands</td>
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<td>14.00 – 14.30</td>
<td>Gene Testing Of Inherited Cardiac Conditions - A Diagnostic Laboratory Perspective</td>
<td>Single Cell vs Single Molecule Imaging</td>
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<td>Human Topologically Associated Domains As Natural Integration Units Of Epigenetic Signalling</td>
<td>Genetic Testing Of Inherited Cardiac Conditions - A Diagnostic Laboratory Perspective</td>
<td>Single Cell vs Single Molecule Imaging</td>
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<td>• Transcription factor-mediated signalling to the genome often takes place through very distant interactions between transcription enhancers and gene promoters</td>
<td>• An insight into how and why our lab carries out genetic testing, and how we interpret our findings</td>
<td>Single Cell vs Single Molecule Imaging</td>
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<td>• What testing means for our patients, including case studies to demonstrate the importance of a genetic diagnosis</td>
<td>Matthew Edwards, Senior Clinical Scientist, Royal Brompton Hospital</td>
<td>Marisa Martin-Fernandez, Functional Biosystems Imaging Group Leader, Science and Technology Facilities Council</td>
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<td>Colin Logie, Associate Professor, Radboud Institute for Molecular Life Sciences</td>
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<td>Assia El Maghraoui, Assistant Professor, Heriot-Watt University</td>
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<td><strong>Exploring Emerging Trends In NGS Data Analysis &amp; NGS Application Strategies</strong>&lt;br&gt;<strong>14.30 – 15.00</strong>&lt;br&gt;Using NGS To Determine The Changes In mRNAs And Long Non-Coding RNAs In Inflammatory Diseases&lt;br&gt;• Using NGS to identify novel targets in the clinical samples&lt;br&gt;• Characterizing the role of long non-coding RNAs in inflammatory disease&lt;br&gt;• Single cell sequencing as a novel approach to identifying targets in inflammatory disease&lt;br&gt;Mark Lindsay, Professor in Molecular Pharmacology, University of Bath</td>
<td><strong>NGS, Genomics And Clinical Diagnostics In Healthcare</strong>&lt;br&gt;Clinical Metagenomics Of Infectious Diseases&lt;br&gt;• Concept of the use of NGS in infectious diseases&lt;br&gt;• Concrete examples in bone and joint infections, pneumonia and endocarditis&lt;br&gt;• Promises and current limitations&lt;br&gt;Etienne Ruppe, MCU-PH/Associate Professor, Paris Diderot University</td>
<td><strong>Translation To Diagnostic And Therapeutic Applications</strong>&lt;br&gt;Use Of Single Cell Analysis In Forensic Science For Phenotypic Characteristics&lt;br&gt;• Recovering single cells in forensics using novel approaches&lt;br&gt;• Laser Capture Microscopy for recovering cells from a single individual&lt;br&gt;• Whole Genome Amplification fromaged single cells, follow ed by SNP analysis&lt;br&gt;Jari Louhelainen, Associate Professor of Biochemistry, University of Helsinki / Liverpool John Moores University</td>
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<td><strong>15.00 – 15.30</strong>&lt;br&gt;Afternoon Coffee &amp; Refreshments, Poster Presentation Sessions</td>
<td><strong>15.30 – 16.00</strong>&lt;br&gt;Recent Advances In Antibody Repertoire Sequencing&lt;br&gt;• Sequencing strategies for high throughput antibody repertoire analysis&lt;br&gt;• The impact of antibody repertoire analysis on basic and translational immunology&lt;br&gt;Louisa James, Lecturer in Immunology, Queen Mary University of London</td>
<td><strong>Microbiome Dynamics - From Cytometric Fingerprints To Ecological Concepts</strong>&lt;br&gt;Microbial community structure and function can be analyzed and evaluated nearly online and w ith high sample density on the single cell level&lt;br&gt;Ecological theories can be tested such as concepts for community assembly, function, and evolution&lt;br&gt;Susann Müller, Professor and Group Leader Flow Cytometry, Helmholtz Centre</td>
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<td>16.00 – 16.30</td>
<td><strong>Bacterial Genomics in Public Health Microbiology</strong>&lt;br&gt;• Strain typing using whole genome sequencing (WGS)&lt;br&gt;• The added value of WGS to disease surveillance and outbreak investigations&lt;br&gt;• Future perspectives</td>
<td>David Litt, Clinical Scientist, Public Health England</td>
<td>Sheffield Diagnostic Genetics Service, University of Cambridge</td>
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<td>16.30 – 17.00</td>
<td><strong>Applications Of Next Generation Sequencing For Newborn Screening</strong>&lt;br&gt;• We are investigating the technical feasibility of Next Generation Sequencing (NGS) for Newborn Screening (NBS) in an NHS Diagnostic Genetics laboratory setting&lt;br&gt;• A custom Ion AmpliSeq panel covering five genes relevant to UK NBS disorders has been designed and validated&lt;br&gt;• Our automated laboratory pipeline for dried blood spot DNA extraction, library preparation and bioinformatic analysis is capable of screening 1000-2000 samples a week</td>
<td>Julia van Campen, Development Specialist</td>
<td>Sheffield Diagnostic Genetics Service, University of Cambridge</td>
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<td>17.00 – 17.30</td>
<td><strong>Translating Microbial Genomics In Clinical Microbiology</strong>&lt;br&gt;• Rapid microbial whole genome sequencing (WGS) is an emerging technology&lt;br&gt;• WGS can be used to investigate outbreaks of infection and for surveillance of antimicrobial resistance&lt;br&gt;• Significant challenges remain to clinical implementation</td>
<td>Estee Torok, Senior Research Associate</td>
<td>University of Cambridge and Honorary Consultant in Infectious Diseases &amp; Microbiology, Addenbrooke’s Hospital</td>
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<td>17.30 – 18.00</td>
<td><strong>The Rationale And Challenges Of Micro-Scale Profiling Of Gut Microbiota</strong>&lt;br&gt;• Impact of Genomics on understanding the human microbial community&lt;br&gt;• The case for characterizing diversity and cell-cell interaction of the gut flora&lt;br&gt;• Application of single cell analysis in reconstructing the dynamic of gut flora</td>
<td>Saheer Gharbia, Professor and Head of Genomic Research</td>
<td>Public Health England</td>
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<td>18.00 – 18.30</td>
<td><strong>High Throughput Metagenomic Sequencing Complements Routine Diagnostics In Identifying Viral Pathogens In Immunocompromised Patients</strong>&lt;br&gt;• A protocol for unbiased metagenomic virus sequencing in clinical samples&lt;br&gt;• Cases of rare virus infections in immunocompromised patients detected by NGS&lt;br&gt;• Virus infection and transmission in cohorts of lung and kidney transplant patients</td>
<td>Michael Huber, Junior Group Leader and Deputy Head of Diagnostics and Development</td>
<td>University of Zurich</td>
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<td>18.30</td>
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Included in this rate is: Access to over 80 presentations, including keynote and strand keynote, lunch & refreshments, access to the exhibition hall, networking drinks, congress workbook and access to the online speaker presentations

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