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:
  o Oncology
  o Inflammatory diseases
  o 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:
  o Genomics & epigenomics
  o Transcriptomics
  o Proteomics
  o 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:
  o Single cell data analysis
  o Single cell data handling
  o Identifying mutated genes in tumor samples
  o 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 topical 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

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, Pubic 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
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 Paterlini-Bächtot, 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 Festeinstein, 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 Ameer-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 Tzafaty, 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, Heriot-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 Saïba, 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, Cellebion
- Anja Smith, Director, Research and Development, Dharmacon
- Chris Wetzel, Director Sales and Marketing, MMI
- Kevin Holden, Head of Synthetic Biology, Synthego
- Guillaume Pavlovic, 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:

Bronze Sponsors:

Congress Sponsors:

Congress Sponsors Continued:
### 9th Annual Next Generation Sequencing and Clinical Diagnostics Congress & 5th Annual Single Cell Analysis Congress

**Day One – 9 November 2017**

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>07.30 – 08.20</td>
<td>Registration - Champagne Foyer</td>
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<tr>
<td>08.20 – 08.25</td>
<td>Oxford Global’s Welcome Address</td>
</tr>
<tr>
<td>08.25 – 08.30</td>
<td>Chairperson’s Opening Address - Jan Komorowski, Professor and Chair of Bioinformatics, Uppsala University</td>
</tr>
</tbody>
</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.  

Ken Chang, Director of Clinical Biomarkers, Daiichi Sankyo |

<table>
<thead>
<tr>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 2: Chalon</th>
<th>Conference Room 3: Epernay &amp; Reims</th>
</tr>
</thead>
<tbody>
<tr>
<td>Exploring Emerging Trends In NGS Data Analysis &amp; NGS Application Strategies</td>
<td>Data Analysis, Biomarker Development, Precision Medicine and Clinical Diagnostics</td>
<td>Single Cell ‘Omic Analysis: Current And Emerging Tools</td>
</tr>
<tr>
<td>Stream Chair: Jan Komorowski, Professor and Chair of Bioinformatics, Uppsala University</td>
<td>Stream Chair:</td>
<td>Stream Chair: Akos Vertes, Professor of Chemistry, George Washington University</td>
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<tr>
<th>Time</th>
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| 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 system 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  

Satu Nahkuri, Principal Data Scientist, F. Hoffmann-La Roche |

| Stream Keynote Address: Discovery Of Potential Biomarkers Using Combined Proteomics And Transcriptomics | Single Cell RNA-Seq In Target Identification  
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 with drug mechanism of action.  

Harpreet Saini, Associate Director, Bioinformatics, Astex Pharmaceuticals |

| Stream Keynote Address: | Single Cell RNA-Seq In Target Identification  
- At Boehringer Ingelheim over the last few years bulk RNA-Seq for expression profiling of tissues and cell populations have been complemented by various single cell RNA-Seq approaches, carried out in-house and at the sites of collaboration partners.  
- For target identification, we analyzed material from the same samples using both approaches, allowing for different views on the same biological material.  

Holger Klein, Head of Computational Biology Expert Function, Boehringer Ingelheim |

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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</table>
| 09.30 – 10.00 | **The Current And Future Trends In Sequencing**  
- Clinical adoption of NGS techniques: panels, exomes and WGS  
- Leveraging single-cell genomics to answer the previously unknown  
- The state of sequencing in precision medicine  

Joe Whittaker, Sr Technical Marketing Specialist, Illumina |
<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
<th>Speaker/Institution</th>
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<tbody>
<tr>
<td>10.00 – 11.20</td>
<td>Morning Coffee &amp; Refreshments, Poster Presentation Sessions, One to One Meetings x3</td>
<td>Exhibition Room – Mancy and Avize</td>
</tr>
<tr>
<td>11.20 – 11.50</td>
<td>Advanced Network Analytical Approaches For The Interpretation Of NGS Data</td>
<td>Tom Freeman, Professor, Roslin Institute</td>
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<tr>
<td>11.20 – 11.50</td>
<td>Quantifying Low-Frequency Revertants In Oral Poliovirus Vaccine Using Next Generation Sequencing</td>
<td>Eric Sarcey, Senior Scientist in Analytical Microbiology, Sanofi</td>
</tr>
<tr>
<td>11.20 – 11.50</td>
<td>Leveraging Single-Cell Genomics For Target Discovery</td>
<td>Ana Leite, Computational Biologist, GlaxoSmithKline</td>
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<tr>
<td>11.50 – 12.20</td>
<td>Rule Networks – Discovering Molecular Interactions From High-Throughput Data</td>
<td>Jan Komorowski, Professor and Chair of Bioinformatics, Uppsala University</td>
</tr>
<tr>
<td>11.50 – 12.20</td>
<td>Challenges Of NGS In Clinical Trials</td>
<td>Marc Sultan, Group Head, Human Genetics and Genomics, Novartis Institutes for BioMedical Research</td>
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<tr>
<td>11.50 – 12.20</td>
<td>Small Molecules In Dividing Cells And Single Neurons Of Known Function</td>
<td>Akos Vertes, Professor of Chemistry, George Washington University</td>
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<tr>
<td>12.20 – 12.50</td>
<td>Solution Provider Presentation</td>
<td>Bogdan Milojkovic, Head of Medical Affairs, Roche Diagnostics</td>
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<tr>
<td>12.50 – 13.50</td>
<td>Lunch, Poster Presentation Sessions</td>
<td>Stream Chair: Akos Vertes, Professor of Chemistry, George Washington University</td>
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<tr>
<td>13.50 – 14.20</td>
<td>Solution Provider Presentation</td>
<td>Stream Chair:</td>
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14.20 – 14.50

**Data-Driven Genomic Computing: Making Sense Of The Signals From The Genome**
- 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
- Presentation of GDM (Genomic Data Model) and GMQL (GenoMetric Query Language) with description of available prototypes and implementations
- Scenarios of use of GMQL in order to respond to biological questions

*Stefano Ceri, Professor, Politecnico di Milano*

**Application Of Academic Knowledge To Clinical Diagnostics & Enhancing Collaborations Between Pharma & Academics**

*Marina Granovskaya, Adjunct Associate Professor, University College Dublin*

**The Human Cell Atlas**
- 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
- 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
- I will introduce this nascent initiative and discuss how it will be achieved by groups working together throughout the world

*Mike Stubbington, Principal Staff Scientist, Wellcome Trust Sanger Institute*

14.50 – 15.20

**High-throughput targeted sequencing of cancer susceptibility genes**
Sequencing of cancer susceptibility genes using targeted gene panels has become commonplace in cancer genetics clinics. However, their validity depends critically on the availability of reliable data, from large well-designed epidemiological studies, on which genes and variants are disease associated, and the magnitude of those risks. As part of the EU funded BRIDGES project, we are performing targeted sequencing of 35 known or suspected breast cancer susceptibility genes in >100,000 individuals from studies in the Breast Cancer Association Consortium. Barcoded libraries of 768 samples are prepared using the Fluidigm Juno™ system and sequenced on an Illumina HiSeq400™. Initial results on variant calling, coverage and sensitivity will be presented.

*Douglas Easton, Professor of Genetic Epidemiology, University of Cambridge*

**Single-Cell RNA-Seq Analysis With Partek Flow Software**
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**

**15.40 – 16.30**

Afternoon Coffee & Refreshments, Poster Presentation Sessions, One to One Meetings x2

**SLAMseq Kit – A New Method For Metabolic RNA Sequencing**
- 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

*Lukas Paul, Senior Manager of Scientific Affairs, Lexogen*

**Isolating Adherent Single Cells – The Taming Of The Shrew**
- Applications: Why analyse a single cell
- Tools: How to precisely isolate a single cell
- Case study: Isolating adherent single cells selectively

*Chris Wetzel, Microscopic Single Cell Isolation, MMI*
### Academic Talks

**17.00 – 17.30**

<table>
<thead>
<tr>
<th>Title</th>
<th>Speaker</th>
<th>Location</th>
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<tbody>
<tr>
<td>Utilizing RNA-Seq To Assess RNA Editing Levels, As A Diagnostic Tool In Cancer</td>
<td>Eli Eisenberg, Professor, Tel Aviv University</td>
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<tr>
<td>- Level of A-to-I RNA editing by ADAR enzymes is altered in various cancer types</td>
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<td>- Extensive editing in cancer introduces RNA diversity or RNA mutations in mRNAs and micro-RNAs</td>
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<td>- RNA modification events in tumours are as abundant as genomic DNA mutations</td>
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<td>- Altered editing activity is associated with poor prognosis</td>
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<td>Integrating ‘Omics Application In Complex Disease: Applications To Paediatric Inflammatory Bowel Disease (IBD)</td>
<td>Sarah Ennis, Professor of Genomics, University of Southampton</td>
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<tr>
<td>- Multiple contemporary sequencing approaches support better understanding of pathoetiology in complex disease. 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 microbe analyses alongside clinical, metabolomic and immuno-profiling to inform on individual risk factors and their interpretation.</td>
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<tr>
<td>Application Of Single-Cell RNA Sequencing In Diseased Tissues</td>
<td>Holger Heyn, Head, Single Cell Genomics Group, National Centre for Genomic Analysis</td>
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<tr>
<td>- Single-cell RNA sequencing elucidates composition and dynamics of complex tissues</td>
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<td>- Cell type deconvolution of diseased tissues pinpoints driving mechanisms</td>
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<td>- Understanding genome activity through single-cell resolution screenings</td>
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**17.30 – 18.00**

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<tr>
<th>Title</th>
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<tbody>
<tr>
<td>Computational Tools For Studies Of RNA Regulation In Neurologic Diseases With ICLIP And RNA-Seq</td>
<td>Jernej Ule, Group Leader and Professor of Molecular Neuroscience, The Francis Crick Institute</td>
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<tr>
<td>- An interactive online platform for processing, management and secure storage of ICLIP and RNA-seq data</td>
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<td>- Use of the platform for collaborative analysis, visualization and distribution of processed transcriptomic data</td>
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<td>- RNA maps: integrating multiple types of NGS data to unravel the position-dependent RNA regulatory principles</td>
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<tr>
<td>Aggressive Lymphomas: Taking Genome Scale Data And Bioinformatics To The Clinic</td>
<td>David Westhead, Head of the School of Molecular and Cellular Biology, Professor of Bioinformatics, University of Leeds</td>
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<td>- The practical and biological challenges of applying large-scale data in clinical trials and real populations</td>
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<td>- Building prognostic and individual models and dealing with disease heterogeneity</td>
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<td>- Precision medicine for lymphoma</td>
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<td>Clinical Impact Of Molecular Analysis Of Circulating Rare Cells</td>
<td>Patrizia Paterlini-Bréchot, Professor of Cell Biology, Paris Descartes University</td>
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<td>- Circulating rare cells represent a new field of medicine with potential clinical impact</td>
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<td>- Their immunomolecular characterization is meant to improve personalized medicine</td>
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<td>- Technical challenges have limited this field in the past but recent developments open new pathways for their analysis</td>
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**18.00 – 18.30**

<table>
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<tr>
<th>Title</th>
<th>Speaker</th>
<th>Location</th>
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<tbody>
<tr>
<td>Cheap Sequencing Is Disrupting Research On Emerging Model Organisms</td>
<td>Yannick Wurm, Senior Lecturer in Bioinformatics, Queen Mary University of London</td>
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<tr>
<td>- 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</td>
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<td>- 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>
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<tr>
<td>Single-Cell Multi-Omics To Understand The Biology Of Cellular Heterogeneity In Health And Disease</td>
<td>Thierry Voet, Associate Professor and Group Leader, University of Leuven and Wellcome Trust Sanger Institute</td>
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<tr>
<td>- Single-cell multi-omics technologies</td>
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<td>- Single-cell genome analysis</td>
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<td>- Somatic genetic variation</td>
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<tr>
<td>Liquid Biopsies: The Potential Of Single Cell Analysis On CTCs</td>
<td>Evi Lianidou, Professor of Analytical Chemistry and Clinical Chemistry, University of Athens</td>
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<tr>
<td>- “Liquid biopsy”, is based on minimally invasive blood-based tests that can be serially repeated</td>
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<tr>
<td>- “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 miRNAs or exomes</td>
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<tr>
<td>- 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>
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**18.30 – 19.00**

<table>
<thead>
<tr>
<th>Title</th>
<th>Speaker</th>
<th>Location</th>
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<tbody>
<tr>
<td>Single Cell Transcriptomics Reveals Specific RNA Editing Signatures In The Human Brain</td>
<td>Holger Heyn, Head, Single Cell Genomics Group, National Centre for Genomic Analysis</td>
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</tr>
<tr>
<td>- 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</td>
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<tr>
<td>- 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)</td>
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<tr>
<td>- To characterize the complexity of A-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</td>
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</tbody>
</table>
**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**

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**9th Annual Next Generation Sequencing and Clinical Diagnostics Congress & 5th Annual Single Cell Analysis Congress**  
**Day Two – 10 November 2017**

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<thead>
<tr>
<th>Conference Room 1: Morangis</th>
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<th>Conference Room 3: Epernay</th>
<th>Conference Room 4: Reims</th>
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<tbody>
<tr>
<td><strong>NGS General Talks</strong></td>
<td><strong>Healthcare Talks</strong></td>
<td><strong>Translation To Diagnostic And Therapeutic Applications</strong></td>
<td><strong>Single Cell Data Analysis &amp; Advances In Microfluidic Technologies</strong></td>
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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>Stream Chair: Miika Ahdesmäki, Associate Director Bioinformatics, AstraZeneca</strong></td>
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**08.00 – 08.30**  
**Keynote Address:**  
**Improved Single Cell Full-Length Transcriptome Sequencing Protocol Enables Long-Term Storage And RNAse Protection**  
- Modifications of Smartseq-2 protocol enable long-term single cell RNA storage  
- Increased resistance of archived samples to RNAse degradation from endogenous and exogenous RNAs  
- Preparation of single nucleus RNA

**Stephan Lorenz, Head, Single Cell Genomics Core Facility, Wellcome Trust Sanger Institute**

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**08.30 – 09.00**  
**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**  
- In this talk I highlight how novel bioinformatics algorithms combined with unique molecular identifiers allow us to reduce noise and monitor cancer drivers in poor quality FFPE DNA as well as liquid biopsies  
- I will also describe how we visualise the results in a user-friendly browser to better enable non-bioinformaticians to explore NGS results

**Miika Ahdesmäki, Associate Director Bioinformatics, AstraZeneca**

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**08.30 – 09.00**  
**Stream Keynote Address:**  
**Cell Dispersal – A Source Of Bias In The Clinical Utilization Of Next Generation Sequencing**  
- Cell movement strongly influences tumour composition and intratumor heterogeneity. A malignant mutation can go undetected in case it also rises cellular motility  
- Mixing leads to a technical bias in current next generation sequencing because of high detection cutoffs  
- Coding mutations in genes affecting cell dispersal lead to improved survival in melanoma

**Balázs Györrfy, Scientific Advisor, Semmelweis University and Hungarian Academy of Sciences**

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**08.30 – 09.00**  
**Stream Keynote Address:**  
**Sex, Disease, Stochastic Gene Silencing And The Epigenetic Code**  
- Heterochromatin-induced gene silencing (position effect variegation) was instrumental in the elucidation of the epigenetic code  
- Repetitive DNA induces stochastic gene silencing in mammals – Locus Control Regions can overcome this effect  
- Such stochastic silencing allowed the identification of a previously hidden epigenetic layer in the regulation of sex dimorphism which operates very early in development with implications for understanding sex bias in physiology and disease

**Richard Festenstein, Clinical Professor of Molecular Medicine, Imperial College London**

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**08.30 – 09.00**  
**Stream Keynote Address:**  
**The Role Of Mathematical Modelling In Informing Single Cell Studies**  
- Provide an introduction to and motivation for the use of mathematical modelling in informing single cell studies  
- Demonstrate through case studies how biological knowledge/data can be integrated into mathematical models at the single cell to increase understanding of the system, test hypotheses and guide future experimentation

**Marcus Tindall, Associate Professor of Mathematical Biology, University of Reading**

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**Graziano Pesole, Professor of Molecular Biology, Head of the Italian Node of ELIXIR, University of Bari Aldi Moro**

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**Thermal 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**
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<th>Time</th>
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<th>Speaker/Institution</th>
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<td>09.00 – 09.30</td>
<td>Solution Provider Presentation</td>
<td>Andreas Klingenhoff, Field Application Specialist</td>
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<td>Conference Room 1: Morangis&lt;br&gt;University of Florence&lt;br&gt;Pamela Pinzani, Associate Professor, University of Florence</td>
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<td>NGS General Talks</td>
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<tr>
<td>09.30 – 10.00</td>
<td>Improving Exome Sequencing, Targeted Sequencing, And Low Frequency Variant Detection With Better Coverage Uniformity, Higher On-Target Rates, And Unique Molecular Identifiers</td>
<td>Xiangyu Rao, NGS Field Application Manager, Europe, Integrated DNA Technologies</td>
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<td>Single Cell Analysis General Talks</td>
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<tr>
<td>10.00 – 10.40</td>
<td>Morning Coffee &amp; Refreshments, Poster Presentation Sessions, One to One Meetings x2</td>
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<td>Healthcare Talks</td>
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<tr>
<td>10.40 – 11.10</td>
<td>Analysis Of The Liquid Biopsy By Next Generation Sequencing</td>
<td>Michael Pfaff, Professor of Molecular Physiology, Technical University of Munich</td>
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<td></td>
<td>Single Cell Analysis General Talks</td>
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<td>Exosomal Biomarkers In Clinical Diagnostics – Micro-Vesicle Purification And microRNA Sequencing In Sepsis Patients&lt;br&gt;Live-cell microscopy-based single cell tracking to reveal normal and malignant stem cell behavior&lt;br&gt;Personalised Breast And Ovary Cancer Therapy Based On Single Cell Motility</td>
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### 11.10 – 11.40
**Solution Provider Presentation**
**Library prep for carrier screening test by NGS using the Echo Liquid Handler**
- Library prep for Illumina NGS using the Echo Liquid Handler
- Carrier Genetic Test for single gene disorders by NGS

**David Blesa, Head of Product Development, IGENOMIX**

**Single Cell RNA Sequencing Of Dormant Myeloma Cells Identifies Therapeutic Targets**
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.

**Weng Hua, Khoo – PhD student at The Garvan Institute, Bone Biology Division**

### 11.40 – 12.00
**Solution Provider Presentation**
**Advances In Automated Cell Isolation For Single-Cell Analysis**
- 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
- cytena’s patented single-cell printing technology enables fully automated isolation of single cells into standard microwell and PCR plate formats
- 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

**Elly Sinkala, Application Scientist, cytena**
<table>
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<tr>
<th>Time</th>
<th>Talks Session</th>
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| 12.10 – 12.40 | A Systems Approach For Drug/Target Discovery And Prioritization In Alzheimer’s Disease  
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  
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  
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  
We are developing a framework to predict those drugs that appear to most specifically interact to correct these perturbations that result in disease  
Winston Hide, Chair of Computational Biology, Center for Genome Translation, Sheffield Institute for Translational Neuroscience, University of Sheffield |
|          | Implementation Of NGS In Healthcare With A Particular Focus On Rare Disease  
- Standardization and benchmarking in the Nordic countries  
- Ongoing initiatives for national as well as cross country data sharing  
- Development and sharing of ICT Tools  
Dag Erik Undlien, Professor and Group Leader, Oslo University Hospital and University of Oslo |
|          | Advanced Microscopy Solutions For Functional Imaging From Single Molecules To Humans  
- Novel imaging methodologies for protein interaction monitoring  
- Measuring FRET at the cellular interface with fluorescence anisotropy and fluorescence lifetime imaging  
- High content screening applications  
- Towards Super-resolved functional imaging - seeing more by imaging less  
Simon Ameer-Beg, Group Leader and Principal Investigator, King’s College London |
|          | Mesenchymal Stem Cells Niche, The Analysis At The Single Cell Level  
- High resolution of stem cell lineage  
- Heterogeneity in CFU-F cells  
- Markers for mesenchymal cells  
- Adipocyte differentiation at the single cell level  
Dafna Benayahu, Professor and Chair, Department of Cell and Developmental Biology, Tel Aviv University |
| 12.40 – 13.30 | Lunch Exhibition Room – Mancy and Avize |
| 13.30 – 14.00 | Next Generation Sequencing (NGS) In Rare Disorders: Scientific Impact And Clinical Utility  
- NGS  
- Whole exome sequencing (WES)  
- Whole genome sequencing (WGS)  
- Diagnostic yield  
- Clinical utility  
- HTA  
- Ethical and legal issues  
Jonathan Strefford, Professor of Cancer Molecular Genetics, University of Southampton |
|          | Global Preamplification: Linking Single-Cell RT-qPCR And RNA-Sequencing  
Current gold standard for preamplification of minute amounts of template (e.g. RNA from single-cells) for quantitative PCR is target-specific preamplification. This comes with some restrictions: Analysis is limited to the targets preamplified, testing and optimizing the primer pool for target-specific preamplification is tricky and time consuming, and every new set of primer pool needs to be tested. Global preamplification, which is based on full-length mRNA reverse transcription followed by adapter-based preamplification allows preamplification of the total mRNA thereby offering an alternative that is not restricted to preselected target genes. In addition, the globally preamplified cDNA can be used for generating RNA-seq libraries. Thus, global preamplification links target-specific analysis (qPCR) with screening approaches (RNA-seq) on the single (rare)-cell level.  
Thomas Kroneis, Head of Research Unit for Single Cell Analysis and Senior Scientist, Medical University of Graz |
|          | Single Cell Sequencing QC And MIASe  
Single-cell RNA sequencing methods delivers high quality RNA-Seq data in most cases. Our experiences over the past year have shown us that quality control is as important as ever: quality of cells, quality of processing, and quality of sequencing. Unfortunately, much of the information required to improve experiments can only be revealed by the final sequencing of single-cell libraries. I will describe our efforts in building a QC portal for 10X Genomics Cell Ranger reports that allows users to share experiences by uploading reports and experimental metadata, and discuss our continued efforts to open this up to other single-cell technologies. We have also made some progress in understanding the impact of Illumina index-swapping on single-cell experiments, and I will also present our initial findings.  
James Hadfield, Head of Genomics, Cancer Research UK Cambridge Institute |
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<td>14.00 – 14.30</td>
<td>Human Topologically Associated Domains As Natural Integration Units Of Epigenetic Signalling</td>
<td>Colin Logie, Associate Professor, Radboud Institute for Molecular Life Sciences</td>
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<td>Genetic Testing Of Inherited Cardiac Conditions – A Diagnostic Laboratory Perspective</td>
<td>Matthew Edwards, Senior Clinical Scientist, Royal Brompton Hospital</td>
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<td>Investigating EGFR oligomerisation at high resolution on the cellular context</td>
<td>Mark Lindsay, Professor in Molecular Sciences</td>
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<td>Microfluidics For Single Cell Analysis</td>
<td>Colin Edwards, Functional Biosystems Imaging Group Leader, Science and Technology Facilities Council</td>
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<td>14.30 – 15.00</td>
<td>Using NGS To Determine The Changes In mRNAs And Long Non-Coding RNAs In Infectious Diseases</td>
<td>Clinical Metagenomics Of Infectious Diseases</td>
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<td>Use Of Single Cell Analysis In Forensic Science For Phenotypic Characteristics</td>
<td>Jari Louhela, Associate Professor of Biochemistry, University of Helsinki / Liverpool John Moores University</td>
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<td>Single Cell Protein Analysis For Clinical Problems</td>
<td>Single Cell Protein Analysis For Clinical Problems</td>
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<td>Microfluidics For Single Cell Analysis</td>
<td>Graeme Whyte, Associate Professor, Heriot-Watt University</td>
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<td>15.00 – 15.30</td>
<td>Afternoon Coffee &amp; Refreshments, Poster Presentation Sessions</td>
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<td>15.30 – 16.00</td>
<td>Recent Advances In Antibody Repertoire Sequencing</td>
<td>Microbiome Dynamics - From Cytometric Fingerprints To Ecological Concepts</td>
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<td>Dissecting Host-Pathogen Interactions One Cell At The Time Using Single-Cell RNA-Seq</td>
<td>Liming Yung, Senior Lecturer, Imperial College London</td>
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<td>Single Molecule Single Cell Imaging Of Protein Oligomers</td>
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<td><strong>16.00 – 16.30</strong></td>
<td><strong>Bacterial Genomics in Public Health Microbiology</strong></td>
<td><strong>Strategy Of Sequencing The Whole Genome And Its Impact Of Next Generation Medicine</strong></td>
<td><strong>Uncovering Genomic Trajectories With Heterogeneous Genetic And Environmental Backgrounds Across Single-Cells And Populations</strong></td>
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<td>• Strain typing using whole genome sequencing (WGS)</td>
<td>• The potential of Whole Genome Sequencing (WGS) for cancer diagnosis</td>
<td>• Modelling molecular progression underlying cellular and disease processes</td>
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<td>• The added value of WGS to disease surveillance and outbreak investigations</td>
<td>• Challenges and solutions for research applications of WGS</td>
<td>• Stratification by cellular or patient phenotypes</td>
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<td>• Future perspectives</td>
<td>• Challenges in Bioinformatics and IT in the area of huge data deluge</td>
<td>• Applications to single cell genomics and beyond</td>
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<td></td>
<td>David Litt, Clinical Scientist, Public Health England</td>
<td>Jürgen Eils, Head of Data Management and Genomics IT, German Cancer Research Centre</td>
<td>Christopher Yau, Associate Professor and Reader in Computational Biology, University of Birmingham and University of Oxford</td>
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### Healthcare Talks

**NGS, Genomics And Clinical Diagnostics In Healthcare**

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<tr>
<th><strong>16.30 – 17.00</strong></th>
<th><strong>Applications Of Next Generation Sequencing For Newborn Screening</strong></th>
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<tbody>
<tr>
<td></td>
<td>• We are investigating the technical feasibility of Next Generation Sequencing (NGS) for Newborn Screening (NBS) in an NHS Diagnostic Genetics laboratory setting</td>
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<td>• A custom Ion AmpliSeq panel covering five genes relevant to UK NBS disorders has been designed and validated</td>
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<td>• 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>
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<td>Julia van Campen, Development Specialist, Sheffield Diagnostic Genetics Service</td>
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<tr>
<th><strong>17.00 – 17.30</strong></th>
<th><strong>Translating Microbial Genomics In Clinical Microbiology</strong></th>
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<tr>
<td></td>
<td>• Rapid microbial whole genome sequencing (WGS) is an emerging technology</td>
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<td>• WGS can be used to investigate outbreaks of infection and for surveillance of antimicrobial resistance</td>
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<td>• Significant challenges remain to clinical implementation</td>
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<td></td>
<td>Estee Torok, Senior Research Associate, University of Cambridge and Honorary Consultant in Infectious Diseases &amp; Microbiology, Addenbrooke’s Hospital</td>
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<thead>
<tr>
<th><strong>17.30 – 18.00</strong></th>
<th><strong>The Rationale And Challenges Of Micro-Scale Profiling Of Gut Microbiota</strong></th>
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<tbody>
<tr>
<td></td>
<td>• Impact of Genomics on understanding the human microbial community</td>
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<td>• The case for characterizing diversity and cell-cell interaction of the gut flora</td>
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<td>• Application of single cell analysis in reconstructing the dynamic of gut flora</td>
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<td>Saheer Gharbia, Professor and Head of Genomic Research, Public Health England</td>
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<tr>
<th><strong>18.00 – 18.30</strong></th>
<th><strong>High Throughput Metagenomic Sequencing Complements Routine Diagnostics In Identifying Viral Pathogens In Immunocompromised Patients</strong></th>
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<tr>
<td></td>
<td>• A protocol for unbiased metagenomic virus sequencing in clinical samples</td>
</tr>
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<td>• Cases of rare virus infections in immunocompromised patients detected by NGS</td>
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<td>• Virus infection and transmission in cohorts of lung and kidney transplant patients</td>
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<tr>
<td></td>
<td>Michael Huber, Junior Group Leader and Deputy Head of Diagnostics and Development, University of Zurich</td>
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**18.30** | **End of Conference** |
## Delegate Details

Please complete fully and clearly. Please photocopy for additional delegates.

- **Title:**
- **Surname:**
- **Job Title:**
- **Company/Organisation:**
- **Email:**
- **Address:**
- **Postcode:**
- **Country:**
- **Direct Telephone:**
- **Direct Fax:**
- **Mobile:**
- **Switchboard:**
- **Signature:**
- **Date:**

## Registration Fees

### Standard Rate Registration (Please tick as appropriate)

<table>
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<tr>
<th>Category</th>
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<tbody>
<tr>
<td>Industry Delegate</td>
<td>250 plus VAT</td>
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<tr>
<td>Academic Delegate</td>
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<tr>
<td>Vendor Delegate</td>
<td>1350 plus VAT</td>
</tr>
<tr>
<td>Academic &amp; Industry Poster Presentation</td>
<td>125 plus VAT</td>
</tr>
<tr>
<td>Vendor Poster Presentation</td>
<td>250 plus VAT</td>
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Poster presentations can be chosen at the standard price with a £50 surcharge.

This price is for a poster only and does not cover attendance, please also choose a registration option.

### Complimentary Visitor Registration (Please tick as appropriate)

Included in this rate is: Access to over 80 presentations, including keynote and stream keynote, lunch & refreshments, access to the exhibition hall, networking drinks, congress workbook and access to the online speaker presentations.

- Industry Delegate (Biopharma, Pharma or Biotech Companies Only)
- Academic Delegate
- Vendor Delegate (CROs, Consultants, Technology & Service Providers)
- Academic & Industry Poster Presentation
- Vendor Poster Presentation
- Poster presentations can be chosen at the standard price with a complimentary booking

### How to Pay (choose one of the following payment options)

- **CREDIT CARD:**
  - Visa
  - MasterCard
  - Maestro
  - Amex

Credit Card Number:

- **Expiry Date:**
- **Security code:**

### Number of delegates:

- **Industry del(s):**
- **Academic dels(s):**
- **Vendor dels(s):**

### Invoice Address (if different from above):

- **Country:**
- **Address:**
- **Email:**
- **Company/Organisation:**
- **Job Title:**
- **Title:**
- **Forename:**
- **Surname:**

*Please note there is a £50 plus VAT handling charge for payment via invoice. All card payments will be subject to a 3% bank charge or 4% AMEX charge.

## Terms & Conditions of Booking

**Agreed Terms between the Organiser (Oxford Global) and the Delegate:**

### Standard Booking Fee

For attendees who are opting for standard registration, the standard Booking Fee is £250 plus VAT (Industry & Academic) and £1350 plus VAT for Vendor Companies and consultants. An admin surcharge of £50 plus VAT will be applied to payments settled following the receipt of an invoice. This charge will not be applied to payments settled online.

Vendor Delegates and Consultants will not be eligible for one to one meetings unless they purchase a sponsorship meetings package. These can only be purchased directly from Oxford Global and not via the online booking facility.

### Cancellation Fee

There is no cancellation charge upon withdrawal of your booking if you attend as a complimentary visitor or standard rate delegate.

### Poster Presentations

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### Refunds

If you’re unable to make the event we can offer a credit note which will allow you to attend next year’s event. Please note as part of our T&Cs we cannot offer this if the event is closer than two weeks out.

### Data Protection

The data controller is the Organiser. The Organiser may disclose such personal information to Registered Event Sellers (Solution Providers) and other Delegates but solely for the purposes of the Event. The Delegate consents to the use of his/her personal and company information on the terms set out herein.

### Miscellaneous

This Agreement may not be transferred or assigned by either the Delegate or the Delegate’s Company. The Organiser will determine the scope and content of Conference conference events, seminars, workshops and activities throughout the Event. The Organiser reserves the right to cancel or postpone the Event without liability to the Delegate’s Company or individual Delegate. If for any reason the Organiser has to cancel or postpone this Event, the Organiser reserves the right to transfer this Booking to another Congress within the same sector to be held within twelve months. Should another Congress in the same sector not be available within this period, the Booking Fee will be refunded.

- I agree to the above Terms and Conditions

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