8th Annual Next Generation Sequencing Congress
4th Annual Single Cell Analysis Congress

10-11 November 2016, London, UK

Day 1 Stream 1 – Advances in NGS Platforms and Key Therapeutic Applications

- DNA, RNA & proteins sequencing technologies
- Effective sample preparation
- Assessment of NGS technologies and platforms
- Latest innovations: gene editing technologies in NGS
- Applications of NGS in medicine and therapeutic case studies:
  - Cancer
  - Immunotherapy
  - Biomarkers
  - Genomic medicine
  - Infectious diseases
  - HIV

Day 1 Stream 2 – NGS Data Management and Bioinformatics

- Developments in NGS data analysis techniques and technologies
- Comparison in practical use of NGS platforms and software
- Integration of ‘omic’ data sets
- Genetic and genomic data analysis
- Advanced bioinformatics & computational genomic analysis tools
- Big Data, & cloud computing & data storage strategies in NGS

Day 2 Stream 1– NGS Clinical Applications & Diagnostics

- NGS in the clinic: case studies including cancer and tumour testing
- Using NGS for precision & personalised medicine
- Supporting clinical decision-making through genomic sequencing
- Novel technology and platforms for NGS data analysis
- Integration of technologies and data sets

4th Annual Single Cell Analysis Congress

Day 1 Stream 3 – Single Cell Analysis, Transcriptomics & ‘Omics

- Single cell ‘omics case studies and therapeutic applications:
  - Genomics
  - Transcriptomics
  - Proteomics
  - Metabolomics
- Using single cell analysis in clinical & diagnostic development
- Methods and applications of single cell study for CTCs and rare cell diseases
- Single cell genomics for understanding tumour heterogeneity
- Single cell RNA sequencing technologies and applications

Day 2 Stream 2 – Applications and Technologies in Different Therapeutic Areas

- Case studies: oncology, immunotherapy and autoimmune diseases
- Methods for single cell isolation, capture & purification
- Single cell analysis tools including PCR analysis technologies
- Clinical applications & future perspectives
- High throughput in-situ sequencing approaches
- Microfluidics technologies and advances in applications
- The potential applications of single cell manipulation

Day 2 Stream 3 – Overcoming Single Cell Analysis Challenges

- Sample preparation for single cell analysis
- Bioinformatics challenges:
  - Calling copy number variations
  - Single cell data-handling
  - Identifying mutated genes in tumor samples
  - Improving the accuracy of quantitative analysis of transcripts
- Data analysis and interpretation hurdles
- Strategies and applications for single cell gene expression study

Benefits to Attending

- Hear from and meet with the key innovators in next generation sequencing and single cell analysis. Attendees include: Professor of Genomics, University of Southampton; Professor of Chemistry, George Washington University; Professor of Cell Biology, Paris Descartes University
- Discover collaborative solutions to next generation sequencing challenges. This prestigious congress brings together key opinion leaders to discuss topic areas ranging from advancements in next generation sequencing platforms & technologies, novel NGS data analysis techniques and NGS case studies in the clinic
- Learn more about the application of next generation sequencing in medicine. Hear therapeutic case studies from cancer, immunotherapy, HIV and infectious diseases
- Discuss the latest innovations in single cell analysis. Case studies include the areas of genomics, transcriptomics & proteomics, metabolomics, bioinformatics and data interpretation
- Examine novel advancements in single cell applications and technologies. The conference will cover using single cells in different therapeutic applications and updates in microfluidics technologies
- A high quality programme devised with the help of our esteemed advisory board. Presentations will cover areas including latest innovations in gene editing technologies in NGS, single cell RNA sequencing technologies and advances in circulating single tumor cells
- Co-located with the highly anticipated 2nd Annual Genome Editing Congress

Complimentary Webinars:

- Advances In Rapid Transgeneration Adaptation – Download for free
- Single Cell Analysis Research – Download for free
- Advances In Genome Editing – Download for free

Register for free - email marketing@oxfordglobal.co.uk

2016 Speakers Include:

- Akos Vertes – George Washington University
- Päivi Saavalainen – University of Helsinki
- Nic Mermod – University of Lausanne

Meet Senior Decision Makers

450 delegates from leading research & academic institutions, clinical research institutions, food & nutrition companies as well as major pharmaceutical and biotech companies will attend the event. Delegate job titles include:

Next Generation Sequencing
Developmental Biology
Genomics
Bioinformatics

Single Cell Analysis
Cellular Biology
Gene Expression
Bioengineering

Discover New Solutions

Formal and informal meeting opportunities offer delegates the chance to discuss key solutions with leading service providers. Services to be discussed include:

- Sequencing Technologies
- NGS Data Analysis
- NGS Data Generation
- Bioinformatics Development

- Diagnostics Technologies
- Microfluidic Solutions
- Molecular Profiling
- Single Cell Analysis Products

For booking details & registration fees please refer to the last page or visit: www.nextgenerationsequencing-congress.com/marketing
2016 8th Annual Next Generation Sequencing Congress Confirmed Speakers Include:

- Jane Wilkinson, Senior Director, Broad Genomics Alliance Management, Broad Institute
- Edward Oakley, Global Head ASI Informatics, Novartis Pharma AG
- Miika Ahdesmäki, Associate Principal Scientist, AstraZeneca
- Tim Hubbard, Head of Genome Analysis, Genomics England / King’s College London
- Nickolas Papadopoulos, Professor of Oncology, Johns Hopkins
- Antoine van Kampen, Professor Medical Bioinformatics, Academic Medical Center (AMC), University of Amsterdam (UvA)
- Shamima Rahman, Professor of Paediatric Metabolic Medicine, UCL Great Ormond Street Institute of Child Health
- Nic Mermod, Professor and Director of Institute of Biotechnology, University of Lausanne
- Sarah Ennis, Professor of Genomics, University of Southampton
- Filip Van Nieuwerburgh, Professor, Ghent University
- Jürg Bähler, Professor of Systems Biology, University College London
- Hubert Smeets, Professor in Clinical Genomics with focus on Mitochondrial Diseases, Maastricht University
- Dhavendra Kumar, Consultant in Clinical Genetics/ Genomic Medicine, Institute of Medical Genetics, Cardiff University School of Medicine
- Ole Lund, Professor, Technical University of Denmark
- Jonathan Strefford, Professor of Molecular Oncology, University of Southampton
- Niels Tommerup, Professor, University of Copenhagen
- Anthony V Moorman, Professor of Genetic Epidemiology, Newcastle University
- Ettore Capoluongo, Adjunct Professor, Catholic University and Teaching Hospital Foundation “A Gemelli” of Rome (Italy)
- Alberto Paccanaro, Professor in Computational Biology, Royal Holloway, University of London
- Timothy Ravasi, Professor, King Abdullah University of Science and Technology (KAUST)
- Rob Krams, Professor of Molecular Bioengineering, Imperial College London
- Ross McManus, Professor in Molecular Medicine, Trinity College Dublin
- Noam Shomron, Head of Genomics Research Team, Tel Aviv University
- Sven Nahmisen, Head of the Quantitative Biology Center (QBiC), Quantitative Biology Center (QBiC), Tübingen
- Patrick Descombes, Head of Functional Genomics, Nestle Institute of Health Sciences
- Vicki Chalker, Head, Respiratory and Vaccine Preventable Bacteria Reference Unit, Public Health England
- Christoph Woelk, Associate Professor of Genomics and Bioinformatics, University of Southampton
- Mikael Rørdam Andersen, Associate Professor, Technical University of Denmark
- Abdul Khalid Siraj, Senior Scientist / Deputy Director, King Faisal Specialist Hospital and Research Centre
- Neil Ward, EMEA Market Development Manager, Illumina

2016 Co-located 4th Annual Single Cell Analysis Congress Confirmed Speakers Include:

- Patrizia Paterlini-Bréchet, Professor of Oncology/Molecular Biology, University Paris Descartes, Paris, France
- Akos Vertes, Professor of Chemistry, George Washington University
- Aldo Jesorka, Professor, Chalmers University of Technology
- Michael A. Rieger, Professor, Goethe University Hospital Frankfurt
- Neil Avent, Professor of Molecular Diagnostics and Transfusion Medicine, Plymouth University Peninsula Schools of Medicine and Dentistry
- Yaron Shav-Tal, Professor, Bar-Ilan University
- Jörg Vogel, Director, Institute for Molecular Infection Biology, University of Würzburg, Germany
- Giuseppe Battaglia, Professor, University College London
- Andrew Ewing, Professor, University of Gothenburg and Chalmers University of Technology
- Raffaele Calogero, Professor, University of Torino
- Claas Nerlov, Professor, University of Oxford
- Saheer Gharbia, Professor and Head of Genomic Research, Public Health England
- Valerie Taly, Group Leader and CNRS Research Director, INSERM / Paris Descartes University
- Jonathan Chubb, Principal Investigator, MRC LMCB, University College London

If you’re on Twitter, make sure to follow us @xgenseq and join the Congress conversation on #xgenseq16

For more information please contact marketing@oxfordglobal.co.uk
2016 Co-located 4th Annual Single Cell Analysis Congress Confirmed Speakers Continued:
- Samuel Marguerat, Group Head, MRC Clinical Sciences Centre / Imperial College London
- Päivi Saavalainen, University Researcher, University of Helsinki
- Christian Depeursinge, Visiting Professor, King Abdullah University of Science and Technology
- Pamela Pinzani, Associate Professor, University of Florence
- Björn Önfelt, Professor, KTH – The Royal Institute of Technology
- Catherine Alix-Panabières, Director of the Laboratory of Rare Circulating Human Cells (LCCRH), University Medical Center of Montpellier
- Jose Gutierrez-Marcos, Professor, University of Warwick
- Stephan Lorenz, Head of Single Cell Genomics Core Facility, Wellcome Trust Sanger Institute
- Joshua Edel, Professor, Imperial College London
- Erez Mills, Scientist, Weizmann Institute of Science
- Esther Mellado, Research Assistant, Wellcome Trust Centre for Human Genetics (University of Oxford)

2016 Co-located 2nd Annual Genome Editing Congress Confirmed Speakers Include:
- Barry Rosen, Senior Principal Scientist, Reagents and Assay Development, Discovery Sciences, AstraZeneca
- Danilo Maddalo, Laboratory Head, Novartis Oncology
- Morten Frödin, Associate Professor, Biotech Research & Innovation Centre (BRIC), University of Copenhagen
- Stephen Hart, Professor in Molecular Genetics, UCL Great Ormond Street Institute of Child Health
- Virginijus Siksnys, Professor, Institute of Biotechnology, Vilnius University
- Tara Moore, Director of Biomedical Sciences Research Institute, Ulster University
- Uta Griesenbach, Professor of Molecular Medicine, Imperial College London
- Zsuzsanna Izsvák, Group Leader, Max Delbrück Center for Molecular Medicine
- Eric Paul Bennett, Associate Professor, University of Copenhagen
- Zoltan Ivics, Head of Division, Paul Ehrlich Institute
- Helene Fastrup Kildegaard, Senior Researcher and Co-PI, Technical University of Denmark, DTU Biosustain
- A. Francis Stewart, Professor, Dresden University of Technology
- Peter Rugg-Gunn, Group Leader, Babraham Institute
- Victor Turcanu, Senior Lecturer in Allergy, King’s College London
- Rafael J. Yáñez-Muñoz, Reader in Advanced Therapy, Royal Holloway, University of London
- Aleksandar Vojta, Assistant Professor, University of Zagreb, Faculty of Science
- Hiroshi Nishimasu, Assistant Professor, The University of Tokyo

2016 Vendor Speakers Include:
- Mike Hawes, Chief Executive Officer, Dolomite Bio
- Steve Siembieda, Vice President Commercialization, Advanced Analytical Technologies
- Christophe Lancrin, Group Leader, EMBL
- Xin Liu, Principal Scientist, Sphere Fluidics Limited
- Ruth Kläver, Scientist Product Development, QIAGEN
- Wieland Keilholz, Field Application Specialist, BD Life Sciences Genomics
- Raimo Tanzi, Chief Commercial Officer, Menarini Silicon Biosystems
- Jean-Noël Billaud, Principal Scientist, QIAGEN
- Sara Gonzalez-Hilarion, Product Manager and Scientific Support Specialist, Takara Bio Europe SAS
- Yannis Pitsiladis, Professor of Sport and Exercise Science and Director, FIMS Reference Collaborating Centre of Sports Medicine for Anti-Doping Research
- Celia P. Martinez-Jimenez, Postdoctoral Fellow, Wellcome Trust Sanger Institute and University of Cambridge, Cancer Research UK Cambridge Institute
- Dominic Graham Rothwell, CEP Staff Scientist, Cancer Research UK Manchester Institute, The University of Manchester

For more information please contact marketing@oxfordglobal.co.uk
For more information please contact marketing@oxfordglobal.co.uk
<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>07.30 – 08.20</td>
<td>Registration: Champagne Foyer&lt;br&gt;Conference Room 1: Morangis</td>
</tr>
<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: Noam Shomron, Head of Genomics Research Team, Tel Aviv University</td>
</tr>
<tr>
<td>08.30 – 09.00</td>
<td>Co-located Event Keynote Address:&lt;br&gt;The 100,000 Genomes Project&lt;br&gt;Tim Hubbard, Head of Genome Analysis, Genomics England / King’s College London</td>
</tr>
</tbody>
</table>

### 8th Annual Next Generation Sequencing Congress

<table>
<thead>
<tr>
<th>Session</th>
<th>Speaker, Institution</th>
</tr>
</thead>
<tbody>
<tr>
<td>Advances In NGS Platforms And Key Therapeutic Applications</td>
<td>Noam Shomron, Head of Genomics Research Team, Tel Aviv University</td>
</tr>
<tr>
<td>NGS Data Management And Bioinformatics</td>
<td>Matthew Keyser, Senior Manager for NGS Applications, DNASTAR</td>
</tr>
<tr>
<td>Mornigis</td>
<td>Daniel Liber, Business Development, Director, Wafergen Biosystems</td>
</tr>
<tr>
<td>Conference Room 1: Morangis</td>
<td>Nic Mermod, Professor and Director of Institute of Biotechnology, University of Lausanne</td>
</tr>
<tr>
<td>Conference Room 2: Chalon &amp; Reims</td>
<td>Patrizia Paterlini-Bréchot, Professor of Oncology/Molecular Biology, University Paris Descartes, Paris, France</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>09.00 – 09.30</td>
<td>Stream Keynote Address:&lt;br&gt;MITOCHONDRIAL-RELATED DISEASE, TRANSMISSION AND TOXICITY: A TALE OF 2 GENOMES&lt;br&gt;Hubert Smeets, Professor in Clinical Genomics with focus on Mitochondrial Diseases, Maastricht University</td>
</tr>
<tr>
<td></td>
<td>Genetic modification of mtDNA and the exome in mitochondrial disease</td>
</tr>
<tr>
<td></td>
<td>De novo mtDNA mutations and inherited mtDNA mutations in zebrafish and humans</td>
</tr>
<tr>
<td></td>
<td>mtDNA variants and the risk of radiation induced lung toxicity in lung cancer</td>
</tr>
<tr>
<td></td>
<td>De novo mtDNA mutations and inherited mtDNA mutations in zebrafish and humans</td>
</tr>
<tr>
<td></td>
<td>Genetic modification of mtDNA and the exome in mitochondrial disease</td>
</tr>
<tr>
<td></td>
<td>De novo mtDNA mutations and inherited mtDNA mutations in zebrafish and humans</td>
</tr>
<tr>
<td></td>
<td>mtDNA variants and the risk of radiation induced lung toxicity in lung cancer</td>
</tr>
<tr>
<td></td>
<td>Genetically modified cells and proteins derived therefrom must be characterized before use in clinical settings</td>
</tr>
<tr>
<td></td>
<td>Whole genome NGS analysis provides information on the transgene(s) sequence and genomic integration loci</td>
</tr>
<tr>
<td></td>
<td>NGS analysis can also document cell origin, possible clonality, and search for genome integrated viral elements</td>
</tr>
<tr>
<td></td>
<td>Circulating tumor and trophoblastic cells are rare cells. They need powerful enrichment before capture and molecular analysis</td>
</tr>
<tr>
<td></td>
<td>Interest of their molecular analysis covers non-invasive theranostics and non-invasive prenatal diagnosis</td>
</tr>
<tr>
<td></td>
<td>Advantages and disadvantages of different strategies will be discussed</td>
</tr>
</tbody>
</table>

For more information please contact marketing@oxfordglobal.co.uk
<table>
<thead>
<tr>
<th>Time</th>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 2: Chalon &amp; Reims</th>
<th>Conference Room 3: Epernay</th>
</tr>
</thead>
</table>
| 09.30 – 10.00 | **The Path To Successful Sequencing Includes Accurate Nucleic Acid Analysis**  
- Improve library preparation and decrease overall preparation costs by assessing genomic DNA and RNA extraction quality  
- Accurately size and quantify large fragment and standard library smears through proper data imaging  
- Eliminate data loss, increase efficiencies and reduce labour with automated workflow | | **Bringing Innovative Technologies Together: An Integrative Workflow For Single Cell Analysis That Helps To Uncover Hidden Events In A Solid Tumor**  
Following the paradigm of easy-to-use tools for genomics analyses, BD Genomics brings a suite of products to market that focus on single cell applications.  
The Tumor Dissociation reagent makes solid tumors accessible to FACS technology.  
The FACSMelody™ is a benchtop cell sorter that enables inexperienced FACS users to successfully run a sorting experiment through automation of complex tasks. 100s of single cells can be sorted at high throughput.  
BD Precise™ Assays are designed for transcriptome analysis on the single cell level using an efficient workflow that seamlessly integrates with sorted cells. The assays ensure highest precision in gene expression analysis by using molecular indexes to remove PCR bias introduced during library preparation.  
A case study will be presented on the integrated workflow of tumor dissociation, FACS sorting and transcriptome analysis.  
New insights into tumor biology at a currently unprecedented resolution are revealed through this powerful approach. | |
| 10.00 – 11.00 | **Exhibition Room: Mancy and Avize**  
Morning Coffee & Refreshments, Poster Presentation Sessions, One to One Meetings x3 | | |
| 11.00 – 11.30 | **Illumina Technology From Research To The Clinic**  
- Oncology: from targeted resequencing to whole genomes  
- Implementation of non-invasive prenatal testing challenges in rare genetic diseases | **De Novo Genome Assembly In The Cloud**  
- PacBio Sequel  
- Cloud computing  
- Metagenomics  
- De novo assembly | **Detection, Characterisation And Ex Vivo Expansion Of Viable Circulating Tumor Cells**  
- In vitro culture of CTCs: EPISPOT assay and establishment of colon CTC lines  
- In-depth characterization of the colon CTC line CTC-MCC-41  
- Detection of CTCs expressing PD-L1 as liquid biopsy for guiding immunotherapy in breast cancer |
| | Steve Siembieda, Vice President Commercialization, Advanced Analytical Technologies | Edward Oakeley, Global Head ASI Informatics, Novartis Pharma AG | Catherine Alix-Panabières, Director of the Laboratory of Rare Circulating Human Cells (LCCRH), University Medical Center of Montpellier |

For more information please contact marketing@oxfordglobal.co.uk
<table>
<thead>
<tr>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 2: Chalon &amp; Reims</th>
<th>Conference Room 3: Epernay</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>11.30 – 12.00</strong> Saturation Of The Human Genome With Chromosomal Breakpoints</td>
<td>Determination Of The Affinity Distribution Among Expanded B Cells Measured By Repertoire Sequencing</td>
<td>Metabolites, Vital Signs And Cell Cycle Studied In Single Cells</td>
</tr>
<tr>
<td>Niels Tommerup, Professor, University of Copenhagen</td>
<td>Antoine van Kampen, Professor Medical Bioinformatics, Academic Medical Center (AMC), University of Amsterdam (UvA)</td>
<td>Akos Vertes, Professor of Chemistry, George Washington University</td>
</tr>
<tr>
<td>- International Breakpoint Mapping Consortium, a global effort to map thousands of constitutional balanced chromosomal rearrangements (BCR) by NGS</td>
<td>- RNaseq repertoire sequencing strategies are used to identify expanded B-cell clones that are assumed to play a role in the pathogenesis of immune disorders. This approach, however, does not provide information about the affinity of the expanded of the (un)expanded clones. Such information might be useful for the further selection of subclones and their characterization. We used mathematical modelling of the germinal centre to gain more insight in the affinity distribution among (un)expanded subclones. Analysis of expanded B-cell subclones reveals that this group contains both low and high affinity B cells.</td>
<td>- Metabolic analysis of single cells to uncover cellular heterogeneity and metabolic noise</td>
</tr>
<tr>
<td>- Target thousands of protein coding and non-coding genes, with associated phenotypes</td>
<td></td>
<td>- Response to metabolic modulators and oxidative stress studied in individual cells</td>
</tr>
<tr>
<td>- Germline mutations of topological domains, with disease-associated dysregulation</td>
<td></td>
<td>- Adenylate energy charge and [GTP]/[GDP] ratios in single cells at distinct mitotic stages</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>12.00 – 12.30</th>
<th>Use Of Genomics In Bacterial Reference Microbiology For Respiratory And Systemic Pathogens</th>
<th>Genomic And Phenotypic Diversity In Fission Yeast</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Vicchi Chalker, Head, Respiratory and Vaccine Preventable Bacteria Reference Unit, Public Health England</td>
<td>Jürg Bähler, Professor of Systems Biology, University College London</td>
</tr>
<tr>
<td></td>
<td>- Genomics is increasingly being utilized in bacterial infectious disease reference laboratories for respiratory pathogens.</td>
<td>- We sequenced the genomes of 161 strains, quantified 74 traits, and conducted 223 genome-wide association studies, presenting a rich resource to examine genotype-phenotype relationships in a tractable model</td>
</tr>
<tr>
<td></td>
<td>- This presentation will detail how Public Health England are using genomics to enhance existing methodologies for bacterial respiratory and systemic pathogens</td>
<td>- Copy number variations frequently vary within near-clonal populations and substantially contribute to quantitative traits, whereas rearrangements are strongly associated with reproductive isolation but contribute less to traits</td>
</tr>
<tr>
<td></td>
<td>- How genomics is being used to examine and enhance invasive and respiratory cluster analysis</td>
<td></td>
</tr>
<tr>
<td></td>
<td>- How genomics are being used to inform methodologies for fastidious pathogens</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

For more information please contact marketing@oxfordglobal.co.uk
<table>
<thead>
<tr>
<th>Time</th>
<th>Session</th>
</tr>
</thead>
<tbody>
<tr>
<td>12.30 – 13.30</td>
<td>Exhibition Room: Mancy and Avize</td>
</tr>
<tr>
<td></td>
<td>Lunch</td>
</tr>
<tr>
<td></td>
<td>Conference Room 1: Morangis</td>
</tr>
<tr>
<td></td>
<td>Stream Chair: Hubert Smeets, Professor in Clinical Genomics with focus on Mitochondrial Diseases, Maastricht University</td>
</tr>
<tr>
<td>13.30 – 14.00</td>
<td>An Integrative ‘Omics’ Solution To The Detection Of Recombinant Human Erythropoietin And Blood Doping</td>
</tr>
<tr>
<td></td>
<td>• PAST: The history of drugs in sport – the problem with the current approach</td>
</tr>
<tr>
<td></td>
<td>• SCIENCE: How “omics” will revolutionise anti-doping - “omics” technology to the rescue</td>
</tr>
<tr>
<td></td>
<td>• FUTURE: The wider implications of this research for personalised medicine</td>
</tr>
<tr>
<td></td>
<td>Yannis Pitsiladis, Professor of Sport and Exercise Science and Director, FIMS Reference Collaborating Centre of Sports Medicine for Anti-Doping Research</td>
</tr>
<tr>
<td></td>
<td>Delegates are welcome to attend the co-located presentations</td>
</tr>
<tr>
<td></td>
<td>Conference Room 2: Chalon &amp; Reims</td>
</tr>
<tr>
<td></td>
<td>Stream Chair: Hasi Patel, Senior Director, UK &amp; Ireland, Bluebee</td>
</tr>
<tr>
<td>14.00 – 14.30</td>
<td>Tackling All The Genomics Challenges From A Single Patient To Large Clinical Studies</td>
</tr>
<tr>
<td></td>
<td>• Highlighting our process development to tackle difficult samples</td>
</tr>
<tr>
<td></td>
<td>• Reviewing our capabilities in managing high volumes of data generation and analysis</td>
</tr>
<tr>
<td></td>
<td>• Globally collaborating with researchers to drive them closer to the cure</td>
</tr>
<tr>
<td></td>
<td>Jane Wilkinson, Senior Director, Broad Genomics Alliance Management, Broad Institute</td>
</tr>
<tr>
<td></td>
<td>Rapid Transgeneration Adaptation Of A Reef Fish To Climate Change</td>
</tr>
<tr>
<td></td>
<td>• Rapid environmental change (such as climate change) results in perturbations of the environment that threaten the persistence of a variety of organisms</td>
</tr>
<tr>
<td></td>
<td>• There is great concern that the change is outpacing the rate of genetic adaptation. However, a growing body of evidence suggests that some responses can be plastic but also heritable across generations</td>
</tr>
<tr>
<td></td>
<td>• Such trans-generational acclimatization can occur over shorter periods of time compared to, and may also accelerate the pace of, genetic adaptation</td>
</tr>
<tr>
<td></td>
<td>Timothy Ravasi, Professor, King Abdullah University of Science and Technology (KAUST)</td>
</tr>
<tr>
<td></td>
<td>Electrochemistry And Mass Spectrometry Imaging In Cells And Vesicles</td>
</tr>
<tr>
<td></td>
<td>• Electrochemical methods and mass spectrometry imaging are used to provide powerful approaches to investigate neurotransmitter release and storage from and in single cells</td>
</tr>
<tr>
<td></td>
<td>• Electrochemical cytometry is used to measure cell vesicle content and support the concept that only a fraction of transmitter is released during exocytosis</td>
</tr>
<tr>
<td></td>
<td>• Electrochemical cytometry has been used to examine neurochemistry of release and vesicle content to understand cisplatin and the chemobrain</td>
</tr>
<tr>
<td></td>
<td>• Mass spectrometry imaging with resolution down to 40 nm has been used to measure transmitter in subregions of nanometer vesicles</td>
</tr>
<tr>
<td></td>
<td>Andrew Ewing, Professor, University of Gothenburg and Chalmers University of Technology</td>
</tr>
</tbody>
</table>

For more information please contact marketing@oxfordglobal.co.uk
### Conference Room 1: Morangis

**14.30 – 15.00**  
**SMARTer® Way For RNA-seq From Single-cells And Other Challenging Samples**
- Powered by SMART and LNA technologies, our latest kits for NGS push the limits of sensitivity enabling to obtain the highest quality sequencing data from the most difficult samples, including single cells, pico-input amounts of RNA, degraded RNA samples (FFPE) and small RNAs.
- Expanding applications for SMART technology have led to innovative tools for immune profiling, targeted RNA-Seq and ChIP-Seq.
- In this talk we will present newly-developed methods that leverage the strengths of the SMARTer approach for single-cell RNA-seq and other challenging NGS applications.

Sara Gonzalez-Hilarion, Product Manager and Scientific Support Specialist, Takara Bio Europe SAS

### Conference Room 3: Epernay

**14.30 – 15.00**  
**Ageing Of The Immune System From A Single Cell Perspective**
- Single-cell RNA-sequencing in conjunction with cross-species comparisons has been used to understand how aging impacts the transcriptional response to immune activation of naive CD4+ T cells.
- A detailed characterization of cell-to-cell transcriptional variability reveals how ageing destabilizes a conserved transcriptional activation program.

Celia P. Martinez-Jimenez, Postdoctoral Fellow, Wellcome Trust Sanger Institute and University of Cambridge, Cancer Research UK Cambridge Institute

### Conference Room 1: Morangis

**15.00 – 15.30**  
**Integrative Approach To Biomarker Discovery: Comparative Analysis Of Two Cancers Using Genomics And Transcriptomics From RNA Sequencing Data**
Hepatocellular Carcinoma (HCC) and Endometrioid Endometrial Carcinoma (EEC) are two lethal diseases of public health importance worldwide. Understanding the mechanisms of tumor progression in both cancers could be essential for the detection of common biomarkers. Using QIAGEN's RNA sequencing solutions, we were able to highlight key molecular and biological processes that indicate similarities in the tumor progression toward metastasis. This approach may be useful in the context of precision or personalized medicine. Examining the gene expression and variants in tumors from groups of patients with each disease revealed that at a molecular level, early stages of EEC resemble established HBV-positive, HCV-negative, liver cirrhosis positive HCC.

Jean-Noël Billaud, Principal Scientist, QIAGEN

### Conference Room 3: Epernay

**15.00 – 15.30**  
**Use Of Single Cell Transcriptomics To Study Blood Stem Cells Formation**
The presentation will cover:
- How blood stem cells are crucial cells for the continuous formation of blood cells throughout life and how they are formed from the vasculature during embryogenesis.
- Challenges associated with studying this process in vivo due to very low cell number available and how we are using single cell transcriptomics approaches to understand the generation of this very important cell type.

Christophe Lancrin, Group Leader, EMBL

### Conference Room 1: Morangis

**15.30 – 16.00**  
**Exhibition Room: Mancy and Avize**
Afternoon Refreshments, Poster Presentation Sessions, One to One Meetings x2

For more information please contact marketing@oxfordglobal.co.uk
<table>
<thead>
<tr>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 2: Chalon &amp; Reims</th>
<th>Conference Room 3: Epernay</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>16.00 – 16.30</strong></td>
<td><strong>A Network Medicine Approach To Quantify Distance Between Hereditary Disease Modules On The Interactome</strong></td>
<td><strong>Biological Cells Tomography By Digital Holography: An Emerging Technology For Cell Investigation</strong></td>
</tr>
<tr>
<td>Utilizing The Connectivity Map To Inform HIV Cure Strategies</td>
<td>Network Medicine sees hereditary diseases as perturbations in specific regions of the interactome – the disease modules. We have developed a method to quantify the distance between disease modules on the interactome which uses exclusively the phenotypic description of the diseases. We show how this measure can effectively predict novel disease genes for hereditary diseases with no molecular characterization.</td>
<td>For cell and tissue imaging, new technologies are presently emerging which are not based on fluorescence. They do not require tagging and offer easy and quick access to biological matter and cells in particular. The data delivered to the biologists and physicians are complementary and are also intrinsically quantitative. In this presentation, we present a short review of our works and other works as well regarding tomographic imaging of dielectric object, biological cells in particular. The complex electromagnetic wavefield scattered by the specimen, can be obtained by reconstruction of digital holograms or by other methods sometime described as “Quantitative Phase Imaging” (QPI) This approach leads to a growing modality in microscopy, which will find its own path in addition to light intensity based imaging methods like fluorescence. By itself, quantitative phase is acknowledged to provide a wealth of data on the sizes and composition of the specimen by the analysis of the optical pathlength and the refractive index with its dispersion law. Significance of these data has been improving recently in biology and medicine. The exploitation of phase data permits the improvement of the image resolution and new criteria must be envisaged to quantify resolution. From the reconstructed complex wavefield, it is possible synthesizing the aperture of a virtual microscope up to 2π, offering super-resolution images. Live images of micro-organisms and neurons with resolution around 100 nm have been obtained.</td>
</tr>
<tr>
<td>Christopher Woelk, Associate Professor of Genomics and Bioinformatics, University of Southampton</td>
<td>Alberto Paccanaro, Professor in Computational Biology, Royal Holloway, University of London</td>
<td>Christian Depeursinge, Visiting Professor, King Abdullah University of Science and Technology</td>
</tr>
<tr>
<td><strong>16.30 – 17.00</strong></td>
<td><strong>Whole-genus Association Analysis – Using Hundreds Of Microbial Genomes For Linking Of Phenotype To Genotypes</strong></td>
<td><strong>Quantifying Allelic mRNA Expression Of Tagged Endogenous Genes Within Single Cells</strong></td>
</tr>
<tr>
<td>Short And Long Sequencing Reads From Bacteria To Plant Genomes</td>
<td>Comparative genomics with large numbers of genomes. Applying microbial genomes for elucidation of primary metabolism, secondary metabolism, and secretomes, among other things. Studies of microbial speciation through pan-genus analysis.</td>
<td>New approach for tagging endogenous genes and detection of their transcribed mRNAs. The technique is used for single molecule mRNA imaging in single cells. This approach allows to distinguish between mRNAs transcribed from different alleles within the same cell.</td>
</tr>
<tr>
<td>Patrick Descombes, Head of Functional Genomics, Nestle Institute of Health Sciences</td>
<td>Mikael Rørdam Andersen, Associate Professor, Technical University of Denmark</td>
<td>Yaron Shav-Tal, Professor, Bar-Ilan University</td>
</tr>
</tbody>
</table>

For more information please contact marketing@oxfordglobal.co.uk
### Conference Room 1: Morangis

**17.00 – 17.30**  
**Genomic Profiling Of Thyroid Cancer**
- Papillary thyroid carcinoma (PTC) is most common in Saudi Arabia, where it is only second to breast cancer as the most common cancer among females.  
- Genomic profiling of PTC from Saudi Arabia has not been attempted previously. We performed whole-exome sequencing of 101 PTC samples and the corresponding genomic DNA to identify genes with recurrent somatic mutations  
- Additional 785 samples then sequenced for detected recurrent somatic mutations by using a next-generation gene-panel approach.  
- In addition to BRAF, N-RAS, and H-RAS, which have previously been shown to be recurrently mutated in PTC, our analysis highlights additional genes, including thyroglobulin (TG)  
- Further analysis of metastatic PTC tissue revealed significant enrichment for TG mutations, demonstrating unknown role of TG somatic mutations in the pathogenesis of PTC and its malignant evolution

**Day One – 10th November 2016**

**Conference Room 1: Morangis**

**Conference Room 2: Chalon & Reims**

**Conference Room 3: Epernay**

**17.00 – 17.30**  
**Integrating Data, Tools, And Infrastructure To Provide For Efficient Collaboration And Management In Large-scale Biomedical Research**
- Data management for high-throughput experiments  
- Fully automated process from project design to the data archive  
- Scalable mining and searching of NGS data

**Additional 785 samples then sequenced for detected recurrent somatic mutations by using a next-generation gene-panel approach.**

**Sven Nahnsen, Head of the Quantitative Biology Center (QBIC), Quantitative Biology Center (QBIC), Tübingen**

**17.30 – 18.00**  
**Big Data And Genomics: Halting Breast Cancer Metastasis**
- Metastasis is the primary cause for mortality in breast cancer though it lacks effective treatment strategies  
- We performed big data analysis on multiple data-sets identifying new players in the metastatic pathway and possible methods to regulate them  
- We show that breast cancer metastasis can be prevented by local delivery of small RNAs to tumor site in mice  
- Our work will permit a more effective individualized anti-metastatic breast cancer therapy

**Conference Room 3: Epernay**

**The Nature And Nurture Of Cell Heterogeneity:**
- Single-cell Functional Analysis, Temporal Single-cell Sequencing And Imaging Of Gene Edited Macrophages**
- Technical improvements in single-cell perturbation, live-cell imaging and single-cell sequencing are enabling the detailed dissection of heterogeneous cell states. Combining all three modalities with new platforms such as the Polaris lab-on-chip, we are performing temporal studies of CRISPR-edited macrophages to better understand their responses to inflammatory perturbation. We analysed the genetic features (‘nature’) and micro-environmental factors (‘nurture’) of heterogeneity in single cells, cultured in perfect isolation, and studied the relationship between transcriptomics and cell signaling interactions. We will present some genetic effects found in macrophages to be likely microenvironmental specific, indicating the importance of both nature and nurture contributions to be considered in particular single-cell studies.

**Esther Mellado, Research Assistant, Wellcome Trust Centre for Human Genetics (University of Oxford)**

---

For more information please contact [marketing@oxfordglobal.co.uk](mailto:marketing@oxfordglobal.co.uk)
<table>
<thead>
<tr>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 3: Epernay</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>18.00 – 18.30</strong></td>
<td><strong>Novel Strategies For The Detection Of Single Molecules Using Multiphase Microfluidics</strong></td>
</tr>
<tr>
<td><strong>BRCA1/2 Somatic Analysis In Ovarian Cancer Patients: Are We Ready For Routine Setting?</strong></td>
<td>Analytical Sensors plays a crucial role in today’s highly demanding exploration and development of new detection strategies. Whether it be medicine, biochemistry, bioengineering, or analytical chemistry the goals are essentially the same: 1) improve sensitivity, 2) maximize throughput, 3) and reduce the instrumental footprint. In order to address these key challenges, the analytical community has borrowed technologies and design philosophies which has been used by the semiconductor industry over the past 20 years. By doing so, key technological advances have been made which include the miniaturization of sensors and signal processing components which allows for the efficient detection of nanoscale object. One can imagine that by decreasing the dimensions of a sensor to a scale similar to that of a nanoscale object, the ultimate in sensitivity can potentially be achieved - the detection of single molecules. This talk highlights novel strategies for the detection of single molecules using multiphase microfluidics.</td>
</tr>
<tr>
<td>Ettore Capoluongo, Adjunct Professor, Catholic University and Teaching Hospital Foundation &quot;A Gemelli&quot; of Rome (Italy)</td>
<td>Joshua Edel, Professor, Imperial College London</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>18.30</strong></th>
<th>Exhibition Room: Mancy and Avize</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Networking Drinks – Sponsored by Wafergen and End of Day One</strong></td>
<td></td>
</tr>
</tbody>
</table>

For more information please contact marketing@oxfordglobal.co.uk
### 8th Annual Next Generation Sequencing Congress & 4th Annual Single Cell Analysis Congress

**Day Two – 11th November 2016**

<table>
<thead>
<tr>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 3: Epernay</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>08.20 – 08.50</strong></td>
<td><strong>Keynote Address:</strong></td>
<td><strong>Overcoming Single Cell Analysis Challenges</strong></td>
</tr>
<tr>
<td><strong>The Clinical Application Of Cancer Genomics: The Example Of Mature B-cell Malignancies</strong></td>
<td><strong>Stream Chair:</strong> Reserved for Senior Representative, Qiagen</td>
<td><strong>Stream Chair:</strong> Miguel Viribay, Vice President, Expedeon</td>
</tr>
<tr>
<td>Jonathan Strefford, Professor of Molecular Oncology, University of Southampton</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>08.50 – 09.20</strong></td>
<td><strong>Stream Keynote Address:</strong></td>
<td><strong>Stream Keynote Address:</strong></td>
</tr>
<tr>
<td><strong>Detection Of Somatic Mutations In Biological Fluids</strong></td>
<td><strong>Applications And Technologies In Different Therapeutic Areas</strong></td>
<td><strong>Leveraging The Power Of Whole Genome Sequence Analysis For Better Understanding The Role Of The Colonising Flora In The Human Microbiome</strong></td>
</tr>
<tr>
<td>Nickolas Papadopoulos, Professor of Oncology, Johns Hopkins</td>
<td><strong>Stream Chair:</strong> Frank Smith, EMEA Marketing Manager – Oncology &amp; Translational Research, Affymetrix, part of Thermo Fisher Scientific</td>
<td><strong>Rationale for exploring single cell technologies for deciphering complex microbiomes</strong></td>
</tr>
<tr>
<td></td>
<td><strong>Stream Keynote Address:</strong> Deciphering, By Single-cell Sequencing, The Subpopulation Organization Of Innate T-cells</td>
<td><strong>Biological diversity and objectives driving selection of key criteria for analysis</strong></td>
</tr>
<tr>
<td></td>
<td></td>
<td><strong>Establishing a computational framework for biomarker discovery</strong></td>
</tr>
<tr>
<td></td>
<td></td>
<td><strong>Bridging genomics analysis with ecological traits in the human gut microbiome</strong></td>
</tr>
<tr>
<td></td>
<td></td>
<td><strong>Saheer Gharbia, Professor and Head of Genomic Research, Public Health England</strong></td>
</tr>
</tbody>
</table>

For more information please contact marketing@oxfordglobal.co.uk
### 8th Annual Next Generation Sequencing Congress & 4th Annual Single Cell Analysis Congress  
**Day Two – 11th November 2016**

<table>
<thead>
<tr>
<th>Time</th>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 2: Chalon &amp; Reims</th>
</tr>
</thead>
</table>
| 09.20 – 09.50 | **Target Enrichment Products For Clinical Research From Roche NimbleGen**  
- Discussion of the design and performance of the MedExome, a whole exome solution with enhanced coverage of disease-associated regions  
- Description of the HyperCap workflow, an integrated, application-specific approach for efficient, streamlined and automatable targeted sequencing solution  
- Custom design options and considerations for clinical research  
  
  Todd Richmond, Research Informatics Director, NimbleGen | **Restoring The Full Power Of Copy Number Variation Analysis On FFPE Tissues And CTC By Sorting Pure Tumor Cells By DEPArray™ Technology**  
- Low Pass Genome CNV analysis on heterogeneous tumor samples is often hindered by the presence of too many stromal cells  
- High level gains are still detectable but single copy gains and losses are confused in the noise of the system  
- Typically, samples with tumor cellularity below 50% are discarded for this kind of analysis  
- DEPArray™ can isolate 100% pure tumor cells form FFPE samples and pure single CTC from enriched blood  
- The CNV analysis on such pure cells reveals the complete and accurate story of cell aberration, both on primary tumor and on CTC allowing a powerful stratification  
  
  Raimo Tanzi, Chief Commercial Officer, Menarini Silicon Biosystems |
| 09.50 – 10.20 | **Delegates are welcome to attend the co-located presentation**  
  
  | **Microfluidic Picodroplets – An Enabling Platform For Biological Discoveries**  
- Introduction of Sphere Fluidics’s Picodroplet technologies and instrument platforms  
- Discussion about applications in Biopharmaceutical Discovery & Development and others  
  
  Xin Liu, Principal Scientist, Sphere Fluidics Limited |
| 10.20 – 11.00 | **Exhibition Room: Mancy and Avize**  
Morning Coffee & Refreshments, Poster Presentation Sessions, One to One Meetings x2  
  
  Conference Room 1: Morangis  
Conference Room 2: Chalon & Reims  
Conference Room 3: Epernay |
| 11.00 – 11.30 | **NGS Technology: How It Has And Will Improve Precision Medicine In Acute Lymphoblastic Leukaemia**  
- Describe how NGS has and will contribute to deciphering the genomic landscape of acute lymphoblastic leukaemia  
- Outline the somatic genetic abnormalities that are and will soon be used as prognostic and predictive biomarkers in the management of patients with acute lymphoblastic leukaemia  
- Discuss the future role of NGS in deciphering the biology of acute lymphoblastic leukaemia and delivering precision medicine in the clinic  
  
  Anthony V Moorman, Professor of Genetic Epidemiology, Newcastle University | **Continuous Observation Of Hematopoietic Stem Cell Fate Decision Control At Single Cell Resolution**  
- Time-lapse microscopy-based tracking of stem cell behavior  
- Tracking of stem cells and their progeny for many generations  
- Molecular control of hematopoietic stem cell self-renewal and differentiation  
  
  Michael A. Rieger, Professor, Goethe University Hospital Frankfurt |
| 11.00 – 11.30 | **Imaging Transcriptional Dynamics In Single Living Cells**  
- Imaging transcription pulses in living cells using live cell fluorescence imaging  
- Quantitative analysis of pulsing data reveals mechanisms of transcriptional regulation  
- Imaging in mutant backgrounds reveals the causes of specific regulatory features  
  
  Jonathan Chubb, Principal Investigator, MRC LMCB, University College London |

For more information please contact [marketing@oxfordglobal.co.uk](mailto:marketing@oxfordglobal.co.uk)
### 11.30 – 12.00
**Conference Room 1: Morangis**

**NGS To Realize The Clinical Potential Of Liquid Biopsies In Cancer**
- Liquid biopsies, including Circulating Tumour Cells (CTCs) and circulating tumour DNA (ctDNA) have the potential to provide real-time, clinically important molecular insight into disease status.
- Tumour specific mutations and copy number aberrations present in CTCs and ctDNA provide potential therapeutic targets and prognostic or predictive biomarkers.
- NGS can be utilised to detect low frequency mutations in cancer patients, though issues of technical noise and false positives and identification of the clinically relevant aberrations need resolving.
- Initial data from pilot studies of NGS based analysis of liquid biopsies in cancer patients will be presented.

Dominic Graham Rothwell, CEP Staff Scientist, Cancer Research UK Manchester Institute, The University of Manchester

---

**Conference Room 2: Chalon & Reims**

**Solution Provider Presentation**

---

### 12.00 – 12.30
**Conference Room 1: Morangis**

**Evaluation Of Tumour BRCA Testing Methodology Across Clinical Labs Shows Great Variability In Approaches And Analytics**
- As part of correctly identifying patients eligible for novel therapies such as olaparib, a PARP inhibitor, clinical labs have to establish accurate detection and calling of germline and somatic variants in BRCA and other cancer related genes.
- An evaluation of 10 clinical diagnostics laboratories across the world revealed wide differences in the choice of DNA capture protocols as well as bioinformatics analyses.
- An internal dissection of the data received from the laboratories showed that although no false positives were reported by the labs, false negatives were cause often by differences in bioinformatics, variant classification, automated nomenclature, database limitations and in the background levels of noise in each data set.

Miika Ahdesmäki, Associate Principal Scientist, AstraZeneca

---

**Conference Room 2: Chalon & Reims**

**Advances in High-Throughput Single Cell RNAseq**
- Automation & protocol improvements of the Smartseq-2 and Nextera protocols.
- Lessons learnt: advice on experimental design and controls for single cell RNAseq experiments.
- Tracking solution for 100’s of experiments across 1000’s of cells.

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

---

**Conference Room 3: Epernay**

**Dual RNA-seq Unveils Noncoding RNA Functions In Host–Pathogen Interactions**
- Full transcriptomes of both a bacterial pathogen and its eukaryotic host.
- All classes of coding and noncoding RNA detected during infection.
- Fast long noncoding RNA response.

Jörg Vogel, Director, Institute for Molecular Infection Biology, University of Würzburg, Germany

---

### 12.30 – 13.30
**Exhibition Room: Mancy and Avize**

**Lunch**

For more information please contact marketing@oxfordglobal.co.uk
### 8th Annual Next Generation Sequencing Congress & 4th Annual Single Cell Analysis Congress

**Day Two – 11th November 2016**

<table>
<thead>
<tr>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 2: Chalon &amp; Reims</th>
<th>Conference Room 3: Epernay</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>13.30 – 14.00</strong></td>
<td><strong>Technology For High Throughput Single Cell RNA-Seq And Other Single Cell Research</strong>&lt;br&gt;• Microfluidic droplet technology has been proven as an effective tool for High Throughput Single Cell Research&lt;br&gt;• Typical technology is either prototype in nature or highly specialized and inflexible&lt;br&gt;• This presentation investigates flexible technology that enables a broad range of applications including - Single cell RNA-Seq, isolating functional antibody coding sequences, Profiling natively-paired T-cell Receptors, directed evolution by FACS sorting doubly encapsulated expression libraries and Encapsulating cells in hydrogels&lt;br&gt;&lt;br&gt;Mike Hawes, Chief Executive Officer, Dolomite Bio</td>
<td><strong>QIAscout: Overcoming Challenges In Single Cell Isolation</strong>&lt;br&gt;• QIAscout is an effective and fast method to isolate viable single cells ensuring minimal manipulation of the cellular status&lt;br&gt;• This novel single cell isolation method works in conjunction with inverted microscopes and is the ideal method to separate single cells for further downstream analysis or cultivation of clonal sub-populations&lt;br&gt;• Single cell isolation with QIAscout is compatible with multiple downstream applications such as whole genome and transcriptome amplification methods, PCR and NGS&lt;br&gt;&lt;br&gt;Ruth Kläver, Scientist Product Development, QIAGEN</td>
</tr>
</tbody>
</table>

**14.00 – 14.30**<br><br>**Lessons From Whole Exome And Genome Sequencing In The Paediatric Mitochondrial Clinic**<br>• The widespread availability of whole exome sequencing has led to a paradigm shift in the diagnostic approach to mitochondrial diseases<br>• Clinical exome sequencing is emerging as a first line diagnostic test, in combination with careful clinical and metabolic phenotyping<br><br>Shamima Rahman, Professor of Paediatric Metabolic Medicine, UCL Great Ormond Street Institute of Child Health | **The Biopen: Microfluidic Superfusion Of Adherent Single Cells**<br>• Technology foundation: microfluidic chip technology featuring hydrodynamic confinement and flow switching<br>• Application examples: brain tissue, muscle fibers, single cell enzymology<br>• Innovation: multiprobe/multistep experiments, integrated viability testing<br><br>Aldo Jesorka, Professor, Chalmers University of Technology | **Impact Of Growth And Cell Size On Fission Yeast Gene Expression In Single Cells**<br>• mRNA expression levels and transcription rates scale with cell size and growth<br>• Single cell RNA-seq reveals the molecular heterogeneity of fission yeast cells as a function of growth<br><br>Samuel Marguerat, Group Head, MRC Clinical Sciences Centre / Imperial College London |

For more information please contact marketing@oxfordglobal.co.uk
<table>
<thead>
<tr>
<th>Time</th>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 2: Chalon &amp; Reims</th>
<th>Conference Room 3: Epernay</th>
</tr>
</thead>
<tbody>
<tr>
<td>14.30 – 15.00</td>
<td>Shallow Whole Genome Sequencing Is Well Suited For The Detection Of Translocations In Human Blastocysts&lt;br&gt;Recent advances in in vitro fertilization techniques such as vitrification and trophoblast biopsy, as well as massively parallel sequencing, brings new possibilities for more straightforward preimplantation genetic diagnosis and screening. Human day-5 embryo biopsy combined with massively parallel sequencing is well suited for the detection of aneuploidy, translocations and small copy number aberrations.</td>
<td>Single Cell Transcriptome Profiling Of Human Leukocyte Populations&lt;br&gt;- We utilize the high-throughput Drop-seq RNAseq method by Macosco et al (2015)&lt;br&gt;- We study various human leukocyte populations both from healthy donors and in various autoimmune conditions&lt;br&gt;- A modified version of the method to capture also the clonality, i.e. the T and B cell receptor variable sequences is under development</td>
<td>Host And Pathogen Simultaneous Single-cell Transcriptome Analysis Reveals Interacting Sub-populations During Infection&lt;br&gt;The interaction between a pathogen and a host is a highly dynamic process in which both agents activate complex programs. Single-cell RNA-Seq is typically limited to the polyadenylated component of the transcriptome, thereby preventing the study of both the host and intracellular bacterial pathogens. Here, I will introduce a single-cell RNA-Seq method that simultaneously captures both host and pathogen transcriptomes. I will present application of this method to study the transcriptomes of individual mouse macrophages along with that of their intracellular pathogen Salmonella typhimurium, and identify their sub-population structure and expression heterogeneity throughout infection. Further, I will demonstrate the ability to study the biological significance of these sub-populations, most importantly the relationships among the co-existing sub-populations, their molecular details and the interplay between host and bacteria subpopulations. I will introduce novel insights into the biology of infection through the molecular study of both host and bacterium in individual encounters.</td>
</tr>
<tr>
<td>15.00 – 15.30</td>
<td>Exhibition Room: Mancy &amp; Avize&lt;br&gt;Afternoon Refreshments, Poster Presentation Sessions</td>
<td>Conference Room 1: Morangis</td>
<td>Erez Mills, Scientist, Weizmann Institute of Science</td>
</tr>
<tr>
<td>15.30 – 16.00</td>
<td>Case Studies In Personalised Diagnostics – Pre-clinical Diagnoses And New Phenotypes For Old Genes&lt;br&gt;This talk will describe identification of patient specific mutations using various next generation sequencing platforms where variant identification modified management and informed appropriate treatment pathways.</td>
<td>Droplet-based Microfluidics For Single Cell Analysis&lt;br&gt;Droplet based microfluidics allows to perform single cell experiments with high efficiency and high throughput.&lt;br&gt;We will illustrate capabilities of newly developed microfluidic platforms for single cell encapsulation, phenotypic characterization and sorting.&lt;br&gt;Finally, we will emphasize on its potential applications for cancer research and resistance to treatment analysis.</td>
<td>Valerie Taly, Group Leader and CNRS Research Director, INSERM / Paris Descartes University</td>
</tr>
<tr>
<td>Time</td>
<td>Conference Room 1: Morangis</td>
<td>Conference Room 2: Chalon &amp; Reims</td>
<td></td>
</tr>
<tr>
<td>------------</td>
<td>---------------------------------------------------------------------------------------------</td>
<td>---------------------------------------------------------------------------------------------------</td>
<td></td>
</tr>
<tr>
<td>16.00 – 16.30</td>
<td><strong>Next Generation Sequencing in Rare Inherited Cardiac Conditions</strong></td>
<td><strong>Fetal Erythroid Surface Biomarkers – Targets For Fetal Cell Enrichment From Maternal Blood</strong></td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Diagnostic challenges of rare inherited cardiac conditions</td>
<td>• The selection of fetal nucleated red cells as targets for fetal cell isolation</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Experience with multi-gene next generation sequencing diagnostic panels</td>
<td>• Differential proteomics of fetal cells compared to adult red cells</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Multi-disciplinary management of rare inherited cardiac conditions</td>
<td>• Characterisation of fetal erythroid Hsp60 as a candidate biomarker</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Dhavendra Kumar, Consultant in Clinical Genetics/Genomic Medicine, Institute of Medical Genetics, Cardiff University School of Medicine</td>
<td>Neil Avent, Professor of Molecular Diagnostics and Transfusion Medicine, Plymouth University Peninsula Schools of Medicine and Dentistry</td>
<td></td>
</tr>
<tr>
<td>16.30 – 17.00</td>
<td><strong>Genomic Epidemiology</strong></td>
<td><strong>Mutational Analysis Of Single Circulating Tumor Cells By Next Generation Sequencing</strong></td>
<td></td>
</tr>
<tr>
<td></td>
<td>• European collaboration in COMPARE, a large EU project with the intention to speed up the detection of and response to disease outbreaks among humans and animals worldwide through the use of new genome technology: <a href="http://www.compare-europe.eu">http://www.compare-europe.eu</a></td>
<td>• CTCs are a real-time “liquid biopsy” of the tumor reflecting the disease complexity at any stage of cancer progression</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Online methods at the Center for Genomic Epidemiology (CGE) for analysis and comparison of isolates and metagenomic samples</td>
<td>• Technical advances have enabled molecular analyses at the single-cell level allowing the profiling of rare cancer cells in clinical samples</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Colaboration at Global Microbial Identifier (GMI) to develop a global system to aggregate, share, mine and use microbiological genomic data</td>
<td>• Several steps are needed to achieve the analysis of CTCs at the single-cell level. The procedure is not yet integrated in a single device, but implies the performance of CTC selection, whole genome amplification and single cell sequencing. Each phase can be conducted by several approaches that can be combined in different workflows</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>Ole Lund, Professor, Technical University of Denmark</strong></td>
<td>• On the basis of the results obtained in a pilot study on breast cancer, single CTC sequencing seems to hold promise for future clinical applications by the development of cancer diagnostics focused on non-invasive disease management aimed at personalized medicine</td>
<td></td>
</tr>
<tr>
<td>17.00 – 17.30</td>
<td><strong>Coeliac T Cell Interiors: Insights From Transcriptomics</strong></td>
<td><strong>Immune Surveillance At The Single Cell Level</strong></td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Case control transcriptomic study</td>
<td>• Microchip tools for studies of immune cell heterogeneity</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Transcriptome of purified CD4+ T cells</td>
<td>• Serial killing by individual natural killer cells and T cells</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• Identification of transcriptional control networks</td>
<td>• Ultrasound-mediated formation 3D “microtumors”</td>
<td></td>
</tr>
<tr>
<td></td>
<td>• BACH2 as an important regulator of T cell development in coeliac disease</td>
<td>• Applications in cancer research and cell therapy</td>
<td></td>
</tr>
<tr>
<td></td>
<td><strong>Ross McManus, Professor in Molecular Medicine, Trinity College Dublin</strong></td>
<td><strong>Björn Önfelt, Professor, KTH – The Royal Institute of Technology</strong></td>
<td></td>
</tr>
</tbody>
</table>

For more information please contact marketing@oxfordglobal.co.uk
### 17.30 – 18.00

<table>
<thead>
<tr>
<th>Conference Room 1: Morangis</th>
<th>Conference Room 2: Chalon &amp; Reims</th>
</tr>
</thead>
</table>
| **Identifying A New Mechanosensitive Gene Network By Fusing World-wide Studies**  
Blood flow is an essential contributor to plaque growth, composition and initiation. It is sensed by endothelial cells, which react to blood flow by expressing >1000 genes. The sheer number of genes implies that one needs genomic techniques to unravel their response in disease. Individual genomic studies have been performed but lack sufficient power to identify subtle changes in gene expression. In this study, we investigated whether a systematic meta-analysis of available microarray studies can improve their consistency.  
We identified 17 studies using microarrays, of which 6 were performed in vivo and 11 in vitro. The in vivo studies were disregarded due to the lack of the shear profile. Of the in vitro studies, a cross-platform integration of human studies (HUVECs in flow cells) showed high concordance (>90%). The human data set identified >1600 genes to be shear responsive, more than any other study and in this gene set all known mechanosensitive genes and pathways were present. A detailed network analysis indicated a power distribution (e.g. the presence of hubs), without a hierarchical organization. The avg. cluster coefficient was high and further analysis indicated an aggregation of 3 and 4 element motifs, indicating a high prevalence of feedback and feed forward loops, similar to prokaryotic cells.  
In conclusion, this initial study presented a novel method to integrate human-based mechanosensitive studies to increase its power. The robust network was large, contained all known mechanosensitive pathways and its structure revealed hubs, and a large aggregate of feedback and feed forward loops.  
Rob Krams, Professor of Molecular Bioengineering, Imperial College London | **Single-cell Epigenomic Analysis In Arabidopsis**  
- Induced cell reprogramming does not require global epigenetic changes  
- Environmental stress creates epigenomic changes that are heritable  
Jose Gutierrez-Marcos, Professor, University of Warwick |

### 18.00
End of Conference