PROGRAM | MONDAY MARCH 20

Parallel Session AM1 Okapi Room	Darwin Hall Parallel session AM 2
Chair: Stefaan Derveaux	Chair: Mark Veugelers

08:45 - 09:15 Registration & coffee

09:15 - 09:20 Welcome

POPULATION-SCALE AND CLINICAL SEQUENCING

09:20 - 09:55 Contribution of non-coding DNA to complex traits and cancer
Emmanouil Dermitzakis, *University of Geneva, CH*

09:55 - 10:20 True Single Molecule Sequencing (tSMS™) for the Precision Medicine Era
Elizabeth Reczek, *CEO, SeqLL, US*

10:20 - 10:55 National Scale Cancer Genome Sequencing in the Netherlands
Edwin Cuppen, *UMC Utrecht and Hartwig Medical Foundation, NL*

10:55 - 11:00 Sponsored talk: Covaris: Gold standard sample preparation for NGS
Soraya Mezaib, *Territory Manager Southern Europe, Covaris, FR*

11:00 - 11:25 Coffee break

11:25 - 11:50 Population Scale Sequencing: Genomic Insights From Sequencing Over 10,000 Human Genomes
William Biggs, *Head of Genomic Sequencing , Human Longevity, US*

11:50 - 12:25 From Genomic Variation to Molecular Mechanism
Jan Korbel, *EMBL, DE*

12:25 - 13:30 Lunch

13:30 - 14:15 Poster session

SINGLE CELL GENOMICS

09:20 - 09:55 Single cell Epigenomics
Amos Tanay, *Weizmann Institute of Science, IL*

09:55 - 10:20 High-throughput Clonal Analysis of tumors with droplet Microfluidics
Dennis Eastburn, *CSO, Mission Bio, US*

10:20 - 10:45 Illumina®|Bio-Rad® Single-Cell RNASeq Solution
Ronald Lebofsky, *Sr. Staff Scientist, Advanced Research, Digital Biology Center, Bio-Rad, US*

10:45 - 10:50 Sponsored talk: PerkinElmer genomic solutions to accelerate your NGS workflow from start to finish
Gawain Bennett , *Field Applications Specialist, PerkinElmer, UK*

10:50 - 11:25 Coffee break

11:25 - 11:50 The future of targeted resequencing
Jurgen Del-Favero, *CSO, Multiplicom, BE*

11:50 - 12:25 Computational methods for dissecting the transcriptome and epigenome diversity between single cells
Oliver Stegle, *EMBL-EBI, UK*

12:25 - 13:30 Lunch

13:30 - 14:15 Poster session

Parallel Session PM1   Okapi Room

Darwin Hall   **Parallel session PM 2**

Chair: Diether Lambrechts

Chair: Halina Novak

EMERGING DNA SEQUENCING TECHNOLOGIES

14:15 - 14:50   Nanopore Sequencing and Picometer-Resolution Measurements of Enzymes
Jens Gundlach, *University of Washington, US*

14:50 - 15:15   Roche Nanotag Sequencing Platform
Steven Henck, *Vice President at Genia Subsidiary of Roche Molecular Systems, US*

15:15 - 15:40   The Chromium™ System: Delivering Linked-Reads and Single Cell gene expression for improved genomics
Geoff McDermott, *Senior Staff Scientist, 10x genomics, US*

15:40 - 15:45   Sponsored talk: Using high-throughput QC to democratize NGS sample prep
Tony Montoye, *Head of Marketing and Applications, Trinean, BE*

15:45 - 16:15   Coffee break

16:15 - 16:50   Recognition Tunneling – a Super-sensitive Readout for Sequencing DNA and other Heteropolymers
Stuart Lindsay, *Arizona State University, US*

16:50 - 17:15   Technologies in Single Cell Gene Expression
Willem Welboren, *BD Biosciencesn NL*

17:15 - 17:40   The Latest Developments in Nanopore Sequencing of DNA and RNA
Clive Brown, *CTO, Oxford Nanopore, UK*

17:40 - 18:40   Reception

CURRENT APPLICATIONS AND PLATFORMS FOR APPLIED NGS

14:15 - 14:50   International Space Station and Earth-based remote single-molecule sequencing
Christopher Mason, *Weill Cornell Medicine, US*

14:50 - 15:25   Understanding melanoma intra-tumor heterogeneity and therapy resistance through lineage-tracing and single-cell sequencing approches
Jean-Christophe Marine, *VIB-KU Leuven Center for Cancer Biology, BE*

15:25 - 15:50   Improved Genome Sequencing Using an Engineered Transposase
Molly He, *Senior Director, Protein Engineering & Sequencing, Illumina, US*

15:50 - 15:55   Sponsored talk: Advanced Analytical Technologies: Current Applications and Platforms for Applied NGS
Markus Tilmes, *European Sales Manager, Advanced Analytical Technologies Inc., US*

15:55 - 16:15   Coffee break

16:15 - 16:50   Integrating Genome and Transcriptome NGS Data for Translational Oncology and Biomarker Discovery
Marie-Laure Yaspo, *MPI, DE*

16:50 - 17:15   Ion Torrent Sequencing – tools for oncology, inherited and infectious disease
Andy Felton, *VP Marketing & Product Management, Ion Torrent Business, US*

17:15 - 17:50   Single cell transcriptomics to uncover the rules governing stem cell biology
Ana Martin-Villalba, *DKFZ, DE*

17:40 - 18:40   Reception

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EPIGENOMICS

09:15 - 09:50   Mechanisms of Epigenetic Regulation in Stem cells and Development
Alexander Meissner, *Harvard, US*

09:50 - 10:25   Visualization of transcription initiation genome-wide at single molecule resolution
Dirk Schübeler, *FMI, CH*

10:25 - 10:50   Epigenetics and Human Aging
Xiaojing Yang, *Scientist, Zymo Research Corporation, US*

10:50 - 10:55   Sponsored talk: Lexogen: QuantSeq: an ideal gene expression profiling protocol ensures high multiplexing, sensitivity and reproducibility at lowest costs
Lukas Paul, *Senior Manager of Scientific Affairs, Lexogen GmbH, CH*

10:55 - 11:20   Coffee break

11:20 - 11:55   DNA 5hmC as biomarker for human diseases
Chuan He, *University of Chicago, USA*

11:55 - 12:30   A two-way interaction between hypoxia and DNA methylation in tumors
Diether Lambrechts, *VIB-KU Leuven Center for Cancer Biology, BE*

12:30 - 13:30   Lunch

13:30 - 14:00   Poster session

LONG READS, GENOME STRUCTURE AND GENOME MAPPING

09:15 - 09:50   Towards population-level microbiome monitoring: the Flemish Gut Flora Project
Jeroen Raes, *VIB-KU Leuven Center for Microbiology, BE*

09:50 - 10:25   Multi-Contact Chromosome Conformation Capture and Non-Invasive Prenatal Diagnosis for Monogenetic Diseases
Wouter de Laat, *Hubrecht Institute, NL*

10:25 - 10:50   Advancing biological understanding with chromosome-scale genome assemblies
Todd Dickinson, *CEO, Dovetail Genomics, US*

10:50 - 11:20   Coffee break

11:20 - 11:45   Advancements in Sequel™ SMRT Sequencing to better enable applications such as SV detection, minor variant detection, isoform sequencing and de novo genome assembly
Kevin Corcoran, *Sr. VP of Marketing Development, Pacific Biosciences, US*

11:45 - 12:20   Genomic Drivers and Cellular Determinants of Cancer Metastasis and Immunity at Single Molecule and Cell Resolution
Hanlee Ji, *Stanford School of Medicine, US*

12:30 - 13:30   Lunch

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NEXT-GEN TRANSCRIPTOMICS

14:00 - 14:35	Single-cell genomics: from one cell to millions of cells **Peter Kharchenko,** *Harvard Medical School, US*
14:35 - 15:10	Gene expression regulation at high resolution **Stirling Churchman,** *Harvard, US*
15:10 - 15:35	RNA capture sequencing enabled liquid biopsy screening **Jo Vandesompele,** *CSO, Biogazelle, BE*
15:35 - 16:00	Coffee break
16:00 - 16:35	Single-cell RNA-seq-based characterisation of somatic stem cells **Bart Deplancke,** *EPFL Lausanne, CH*
16:35 - 17:00	Exploring the space of 2D RNA sequencing **Florian Baumgartner,** *Interim CEO Spatial Transcriptomics, SE*
17:00 - 17:35	Ribose-Map: A Bioinformatics Toolkit to Profile rNMPs Embedded in DNA **Alli Gombolay,** *Georgia Institute of Technology, US*
17:35 - 17:45	Closing remarks

COMPUTATIONAL GENOMICS AND DATA ANALYSIS

14:00 - 14:35	Fast, Scalable Prediction of Deleterious Noncoding Variants from Genomic Data **Adam Siepel,** *CSHL, US*
14:35 - 15:10	Assessment of metastatic disease burden through the analysis of cfDNA in patients' circulation **Francesca Demichelis,** *University Trento, IT*
15:10 - 15:35	Genestack – metadata management, reproducible pipelines and interactive analytics for enterprise bioinformatics R&D **Misha Kapushesky,** *CEO, Genestack, UK*
15:35 - 16:00	Coffee break
16:00 - 16:35	The genomic landscape of osteoarthritis **Eleftheria Zeggini,** *Wellcome Trust Sanger Institute, UK*
16:35 - 17:00	Bringing NGS Analytics from the Research Lab to the Clinic **Hans Cobben,** *CEO, Bluebee, NL*
17:00 - 17:25	Improving Algorithms & Research Results with Large Scale Data in Genomics **Deniz Kural,** *CEO, Seven Bridges Genomics, US*
17:25 - 17:35	Closing remarks