

08:30 - 09:00 Registration & coffee

09:00 - 09:05 Welcome

Plenary session 1

Hall: James Cook

## LONG READS, GENOME STRUCTURE AND MAPPING

Chair: Mojca Strazisar

09:05 - 09:40 Long nanopore reads in the clinic  
**Nick Loman**, *University of Birmingham, UK*

09:40 - 10:05 HiFi long reads for comprehensive genomic analysis  
**Ralph Vogelsang**, *Pacific Biosciences, DE*

10:05 - 10:40 Applications of modification detection in nanopore sequencing  
**Winston Timp**, *Johns Hopkins University, Baltimore, Maryland, US*

10:40 - 11:05 From lizards to clinical genomes: the importance of recapturing long range genomic information  
**Todd Dickinson**, *Dovetail Genomics, US*

11:05 - 11:35 Coffee break

11:35 - 12:10 The Bat1k project: bat genomes, biology, and implications  
**Sonja Vernes**, *MPI, NL*

12:10 - 12:35 How will Nanopore Technology develop in 2019?  
**Clive Brown**, *Oxford Nanopore, UK*

12:35 - 12:50 Selected talk: Structural variants identified by long read human genome sequencing  
**Wouter De Coster**, *VIB-UAntwerp Center for Molecular Neurology, BE*  
(Abstract #10)

12:50 - 13:35 Lunch

13:35 - 14:20 Poster session

## EPIGENOMICS

Chair: Bernard Thienpont

- 14:20 - 14:55** Single-cell epigenome landscape of development and ageing  
**Wolf Reik**, Babraham Institute, UK
- 14:55 - 15:20** Enabling ultra-low sample inputs and streamlining NGS workflows for epigenetic and other applications  
**Vladimir Makarov**, Swift Bioscience, US
- 15:20 - 15:55** Hit-and-run epigenetic editing prevents senescence entry in primary breast cells from healthy donors  
**Emily Saunderson**, Barts Cancer Institute, Queen Mary University of London, UK
- 15:55 - 16:10** Selected abstract: Specialization and plasticity of biological systems: when social insects teach us to look further up  
**Solenn Patalano**, Fleming Institute, GR (Abstract #38)
- 16:10 - 16:15** Sponsored talk: TeloPrime for cap-specific full-length RNA sequencing on Nanopore and PacBio platforms  
**Lukas Paul**, Senior Manager of Scientific Affairs, Lexogen, AT
- 16:15 - 16:50** Coffee break
- 16:50 - 17:15** Revealing the living genome: direct decoding of DNA, RNA and modified bases using Depixus' novel technology  
**Gordon Hamilton**, Depixus, FR
- 17:15 - 17:50** Sequencing-based functional readouts to probe genome regulation  
**Bas Van Steensel**, NKI, NL
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- 17:50 - 19:00** Reception
- 19:00 - 20:00** Social program
- 20:00 - 22:30** Conference dinner

## METAGENOMICS

Chair: Jeroen Raes

- 14:20 - 14:55** Tara oceans: Eco-systems biology at planetary scale  
**Chris Bowler**, IBENS, FR
- 14:55 - 15:30** Human skin microbiome: Trans-kingdom, host-immune interactions  
**Julie Segre**, National Human Genome Research Institute, NIH, US
- 15:30 - 16:05** Uncovering extensive species and strain-level diversity in the human microbiome  
**Nicola Segata**, CIBIO - University of Trento, IT
- 16:05 - 16:20** Selected abstract: Characterization of microbial communities in harsh environments  
**Camilla Urbaniak**, NASA-JPL, US (Abstract #50)
- 16:20 - 16:25** Sponsored talk: Fully automated NGS approach for bacterial and fungal communities analysis  
**Pedro Echave**, NGS Sample Prep Expert, Perkin Elmer, BE
- 16:25 - 16:50** Coffee break

08:30 - 09:00 Coffee

Parallel session 3

Hall: James Cook

## EMERGING TECHNOLOGIES

Chairs: Stefaan Derveaux & Silvie Van den Hoecke

- 09:00 - 09:35** Spatial genomics: dynamics and organization of the nascent transcriptome by Intron SeqFISH  
**Long Cai**, *California Institute of Technology, US*
- 09:35 - 10:00** In situ sequencing – the next generation tissue analysis  
**Malte Kühnemund**, *Cartana, SE*
- 10:00 - 10:35** Spatially resolved transcriptomics using targeted in situ sequencing  
**Mats Nilsson**, *Stockholm University, SE*
- 10:35 - 10:40** Sponsored talk: Advances in single-cell RNA-seq for deciphering mechanisms of disease  
**Matthieu Pesant**, *NGS product manager - scientific support specialist, Takara Bio Europe, FR*
- 10:40 - 11:10** Coffee break
- 11:10 - 11:45** The fabric of the neocortex  
**Andreas Tolias**, *Baylor College of Medicine, US*
- 11:45 - 12:10** Development of an automated system to process solid tissues into single cells and nuclei  
**John Bashkin**, *S2 Genomics, US*
- 12:10 - 12:45** Building Chromatin: Histone variants and chaperones at work  
**Genevieve Almouzni**, *Institut Curie, PSL Research University, FR*

**12:45 - 13:30** Lunch

**13:30 - 14:15** Poster session

Hall: Orangerie

Parallel session 4

## POPULATION SCALE AND CLINICAL SEQUENCING

Chair: Bernard Thienpont

- 09:00 - 09:35** Long-read sequencing of structurally variant genomes  
**Evan Eichler**, *University of Washington, US*
- 09:35 - 10:00** An industry interface into population genomics at scale  
**Paul Jones**, *Illumina, US*
- 10:00 - 10:35** Medical genetics: Identification of hidden structural variants with long-read sequencing  
**Alexander Hoischen**, *Radboud University Medical Center, NL*
- 10:35 - 10:40** Sponsored talk: Taking PCR to the next level : Bio-Rad's droplet PCR applications  
**Koen De Gelas**, *Regional Sales Specialist ddPCR, Bio-Rad, BE*
- 10:40 - 11:10** Coffee break
- 11:10 - 11:35** rhAmpSeq™ -- a novel, elegant targeted amplicon sequencing system leveraging the power of IDT's proprietary rhPCR chemistry  
**Allen Nguyen**, *Integrated DNA Technologies, US*
- 11:35 - 12:10** Implementation of clinical grade whole genome sequencing: the Genome Analytics Platform  
**Joris Vermeesch**, *KU Leuven, BE*
- 12:10 - 12:35** Bionano genome mapping: high-throughput mapping of structural variation in cancer and genetic disease  
**Yannick Delpu**, *Bionano Genomics, US*

## SINGLE CELL

Chairs: Bernard Thienpont & Silvie Van den Hoecke

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- 14:15 - 14:50** Reconstructing tissue architecture by single cell genomics  
**Sarah Teichmann**, *Wellcome Sanger institute, UK*
- 14:50 - 15:15** Accelerating biology: 10x Genomics products and vision  
**Serge Saxonov**, *10XGenomics, US*
- 15:15 - 15:50** Preventing therapy-induced cancer stemness  
**Jean-Christophe Marine**, *VIB-KU Leuven Center for Cancer Biology, BE*
- 15:50 - 16:15** Proteomics in the era of high-throughput single-cell sequencing via TotalSeq™  
**Kristopher Nazor**, *BioLegend, US*
- 16:15 - 16:45** Coffee break
- 16:45 - 17:00** Selected abstract: Single cell profiling of different cancer types before and during immune checkpoint therapy  
**Marlies Vanden Bempt**, *VIB-KU Leuven Center for Cancer Biology, BE*  
*(Abstract #55)*
- 17:00 - 17:25** High-resolution analysis of tumor architecture and evolution with single-cell DNA sequencing  
**Dennis Eastburn**, *Mission Bio, US*
- 17:25 - 18:00** Single-cell multi-omics to study DNA mutation, genetic heterogeneity and disease  
**Thierry Voet**, *KU Leuven, BE*
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- 18:00 - 18:10** Closing remarks & poster award