

- 08:30 – 09:30 **Registration**
- 09:30 – 09:45 **Welcome**
Gordon Sanghera, Oxford Nanopore Technologies Ltd
- 09:45 – 10:35 **Plenary session 1**
Karen Miga, *Linear assembly of a human Y centromere using MinION nanopore long read sequences*
Björn Usadel, *Complex tomato genomes: Easy with nanopores*
- 10:35 – 11:30 **Coffee & Live Lounge, Flow cell loading zone, MinKNOW clinic & Albacore clinic**
Mini Theatre: **Josh Quick**, *Thar she blows! Ultra-long read methods for nanopore sequencing*
- 11:30 – 11:55 **Plenary session 2**
Jared Simpson, *Analysis tools for nanopore data*
- 11:55 – 12:45 **Lightning talks** (6 x five minute talks)
- 12:45 – 14:00 **Lunch, posters, Live Lounge, Flow cell loading zone, MinKNOW clinic & Albacore clinic**
Mini Theatre: **Tim Massingham**, *Developments in basecalling*
- 14:00 – 15:15 **Plenary session 3**
Daniel Turner, *Nanopore Applications*
Eric van der Helm & Lejla Imamovic, *Rapid resistome mapping using nanopore sequencing*
Philipp Euskirchen, *Rapid (epi-) genomic classification of brain tumors using nanopore sequencing*
- 15:15 – 16:00 **Coffee, posters & Live Lounge, Flow cell loading zone, MinKNOW clinic & Albacore clinic**
Mini Theatre: **James Brayer**, *Introduction to nanopore sensing*
- 16:00 – 17:10 **Breakout room 1. Applications and Analysis: "Metagenomics" and microbiomes**
Aleida Hommes - de Vos van Steenwijk, *Using MinION for next generation environmental monitoring*
Sarah Stewart Johnson, *Nanopore Sequencing as a Tool for Exploration*
Richard Leggett, *Real-time microbial disease diagnostics with MinION and NanoOK*
Mick Watson, *Mining microbial dark matter in ruminants*
- 16:00 – 17:10 **Breakout room 2. Applications: Epigenetics and methylation**
Marcus Stoiber, *Applications of raw nanopore signal processing: From modified bases to streaming basecalling and beyond*
Winston Timp, *Measuring DNA methylation with the MinION*
Miten Jain, *Recent progress at UCSC: long reads, DNA, and RNA sequencing*
- 16:00 – 17:10 **Breakout room 3. Data Analysis: Consensus accuracy & variant calling**
Chris Wright, *Real-time assembly of MinION sequencing data*
Ryan Wick, *Hybrid Nanopore and Illumina assembly: working towards the perfect bacterial genome*
Damien Tully, *Characterizing the dynamics of HIV and HCV Evolution within hosts using MinION nanopore sequencing*
- 16:00 – 17:10 **Mini Theatre. Data Analysis: Getting started with data analysis**
Amber Wright, Oxford Nanopore Technologies Ltd
Sergey Koren, *Who needs genome assembly in the age of ultra-long reads*
Kim Judge, *The Long and Short of it: understanding your data*
- 17:10 – 18:00 **Prosecco reception**
- 18:00 – 18:45 **Plenary session 4**
Clive Brown, Oxford Nanopore Technologies Ltd
- 18:45 – 23:00 **Drinks reception and dinner plus evening speaker**

- 08:30 – 09:30 **Registration**
- 09:30 – 09:45 **Welcome back**
Gordon Sanghera, Oxford Nanopore Technologies Ltd
- 09:45 – 10:10 **Plenary session 5**
Nick Loman, University of Birmingham, UK
- 10:10 – 11:00 **Lightning talks** (6 x five minute talks)
- 11:00 – 11:45 **Coffee, posters & Live Lounge, Flow cell loading zone, MinKNOW clinic & Albacore clinic**
Mini Theatre: **Denis Milan**, *GeT experience of long read sequencing using the available technologies*
- 11:45 – 13:00 **Breakout room 1. Applications: RNA and cDNA**
John Tyson, *Transcriptomic analysis via direct RNA sequencing and contextual splice variation*
Rachael Workman, *Comparison of direct RNA and cDNA sequencing of C. elegans*
Chris Vollmers, *Identifying and quantifying transcript isoforms in single-cell nanopore RNA-seq data*
Andrew Smith, *Direct nanopore sequencing of canonical and modified bases in 16S ribosomal RNA*
- 11:45 – 13:00 **Breakout room 2. Applications: Targeted techniques**
Andy Heron, *Enrichment and sensitivity methods*
Tsilil Gabrieli, *Cas9-Assisted Targeting of CHromosome segments (CATCH) for targeted nanopore sequencing and optical genome mapping*
Alfonso Benítez-Páez, *Multi-locus amplicon sequencing approach to study microbial diversity at species level*
- 11:45 – 13:00 **Breakout room 3. Applications and Analysis: Pathogens and microbiology**
Oliver Pybus, *Genomic epidemiology of Zika virus in the Americas*
Satomi Mitsuhashi, *A portable system for rapid bacterial composition analysis using the MinION and a laptop computer*
Zamin Iqbal, *Same-day tuberculosis diagnostic and surveillance information direct from sputum*
Justin O'Grady, *Developing rapid sample-to-result diagnostic workflows on the MinION*
- 11:45 – 13:00 **Mini Theatre. Applications and Data Analysis: Structural variation analysis — revealing the "inaccessible genome"**
Wigard Kloosterman, *Mapping and phasing of structural genomic variation in patient genomes using nanopore sequencing*
Tom Sasani, *Tracking adaptive structural variation during host-pathogen conflict*
Sudha Rao, *Balanced translocation breakpoint mapping at single base resolution using long read nanopore sequencing technology*
- 13:00 – 14:15 **Lunch, posters, Live Lounge, Flow cell loading zone, MinKNOW clinic & Albacore clinic**
Mini Theatre: **David Deamer**, *Is there life on Enceladus, Europa and Mars? Nanopore devices as biosensors*
- 14:15 – 15:15 **Plenary panel session (6): Larger genomes**
Raymond Hulzink, *Crop innovation using nanopore sequencing*
Ivo Gut, *Assembly of vertebrate genomes with nanopore sequences*
Christiaan Henkel, *Lightweight sequencing of massive genomes*
- 15:15 – 16:00 **Coffee, posters & Live Lounge, Flow cell loading zone, MinKNOW clinic & Albacore clinic**
Mini Theatre: **Jackie Evans**, *Your Nanopore Community*
- 16:00 – 16:25 **Plenary session 7**
Kazuhara Arakawa, *Untangling the spider silk genes using nanopore long reads*
- 16:25 – 16:40 **Closing remarks**
Gordon Sanghera, Oxford Nanopore Technologies Ltd
- 16:40 – 18:00 **Cheese and wine**

Live Lounge activities: Thursday 4th May 2017

10:35 – 11:30 COFFEE BREAK

- 10:35 – 11:30 MinKNOW and Albacore clinics
- 10:40 – 10:50 Product tables: VoITRAX demo
- 10:55 – 11:10 Data analysis tools: [Marcus Stoiber](#) – nanoraw & basecRAWlller
- 10:55 – 11:25 Mini Theatre: [Josh Quick](#) – *Thar she blows! Ultra-long read methods for nanopore sequencing*
- 11:05 – 11:25 Flow cell loading zone: Session 1

12:45 – 14:00 LUNCH

- 12:45 – 14:00 MinKNOW and Albacore clinics
- 12:50 – 13:05 Data analysis tools: [Matt Loose](#) – MinoTOUR
- 13:10 – 13:20 Product tables: PromethION demo
- 13:15 – 14:00 Posters: Session 1 poster presenters
- 13:25 – 13:45 Mini Theatre: [Tim Massingham](#) – *Developments in basecalling*
- 13:30 – 13:50 Flow cell loading zone: Session 2
- 13:40 – 13:55 Data analysis tools: [Scott Gigante](#) – Picopore

15:15 – 16:00 COFFEE BREAK

- 15:15 – 16:00 MinKNOW and Albacore clinics
- 15:20 – 15:30 Product tables: VoITRAX demo
- 15:30 – 15:50 Mini Theatre: [James Brayer](#) – *Introduction to nanopore sensing*
- 15:35 – 15:55 Flow cell loading zone: Session 3
- 15:40 – 15:55 Data analysis tools: [Christiaan Henkel](#) – TULIP

Live Lounge activities: Friday 5th May 2017

11:00 – 11:45 COFFEE BREAK

- 11:00 – 11:45 MinKNOW and Albacore clinics
- 11:05 – 11:15 Product tables: PromethION demo
- 11:10 – 11:40 Posters: Session 2 poster presenters
- 11:15 – 11:45 Mini Theatre: [Denis Milan](#) – *GeT experience of long read sequencing using the available technologies*
- 11:20 – 11:40 Flow cell loading zone: Session 4
- 11:25 – 11:40 Data analysis tools: [Richard Leggett](#) – NanoOK

13:00 – 14:15 LUNCH

- 13:00 – 14:15 MinKNOW and Albacore clinics
- 13:20 – 13:30 Product tables: VoITRAX demo
- 13:30 – 13:50 Mini Theatre: [David Deamer](#) – *Is there life on Enceladus, Europa and Mars? Nanopore devices as biosensors*
- 13:40 – 14:00 Flow cell loading zone: Session 5
- 13:45 – 14:00 Data analysis tools: [Sergey Koren](#) – CANU

15:15 – 16:00 COFFEE BREAK

- 15:15 – 16:00 MinKNOW and Albacore clinics
- 15:15 – 16:00 Mini Theatre: [Jackie Evans](#) – *Your Nanopore Community*
- 15:30 – 15:40 Product tables: PromethION demo
- 15:40 – 16:00 Flow cell loading zone: Session 6
- 15:45 – 16:00 Data analysis tools: [Wigard Kloosterman](#) – NanoSV