Nanopore Community Meeting 2017
The Metropolitan Pavilion, New York

08:30 – 09:30	**Registration and breakfast**	Full Pavilion
09:30 – 09:45	**Welcome** **Gordon Sanghera**, Oxford Nanopore Technologies Ltd	Auditorium
09:45 – 10:35	**Plenary session 1** **Nick Loman**, The sequencing singularity? **Sissel Juul**, Applications in genetics and genomics using nanopore DNA, cDNA and direct RNA sequencing	Auditorium
10:35 – 11:30	**Coffee, Demo zone, posters, Data analysis tools, Flow cell loading zone, MinKNOW, Albacore & Library preparation clinics**	Full Pavilion
11:30 – 12:45	**Breakout room 1. Applications and analysis: Structural variations** **Joseph Schacherer**, Yeast genome assembly and structural variant mapping using nanopore sequencing **Svetlana Madjunkova**, Nanopore sequencing (MinION) for comprehensive Preimplantation Genetic Diagnosis (PGD) of chromosomal rearrangements **Chia-Lin Wei**, Nanopore sequencing reveals high-resolution structural variation in the cancer genome	Full Pavilion
11:30 – 12:45	**Breakout room 2. Applications and analysis: RNA and cDNA** **Intawat Nookaew**, Transcriptional landscapes analysis through direct RNA sequencing **Stéphane Le Crom**, RNA sequencing and data analysis using the MinION system **Matthew Keller**, Direct RNA sequencing of influenza viral RNA using the MinION nanopore sequencer **Martin Smith**, 'Squiggle'-cell sequencing	The Suite
11:30 – 12:45	**Breakout room 3. Data analysis: Completing genomes** **Sergey Koren**, Can nanopore sequencing finally finish the human genome? **Ryan Wick**, Assembly is still hard: Challenges in genome assembly in the era of long reads **Conrad Stack**, Validation of low-cost, long-read sequencing for crop pangenomics	The Suite
12:45 – 14:15	**Lunch, Demo zone, posters, Data analysis tools, Flow cell loading zone, MinKNOW, Albacore & Library preparation clinics** **Breakout room 1: Baptiste Mayjonade**, Best practice to maximize throughput with nanopore technology & *de novo* sequencing of bacterial strains of *Xanthomonas campestris* and genetic lines of *Arabidopsis thaliana* **Breakout room 1: Winston Timp**, Extracting DNA for nanopore sequencing in the Redwood Genome Project	Full Pavilion
14:15 – 14:55	**Plenary session 2** **Lightning talks** (6 x five-minute talks)	Auditorium
14:55 – 15:20	**Steven Salzberg**, Assembly of large genomes using Oxford Nanopore and Illumina data	Auditorium
15:20 – 16:10	**Coffee, Demo zone, posters, Data analysis tools, Flow cell loading zone, MinKNOW, Albacore & Library preparation clinics**	Full Pavilion
16:10 – 17:10	**Plenary session 3** **Clinical and public health panel plenary** **Justin O'Grady**, Rapid metagenomic diagnosis of hospital-acquired pneumonia **Alban Ramette**, Applications of nanopore sequencing technologies to whole genome sequencing of human viruses in the clinical setting **Claire Jenkins**, Use of Oxford Nanopore technology in the *E. coli* Reference Laboratory at Public Health England	Auditorium
17:10 – 17:35	**Bjarni V. Halldórsson**, Using long-read Oxford Nanopore sequencing for population-scale human genetics	Auditorium
17:35 – 18:00	**The Nanopore Human RNA Consortium** **Winston Timp and Miten Jain,** Direct RNA and cDNA sequencing of the human transcriptome	Auditorium
18:00 – 23:00	**Drinks reception and dinner plus evening speaker**	The Level

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08:30 – 09:00	**Registration**	Full Pavilion
09:00 – 09:10	**Welcome back** **Gordon Sanghera**, Oxford Nanopore Technologies Ltd	Auditorium
09:10 – 09:35	**Plenary session 4** **Patricia Simner**, Applying nanopore sequencing and real-time antimicrobial resistance gene analysis to address the threat of carbapenem-resistant gram-negative organisms	Auditorium
09:35 – 10:00	**Lightning talks** (4 x five-minute talks)	Auditorium
10:00 – 11:00	**Coffee, Demo zone, posters, Data analysis tools, Flow cell loading zone, MinKNOW, Albacore & Library preparation clinics**	Full Pavilion
11:00 – 12:15	**Breakout room 1. Data analysis: Epigenetics** **Alexa McIntyre**, Detecting m6A in bacterial DNA **Marcus Stoiber**, Tombo: Detection of modified nucleotides from raw nanopore sequencing data **Scott Gigante**, Direct determination of mouse genome-wide, allele-specific DNA methylation from nanopore long-read sequencing **Yunfan Fan**, Bacterial DNA modifications with nanopore sequencing	Full Pavilion
11:00 – 12:15	**Breakout room 2. Applications and analysis: Metagenomics, microbiomes and microbiology** **Arwyn Edwards**, MinION microbiome profiling: Going from on-the-go to go-to? **Mads Albertsen**, Genome-centric metagenomics in the long-read era **Anika Kinkhabwala**, Understanding phage-bacterial host interactions for smarter therapeutics **Jon Jerlström Hultqvist**, Nanopore sequencing for genomics of heterotrophic protists	The Suite
11:00 – 12:15	**Breakout room 3. Applications and analysis: Larger genomes** **Kim Judge**, Sanger sequencing: Using GridION for large genomes in a core facility **Taco Jesse**, Exploring new horizons in plant breeding using nanopore sequencing **Todd Michael**, High-molecular-weight DNA enables ultra-long reads for genome assembly	The Suite
12:15 – 13:15	**Lunch, Demo zone, posters, Data analysis tools, Flow cell loading zone, MinKNOW, Albacore & Library preparation clinics** **Breakout room 1: Andy Davies**, Nanopore Services & GridION Certification	Full Pavilion
13:15 – 13:35	**Plenary session 5** **Eshita Sharma**, Nanopore cDNA sequencing produces complex transcriptomes for sensitive and accurate gene expression profiling	Auditorium
13:35 – 14:00	**Lightning talks** (4 x five-minute talks)	Auditorium
14:00 – 14:25	**Michael Clark**, Elucidating the expression and splicing patterns of neuropsychiatric disease genes in the human brain	Auditorium
14:40 – 15:20	**Birds of a Feather** (5 different attendee-selected discussion forums)	
15:20 – 16:00	**Coffee, Demo zone, posters, Data analysis tools, Flow cell loading zone, MinKNOW, Albacore & Library preparation clinics**	Full Pavilion
16:00 – 16:25	**Plenary session 6** **Polling panel plenary** **Jared Simpson, Karen Miga and Sophie Zaaijer**	Auditorium
16:25 – 16:50	**Charles Chiu**, Metagenomic nanopore sequencing for precision diagnosis of infectious diseases	Auditorium
16:50 – 17:00	**Closing remarks** **Gordon Sanghera**, Oxford Nanopore Technologies Ltd	Auditorium

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Demo zone activities: Thursday 30th November 2017

10:35 – 11:30	**Coffee break**

10:45 – 11:25	MinKNOW, Albacore and Library preparation clinics
10:50 – 11:00	Product tables: PromethION demo
10:50 – 11:15	Delegate poster presentations
11:05 – 11:25	Flow cell loading zone: Session 1

12:45 – 14:15	**Lunch**

12:55 – 14:05	MinKNOW, Albacore and Library preparation clinics
12:55 – 13:05	Product tables: VolTRAX demo
13:10 – 13:30	Flow cell loading zone: Session 2
13:10 – 13:35	Breakout room 1: **Baptiste Mayjonade**, Best practice to maximize throughput with nanopore technology & *de novo* sequencing of bacterial strains of *Xanthomonas campestris* and genetic lines of *Arabidopsis thaliana*
13:45 – 14:05	Breakout room 1: **Winston Timp**, Extracting DNA for nanopore sequencing in the Redwood Genome Project
13:25 – 13:35	Data analysis tools: **Oxford Nanopore Technologies**, EPI2ME
13:40 – 14:10	Data analysis tools: **Ryan Wick**, Porechop, Filtlong and Unicycler

15:20 – 16:10	**Coffee break**

15:25 – 15:55	MinKNOW, Albacore and Library preparation clinics
15:25 – 15:50	Delegate poster presentations
15:30 – 15:40	Product tables: PromethION demo
15:45 – 16:05	Data analysis tools: **Alexa McIntyre**, mCaller

Demo zone activities: Friday 1st December 2017

10:00 – 11:00	**Coffee break**

10:15 – 10:55	MinKNOW, Albacore and Library preparation clinics
10:10 – 10:20	Product tables: VolTRAX demo
10:10 – 10:45	Delegate poster presentations
10:25 – 10:35	Data analysis tools: **Oxford Nanopore Technologies**, EPI2ME
10:25 – 10:45	Flow cell loading zone: Session 3
10:40 – 11:00	Data analysis tools: **Jared Simpson**, Nanopolish

12:15 – 13:15	**Lunch**

12:20 – 13:10	MinKNOW, Albacore and Library preparation clinics
12:25 – 12:35	Product tables: PromethION demo
12:25 – 12:50	Breakout room 1: **Andy Davies**, Nanopore services & GridION certification
12:40 – 13:00	Flow cell loading zone: Session 4
12:45 – 13:05	Data analysis tools: **Marcus Stoiber**, Tombo

15:20 – 16:00	**Coffee break**

15:25 – 15:55	MinKNOW, Albacore and Library preparation clinics
15:25 – 15:35	Product tables: VolTRAX demo
15:25 – 16:00	Delegate poster presentations
15:40 – 16:00	Flow cell loading zone: Session 5

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