

London Calling 2020 online – Agenda

17th June 2020 (from 12pm UK time): on-demand content, and Flow cell loading demo
18-19th June 2020: Live talks and on-demand content



LIVE CONTENT

Wednesday 17th June 2020

MINI THEATRE & DATA ANALYSIS THEATRE

Interactive flow cell loading demonstration with live Q&A

Wednesday 17th June at 16:00 UK time (BST) and 11:00 East USA (EDT)

NETWORKING

Chat with other delegates in the human & clinical research, microbiology & metagenomics, plant research, bioinformatics, and general networking rooms. Have one-to-one chats with speakers, poster presenters, and other delegates

Networking will be available:

17th June: 12:00 - 18:00 UK time (BST)
07:00 - 12:00 East USA (EDT)
18th - 19th June: 09:00 - 18:00 UK time (BST)
04:00 - 12:00 East USA (EDT)

LIVE LOUNGE

Product tables: showcasing nanopore technology across the entire sequencing workflow of Prepare, Sequence, and Analyse. Get the latest information and chat directly with the Oxford Nanopore team

Customer Services: order queries, getting started with nanopore, and general enquiries

Technical clinics: one-to-one support with our experts

Customer Services and Technical clinics will be available:

17th June: 12:00 - 18:00 UK time (BST)
07:00 - 12:00 East USA (EDT)
18th - 19th June: 09:00 - 18:00 UK time (BST)
04:00 - 12:00 East USA (EDT)

ON-DEMAND CONTENT

LIVE LOUNGE:

Product tables showcasing nanopore technology across the entire sequencing workflow of Prepare, Sequence, and Analyse

MINI THEATRE & DATA ANALYSIS THEATRE:

Inspirational series of presentations available on demand throughout the conference

Flow cell loading demo

Adam Ameur, Nanopore off-target sequencing (Nano-OTS) reveals unforeseen CRISPR-Cas9 activity

Rebecca Richards, Investigation of Oxford Nanopore sequencing technologies for forensic purposes

Elizabeth Ross, Nanopore sequencing and animal agriculture

Juan Lobaton Garces, Honeybee pollen sequencing in apples

Glen Gowers, Snow, sledges, and sequencing: off-grid metagenomics on a polar expedition

Data Analysis Theatre: Presentations from the creators of a range of nanopore data analysis tools, available throughout the conference

Hasindu Gamaarachchi, Lightweight, portable and real-time embedded computing system for downstream nanopore data processing

Ploy Pratanwanich, xPore: Detection of differential RNA modifications from direct RNA sequencing

SECRET CINEMA:

Short presentations from our Lightning speakers:

Luyi Tian, Characterization of full-length isoforms in single cells with nanopore long-read sequencing

Aditya Deshpande, Nanopore sequencing of DNA concatemers reveals higher-order features of chromatin structure

Steffen Klasberg, kTypeR – accurate and efficient alignment-free HLA genotyping using nanopore sequencing

Kin Fai Au, MeSMLR-seq: identify multiple layers of epigenome at single long DNA molecules

Nick Vereecke, High-quality MinION and Flongle long-read nanopore genome assemblies of *Mycoplasma bovis* using taxon-specific training of the Bonito basecaller

Paola Cristina Resende, Tracking the re-emergence and spread of measles virus in Brazil: a pilot study using nanopore whole genome sequencing

Sarah Reiling, Nanopore PromethION sequencing identified structural variants in the French-Canadian population

Zaka Yuen, Systematic benchmarking of detection tools for CpG methylation from nanopore sequencing

Natalie Ring, DoGsTAiIs: Developing a nanopore-based diagnostic approach for the effective antibiotic treatment of canine infections

Sukanya Punthambaker, A biochemical DNA nanoscope that identifies and localizes over a hundred unique molecular features with nanometer accuracy

Oxford Nanopore Technologies movies:

A selection of inspirational short videos

- Totally off-grid nanopore sequencing
- DNA sequencing on board the Sikuliaq research vessel
- Fighting cassava viruses with nanopore sequencing
- Fighting TB in Madagascar, with real-time portable DNA sequencing
- Introduction to LamPORE

RESOURCE ROOM

Download Zoom backgrounds from the conference platform for selfies and download your certificate of attendance

KEYWORD SEARCH

Find content relative to your research area

POSTERS

View and download posters from Oxford Nanopore Technologies and those selected from abstract submissions, see separate poster agenda. Short narrated summaries also available to view. Don't forget to vote for your favourite poster!




ALL CONTENT AVAILABLE ON-DEMAND UNTIL 17TH JULY 2020




London Calling 2020 online – Agenda



LIVE CONTENT

Thursday 18th June 2020

	6:00 – 6:10	6:10 – 6:35	6:40 – 7:10	7:10 – 7:35	7:35 – 8:35	8:35 – 9:05	9:05 – 9:30	9:30 – 10:00	10:00 – 11:30	11:30 – 11:35
East USA (EDT)										
UK time (BST)										
 <p>Human & clinical research</p>	AUDITORIUM	AUDITORIUM	BREAKOUT ROOM Human & clinical research		Break	AUDITORIUM	AUDITORIUM	Break	AUDITORIUM	AUDITORIUM
	<p>Gordon Sanghera Welcome to London Calling 2020 online</p>	<p>Dafni Glinos Long-read sequencing of human tissues to study allelic effects on transcriptome structure</p>	<p>Human translational research Thidathip Wongsurawat GLIoma Molecular Marker Enrichment & Long-Read Sequencing (GLIMMERS) Matthew Parker Nanopore sequencing of C9orf72 in ALS. Usha R. Dutta Precise break point mapping of balanced reciprocal translocation cases using long-read sequencing</p>			<p>Filippo Martignano Nanopore sequencing and liquid biopsy: copy number variation analysis of short cell-free DNA from plasma of lung cancer patients</p>	<p>Julien Masliah-Planchon Rapid molecular subgrouping of medulloblastoma based on DNA methylation by nanopore sequencing</p>		<p>Dan Turner Rosemary Dokos James Clarke Stuart Reid Update from Oxford Nanopore Technologies</p>	Close out
 <p>Microbiology & metagenomics</p>	AUDITORIUM	AUDITORIUM	BREAKOUT ROOM Microbiology & metagenomics		Break	BREAKOUT ROOM Microbiology & metagenomics		Break	AUDITORIUM	AUDITORIUM
	<p>Gordon Sanghera Welcome to London Calling 2020 online</p>	<p>Dafni Glinos Long-read sequencing of human tissues to study allelic effects on transcriptome structure</p>	<p>Metagenomics Samuel Nicholls Long-read nanopore metagenomics for reconstruction of bacterial genomes Tânia Duarte Deep sequencing of microbial communities in cystic fibrosis airways Oscar Gonzalez-Recio Shedding light onto the causality forces of phenotypic expression in the holobiont organism</p>			<p>Microbiome Sonia Villapol Full-length 16S rRNA enabled analysis highlights the restoration of gut microbiota in a mouse model of Alzheimer's disease Yu Xia Oxford Nanopore-based metagenomic study on high-altitude permafrost microbiome Ryan Ziels Enabling high-accuracy long-read amplicon sequences using unique molecular identifiers</p>	<p>Dan Turner Rosemary Dokos James Clarke Stuart Reid Update from Oxford Nanopore Technologies</p>		Close out	
 <p>Plant research</p>	AUDITORIUM	AUDITORIUM	AUDITORIUM	AUDITORIUM	Break	BREAKOUT ROOM Plant research		Break	AUDITORIUM	AUDITORIUM
	<p>Gordon Sanghera Welcome to London Calling 2020 online</p>	<p>Dafni Glinos Long-read sequencing of human tissues to study allelic effects on transcriptome structure</p>	<p>Bernice Waweru & Allen Van Deynze The African Orphan Crops Consortium, alleviating stunting due to malnutrition one crop at a time</p>	<p>Ian Adams Application of the Flongle to protect UK plant health</p>		<p>Plant genomics Victor A. Albert Sequencing and assembling highly heterozygous and/or repeat-rich plant genomes using Oxford Nanopore technology Peter Emmrich Beware of Ogres: grass pea and the challenges of assembling large legume genomes Larissa Ramsay Bridging the gap: long reads enable more contiguous assembly of repeat-rich plant genomes</p>	<p>Dan Turner Rosemary Dokos James Clarke Stuart Reid Update from Oxford Nanopore Technologies</p>		Close out	

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	Gordon Sanghera Welcome back to London Calling 2020 online	Tracy Murphy Nanopore sequencing in mixed lineage leukemia	Genomic epidemiology panel Joseph Fauver Coast-to-coast spread of SARS-CoV-2 during the early epidemic in the United States Estée Török Rapid implementation of real-time SARS-CoV-2 sequencing to investigate healthcare-associated COVID-19 infections Jing Lu Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China George Githinji Building capacity for public health bioinformatics in East Africa using a portable sequencing platform		Human transcriptomics Chenchen Zu Single-molecule, full-length transcript isoform sequencing reveals disease-associated RNA isoforms Ricardo De Paoli-Iseppi Long-read sequencing of neuropsychiatric disorder risk gene isoforms in human brain Ying Chen The SG-NEX project: a resource for long-read nanopore RNA-Sequencing in 5 human cancer cell lines	Cancer research Mukta Asnani Complex exon structure of CD19 and CD22 mRNA isoforms revealed by long-read Oxford Nanopore sequencing Anna Dolnik Combining genomic and transcriptomic profiling allows real-time stratification of hematologic malignancies Touati Benoukraf Characterising structural variants in acute myeloid leukemia using low-depth nanopore sequencing		Benedict Paten Efficient <i>de novo</i> assembly of phased, telomere-to-centromere human genomes	Ariel Gershman Utilizing nanopore sequencing to investigate sugar flux in Ruby-throated hummingbirds		Close out		
 Microbiology & metagenomics	AUDITORIUM	AUDITORIUM	AUDITORIUM	Break	AUDITORIUM	AUDITORIUM	Break	BREAKOUT ROOM Microbiology & metagenomics		Break	AUDITORIUM	AUDITORIUM	AUDITORIUM
	Gordon Sanghera Welcome back to London Calling 2020 online	Tracy Murphy Nanopore sequencing in mixed lineage leukemia	Genomic epidemiology panel Joseph Fauver Coast-to-coast spread of SARS-CoV-2 during the early epidemic in the United States Estée Török Rapid implementation of real-time SARS-CoV-2 sequencing to investigate healthcare-associated COVID-19 infections Jing Lu Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China George Githinji Building capacity for public health bioinformatics in East Africa using a portable sequencing platform		Chongtao Ge Whole Genome Sequencing (WGS) and the food industry Matt Loose Nanopore adaptive sequencing for mixed samples, whole exome capture and targeted panels	Infectious disease Kayzad Nilgiriwala Diagnosis of tuberculosis by whole genome sequencing of DNA from sputum Amanda Warr Saving your bacon: nanopore sequencing of deadly porcine viruses in the Philippines Jonathan Abrahams Ultra-long nanopore reads uniquely demonstrate genome plasticity in <i>Bordetella pertussis</i>		Benedict Paten Efficient <i>de novo</i> assembly of phased, telomere-to-centromere human genomes	Ariel Gershman Utilizing nanopore sequencing to investigate sugar flux in Ruby-throated hummingbirds		Close out		
 Plant research	AUDITORIUM	AUDITORIUM	AUDITORIUM	Break	BREAKOUT ROOM Plant research		Break	AUDITORIUM	AUDITORIUM	Break	AUDITORIUM	AUDITORIUM	AUDITORIUM
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