

# NANOPORE COMMUNITY MEETING 2023: SINGAPORE **AGENDA**

The following pages will guide you through all we have in store for you at this year's event.

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## **TECHNICAL CLINICS**

One-to-one support session with our experts

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## **FLOW CELL LOADING**

Perfect your flow cell loading technique in this hands-on, expert-led demonstration



**NCM**  
Singapore



## Wednesday 27th September 2023

### 07:45–08:45 Pre-event activities

07:45–08:30 SGT **REGISTRATION AND BREAKFAST**

07:45–08:00 SGT **POSTER REGISTRATION**

### 08:45–10:20 Session 1

08:45–09:00 SGT **WELCOME TO THE NANOPORE COMMUNITY MEETING 2023: SINGAPORE** **AUDITORIUM**  
**Gordon Sanghera** | CEO, Oxford Nanopore Technologies  
**Thomas Bray** | Senior Director Sales, APAC, Oxford Nanopore Technologies

09:00–09:25 SGT **PLENARY 1** **AUDITORIUM**  
Redefining telomere-to-telomere genome assembly strategy using the Oxford Nanopore platform  
**Jianjun Liu** | Genome Institute of Singapore, Singapore  
■ **HUMAN & CLINICAL RESEARCH**

09:25–09:50 SGT **PLENARY 2** **AUDITORIUM**  
Seq&Treat: targeted sequencing to detect drug-resistant TB and inform treatment  
**Anita Suresh** | FIND, Switzerland  
■ **INFECTIOUS DISEASE**

09:50–10:20 SGT

## LIGHTNING TALKS

AUDITORIUM

Ten case studies on the recent applications of nanopore sequencing in Thailand

**Thidathip Wongsurawat** | Siriraj Long-read Lab, Mahidol University, Thailand

■ HUMAN & CLINICAL RESEARCH

Exploring post-transcriptional modifications during myrtle rust pathogen-plant interactions

**Ashley Jones** | The Australian National University, Australia

■ PLANT & ANIMAL

Variant segregation in rare disease singletons and duos using nanopore adaptive sampling

**Min Wang** | Murdoch Children's Research Institute, Australia

■ RARE DISEASE

Novel algorithms for long read analysis and applications

**Kai Ye** | Xi'an Jiaotong University, China

■ BIOINFORMATICS

10:20–11:05

Poster networking break

10:20–11:05 SGT

**FLOW CELL LOADING, CUSTOMER SERVICES, TECHNICAL CLINICS, PRODUCT TABLES**

**PRODUCT DISPLAY AREA**

10:30–11:05 SGT

**POSTER NETWORKING**

**POSTERS**

11:05–12:05

Session 2: Breakouts

11:05–12:05 SGT

**INFECTIOUS DISEASE**

**THE MERLION ROOM**

Advances in rapid, accurate, field-forward sequencing to respond to avian influenza virus at the animal-human interface

**Erik Karlsson** | Institut Pasteur du Cambodge, Cambodia

Identification of YFV-17D human-adaptive mutations with nanopore direct RNA sequencing

**Ruyue Liu** | National University of Singapore, Singapore

Application and history of nanopore sequencing in helping China's CDC system

**Ji Wang** | Chinese Center for Disease Control and Prevention, China

■ INFECTIOUS DISEASE

11:05–12:05 SGT	<p><b>RNA</b></p> <p>Improving long-read single cell transcriptomics with Flexiplex: a noise-tolerant sequence search and demultiplexing tool</p> <p><b>Nadia Davidson</b>   Walter and Eliza Hall Institute of Medical Research, Australia</p> <p>Identification of m6A RNA modifications at single molecule resolution using nanopore direct RNA-Seq data</p> <p><b>Jonathan Göke</b>   Genome Institute of Singapore, Singapore</p> <p>Detecting RNA structures using nanopore sequencing</p> <p><b>Yue Wan</b>   Genome Institute of Singapore, Singapore</p> <p>■ RNA</p> <p>■ EPIGENETICS</p>	<b>THE HELIX ROOM</b>
<b>12:05–13:30 Networking lunch</b>		
12:05–13:20 SGT	<b>FLOW CELL LOADING, CUSTOMER SERVICES, TECHNICAL CLINICS, PRODUCT TABLES</b>	<b>PRODUCT DISPLAY AREA</b>
12:05–13:00 SGT	<b>NETWORKING LUNCH</b>	<b>PRODUCT DISPLAY AREA</b>
13:00–13:20 SGT	<p><b>PRODUCT DEMO</b></p> <p>Anyone and anything: unleashing the power of PromethION from human genomics to conservation</p>	<b>PRODUCT DISPLAY AREA</b>
<b>13:30–15:10 Session 3</b>		
13:30–13:55 SGT	<p><b>PLENARY 3</b></p> <p>Update from the Applications team</p> <p><b>Dan Turner</b>   SVP, Applications, Oxford Nanopore Technologies</p>	<b>AUDITORIUM</b>
13:55–14:20 SGT	<p><b>PLENARY 4</b></p> <p>Comprehensive structural and copy number variant detection: from mosaic to population-level</p> <p><b>Fritz Sedlazeck</b>   Baylor College of Medicine &amp; Rice University, USA</p> <p>■ HUMAN &amp; CLINICAL RESEARCH</p> <p>■ BIOINFORMATICS</p> <p>■ POPULATION GENOMICS</p>	<b>AUDITORIUM</b>

14:20–14:45 SGT	<b>PLENARY 5</b> Revolutionizing agriculture: harnessing the power of nanopore sequencing in genomics <b>Elizabeth Ross</b>   University of Queensland, Australia <b>■ PLANT &amp; ANIMAL</b>	<b>AUDITORIUM</b>
14:45–15:10 SGT	<b>PLENARY 6</b> Long cell-free DNA: the beginning of a new era in liquid biopsy <b>Stephanie Yu</b>   The Chinese University of Hong Kong, China <b>■ CANCER RESEARCH</b>	<b>AUDITORIUM</b>
<b>15:10–15:55</b>	<b>Coffee break</b>	
15:10–15:55 SGT	<b>FLOW CELL LOADING, CUSTOMER SERVICES, TECHNICAL CLINICS, PRODUCT TABLES</b>	<b>PRODUCT DISPLAY AREA</b>
15:25 –15:45 SGT	<b>SHOWCASE STAGE</b> Australia’s National Centre for Indigenous Genomics: enabling the inclusion of First Nations peoples in genomics <b>Hardip Patel</b>   The Australian National University, Australia  Genomics Thailand: a mission to integrate genomic technology into the national health system <b>Manop Pithukpakorn</b>   Siriraj Genomics, Thailand <b>■ HUMAN &amp; CLINICAL RESEARCH</b> <b>■ POPULATION GENOMICS</b>	<b>PRODUCT DISPLAY AREA</b>
<b>15:55–17:45</b>	<b>Session 4</b>	
15:55–16:25 SGT	<b>UPDATE FROM OXFORD NANOPORE TECHNOLOGIES</b> <b>Rosemary Sinclair Dokos</b>   SVP, Product & Programme Management, Oxford Nanopore Technologies	<b>AUDITORIUM</b>

16:25–17:15 SGT	<p><b>PANEL PLENARY: A NEW ERA FOR TRANSLATIONAL RESEARCH</b></p> <p>Measuring skewed X inactivation by adaptive nanopore sequencing</p> <p><b>Quentin Gouil</b>   Walter and Eliza Hall Institute of Medical Research, Australia</p> <p>■ HUMAN &amp; CLINICAL RESEARCH</p>	AUDITORIUM
	<p>Investigating structural variations and complex cancer genomes using Oxford Nanopore sequencing</p> <p><b>Marjan Naeini</b>   Garvan Institute of Medical Research, Australia</p> <p>■ CANCER RESEARCH</p>	
	<p>Direct detection of DNA modifications in human cancer genomes</p> <p><b>Genta Nagae</b>   The University of Tokyo, Japan</p> <p>■ CANCER RESEARCH</p> <p>■ EPIGENETICS</p>	
17:15–17:40 SGT	<p><b>PLENARY 7</b></p> <p>The 1000 Genomes Project Oxford Nanopore Sequencing Consortium: expanding our understanding of human genetic variation</p> <p><b>Danny E. Miller</b>   University of Washington, USA</p> <p>■ HUMAN &amp; CLINICAL RESEARCH</p>	AUDITORIUM
17:40–17:45 SGT	<b>CLOSING REMARKS</b>	AUDITORIUM
<p><b>17:45–19:00</b>      <b>Evening networking event</b></p>		