TIME (EDT)	AGENDA: 16th SEPTEMBER 2024	RESEARCH AREA
10:00–12:55	**Session 1**	
10:00–10:20	**Welcome to the Nanopore Community Meeting 2024: Boston**	
10:20–10:45	**Use of Oxford Nanopore sequencing to evaluate potential transmission of hospital infections** **Samuel Shelburne** | The University of Texas MD Anderson Cancer Center, USA	MICROBIOLOGY & INFECTIOUS DISEASE
10:45–11:10	**Transforming cancer care: redefining cancer characterization and predisposition insights through nanopore sequencing** **Mathilde Filser** | Curie Institute, France	CANCER RESEARCH
11:10–11:35	**Detection of germline alterations in homologous recombination repair genes by adaptive sampling** **Stephanie Chrysanthou** | Memorial Sloan Kettering Cancer Center, USA	HUMAN & CLINICAL RESEARCH
11:40–12:00	**Networking catalysts** HUMAN & CLINICAL RESEARCH | CANCER RESEARCH | BIOINFORMATICS | MICROBIOLOGY & INFECTIOUS DISEASE | PLANT & ANIMAL RESEARCH	
12:00–12:20	**From London Calling 2024: How to get started with nanopore sequencing and plan your experiment**	
12:25–12:45	**From London Calling 2024: How to select the right library prep workflow for your experiment**	
12:55–15:00	**Session 2**	
12:55–13:55	**Breakout: Human clinical research** **Resolving structural configurations of *DMD* intragenic duplications through nanopore long-read sequencing** **Qiliang (Andy) Ding** | Mayo Clinic, USA **needLR: a structural variant filtering and prioritization tool for long-read sequencing data** **J. (Gus) Gustafson** | University of Washington, USA **Diagnostic utility of long-read sequencing for challenging cases in the Undiagnosed Diseases Network** **Shilpa Kobren** | Harvard Medical School, USA	HUMAN & CLINICAL RESEARCH
	Breakout: Bitesize bioinformatics **Evaluating the quality of long-read phasing methods in clinically relevant genes** **Nikhita Damaraju** | University of Washington, Seattle, USA **Detection of mosaic and somatic structural variants with Sniffles2** **Fritz Sedlazeck** | Baylor College of Medicine, USA **Maximizing the power of genomic sequencing in pediatric rare disease** **Wanqing Shao** | Boston Children's Hospital, USA **A survey of RNA modifications across the human transcriptome by direct RNA nanopore sequencing** **Logan Mulroney** | EMBL-EBI, UK & IIT, Italy	BIOINFORMATICS

14:05–14:25	**From London Calling 2024: Nanopore sequencing reveals conservation of chromosome end-specific telomere lengths** **Carol Greider** | University of California, Santa Cruz, USA	HUMAN & CLINICAL RESEARCH
14:30–14:50	**From London Calling 2024: Advancing RNA liquid biopsy technology via nanopore sequencing** **Daniel Kim** | University of California, Santa Cruz, USA	CANCER RESEARCH
15:00–18:00	**Session 3**	
15:00–15:25	**Update from the Oxford Nanopore Technologies Applications team**	
15:25–15:50	**Bulk and single-cell nanopore transcriptomics to identify alternative splicing in renal tubule cells** **Megan L. Noonan** | Washington University School of Medicine in St. Louis, USA	HUMAN & CLINICAL RESEARCH
15:50–16:10	**Lightning talks**	
	Studying disease-causing polymorphic transposable element insertions using nanopore sequencing **Vivien Horvath** | Lund University, Sweden	HUMAN & CLINICAL RESEARCH
	Is the water safe to drink? The rapid test is the missing link! **Noah Bryan** | Bayview Secondary School, Canada	MICROBIOLOGY & INFECTIOUS DISEASE
	Decoding the spliced HIV-1 transcriptome with accurate long-read RNA sequencing **Christian Gallardo** | Seattle Children's Research Institute, USA	MICROBIOLOGY & INFECTIOUS DISEASE
16:10–16:35	**Long-read sequencing for comprehensive genomic profiling of infertile men** **Thomas Garcia** | Baylor College of Medicine, USA	HUMAN & CLINICAL RESEARCH
17:25–18:00	**Poster networking**	
17:35–17:50	**From London Calling 2024: Towards personalised medicine for breast cancer in the Caribbean — a pilot study** **Carika Weldon** | CariGenetics, Bermuda	CANCER RESEARCH
18:00–19:05	**Session 4**	
18:00–19:00	**Tech update**	
19:00–19:05	**Closing remarks**	

TIME (EDT)	AGENDA: 17th SEPTEMBER 2024	RESEARCH AREA
09:00–11:35	**Session 5**	
09:00–09:20	Welcome back to the Nanopore Community Meeting 2024: Boston	
09:20–09:45	Large-scale methylation studies using nanopore sequencing **Brynja Sigurpálsdóttir** | deCODE genetics, Iceland	HUMAN & CLINICAL RESEARCH
09:45–10:10	Precision genomics: the future of food safety **Julie Haendiges** | U.S. Food and Drug Administration, USA	MICROBIOLOGY & INFECTIOUS DISEASE
10:40–11:10	From London Calling 2024: How to analyse your data with EPI2ME	
11:00–11.30	Networking catalysts HUMAN & CLINICAL RESEARCH | CANCER RESEARCH | BIOINFORMATICS | MICROBIOLOGY & INFECTIOUS DISEASE | PLANT & ANIMAL RESEARCH	
11:15–11:30	From London Calling 2024: HERRO — haplotype-aware error correction of ultra-long nanopore reads **Mile Sikic** | Genome Institute of Singapore, A*STAR, Singapore	HUMAN & CLINICAL RESEARCH
11:35–14:15	**Session 6**	
11:35–12:35	Breakout: Cancer research Unraveling gene expression patterns in pediatric germ cell tumors: a nanopore sequencing approach **Ana Peres** | The University of North Carolina at Chapel Hill, USA Nanopore-based random genomic sampling for intraoperative diagnosis of brain tumors and beyond **Chun-Chieh Lin** | Dartmouth Health, USA Diverse structural variants cluster near breakage-fusion-bridge site in cancer genomes **Michael Dean** | National Cancer Institute, USA	CANCER RESEARCH
	Breakout: Microbiology & infectious disease Fieldable sequencing for biothreat identification and characterization **Cory Bernhards** | DEVCOM Chemical Biological Center, USA Detection of hidden antibiotic resistance through real-time genomics **Ela Sauerborn** | Helmholtz AI Institute Munich, Germany How good is good enough? **David Yarmosh** | ATCC, USA	MICROBIOLOGY & INFECTIOUS DISEASE
12:55–14.05	Data for lunch	BIOINFORMATICS

14:15–16:45	**Session 7**	
14:15–14:40	**Long-read sequencing: bridging the diagnostic gap for undiagnosed cases in Chile** **Paula Saffie** | Clinica Santa María, Chile	HUMAN & CLINICAL RESEARCH
14:40–15:05	**Long-read sequencing for detecting methylation dysregulation** **Matthew Bainbridge** | Rady Children's Institute for Genomic Medicine, USA	HUMAN & CLINICAL RESEARCH
15:05–15:25	**Lightning talks**	
	Nanopore sequencing in reproductive care **Svetlana Madjunkova** | CReATe Fertility Centre, Canada	HUMAN & CLINICAL RESEARCH
	Long-read sequencing reveals the molecular landscape of mitochondrial DNA 6mA methylation **Lantana Grub** | Vanderbilt University, USA	HUMAN & CLINICAL RESEARCH
	Consolidation of a long-read sequencing platform in southern South America **Laura Kamenetzky** | CONICET, Argentina	PLANT & ANIMAL RESEARCH
15:25–15:50	**Acute ketamine and electroconvulsive therapy alter prefrontal cortex cell type-specific transcriptomes** **Benjamin C. Reiner** | University of Pennsylvania, USA	HUMAN & CLINICAL RESEARCH
16:20–16:40	**From London Calling 2024: Whole-genome sequencing in PulseNet foodborne molecular surveillance systems** **Heather Carleton** | Centers for Disease Control & Prevention, USA	MICROBIOLOGY & INFECTIOUS DISEASE
16:20–16:40	**Poster networking**	
16:45–17:50	**Session 8**	
16:45–17:45	**Panel plenary: The importance of methylation in genetic diseases**	
	Nanopore sequencing to resolve DNA methylation patterns in developmental disease **Lucia Daxinger** | Leiden University Medical Center, Netherlands	HUMAN & CLINICAL RESEARCH
	Long-read epigenetics of endogenous retroviruses to pinpoint tumor antigens **Justin Becker** | Dana-Farber Cancer Institute & Massachusetts General Hospital, USA	CANCER RESEARCH
	DNA methylation signature detection using ultra-rapid, long-read nanopore genome sequencing **Dmitrijs Rots** | Erasmus MC, Netherlands	HUMAN & CLINICAL RESEARCH
	Brynja Sigurpálsdóttir | deCODE genetics, Iceland **(panellist)**	
17:45–17:50	**Closing remarks**	