TIME (EDT)	AGENDA: 16th SEPTEMBER 2024	RESEARCH AREA
08:30–09:45	**Registration & breakfast**	
10:00–11:45	**Session 1: Auditorium**	
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
11:45–12:55	**Networking lunch**	
	Workflow demo 12:05–12:25 | Showcase Stage **Networking catalyst** 12:25–12:45 | Product Display Area	
12:55–13:55	**Session 2: Breakouts**	

Human clinical research | Blondie	**Bitesize bioinformatics** | Talking Heads	**Plant & animal research** | Ramones
Resolving structural configurations of *DMD* intragenic duplications through nanopore long-read sequencing **Qiliang (Andy) Ding** | Mayo Clinic, USA	**Evaluating the quality of long-read phasing methods in clinically relevant genes** **Nikhita Damaraju** | University of Washington, Seattle, USA	**DNA methylation patterns explain missing heritability in maize** **Jack Colicchio** | Sound Agriculture, USA
needLR: a structural variant filtering and prioritization tool for long-read sequencing data **J. (Gus) Gustafson** | University of Washington, USA	**Detection of mosaic and somatic structural variants with Sniffles2** **Fritz Sedlazeck** | Baylor College of Medicine, USA	**Positional mapping of active versus silenced rRNA gene clusters within *A. thaliana* nucleolus organizer regions** **Anastasia McKinlay** | Indiana University & HHMI, USA
Diagnostic utility of long-read sequencing for challenging cases in the Undiagnosed Diseases Network **Shilpa Kobren** | Harvard Medical School, USA	**Maximizing the power of genomic sequencing in pediatric rare disease** **Wanqing Shao** | Boston Children's Hospital, USA	**Obtaining reference genomes of emblematic and endangered Ecuadorian species** **Gabriela Pozo** | University of San Francisco de Quito, Ecuador
	A survey of RNA modifications across the human transcriptome by direct RNA nanopore sequencing **Logan Mulroney** | EMBL-EBI, UK & IIT, Italy	
HUMAN & CLINICAL RESEARCH	BIOINFORMATICS	PLANT & ANIMAL RESEARCH

13:55–15:00	**Networking break**		
	Networking catalysts 13:55–14:20 | Product Display Area	**Carrier screening** 14:30–14:50 | Showcase Stage	
15:00–16:45	**Session 3: Auditorium**		
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
16:45–18:00	**Poster networking break**		
	ORG.one 17:25–17:45 | Product Display Area	**Data analysis demo** 17:25–17:45 | Data Café	
18:00–19:05	**Session 4: Auditorium**		
18:00–19:00	**Tech update**		
19:00–19:05	**Closing remarks**		
19:05–21:00	**Evening networking event**		

TIME (EDT)	AGENDA: 17th SEPTEMBER 2024			RESEARCH AREA
08:00–08:45	**Registration & breakfast**			
09:00–10:20	**Session 5: Auditorium**			
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
10:20–11:35	**Networking break**			
	Workflow demo 10:40–11:00 | Showcase Stage	**Networking catalyst** 11:00–11:20 | Product Display Area		
11:35–12:35	**Session 6: Breakouts**			
	Cancer research | Blondie	**Microbiology & infectious disease** | Talking Heads	**Functional genomics** | Ramones	
	Unraveling gene expression patterns in pediatric germ cell tumors: a nanopore sequencing approach **Ana Peres** | The University of North Carolina at Chapel Hill, USA	**Fieldable sequencing for biothreat identification and characterization** **Cory Bernhards** | DEVCOM Chemical Biological Center, USA	**Understanding the binding of multiple transcription factors by base-pair-resolution chromatin accessibility** **Ailsa MacCalman** | University of Exeter, UK	
	Nanopore-based random genomic sampling for intraoperative diagnosis of brain tumors and beyond **Chun-Chieh Lin** | Dartmouth Health, USA	**Detection of hidden antibiotic resistance through real-time genomics** **Ela Sauerborn** | Helmholtz AI Institute Munich, Germany	**Methylation- and CTCF-dependent control of 3D chromatin in normal and malignant hematopoiesis** **Aaron Viny** | Columbia University Irving Medical Center, USA	
	Diverse structural variants cluster near breakage-fusion-bridge site in cancer genomes **Michael Dean** | National Cancer Institute, USA	**How good is good enough?** **David Yarmosh** | ATCC, USA	**Genetic regulation of nascent RNA maturation revealed by direct RNA sequencing** **Karine Choquet** | University of Sherbrooke, Canada	
	CANCER RESEARCH	MICROBIOLOGY & INFECTIOUS DISEASE	HUMAN & CLINICAL RESEARCH | CANCER RESEARCH	
12:35–14:15	**Networking lunch**			
	Networking catalysts 12:35–13:00 | Product Display Area	**Data for lunch** 12:55–14.05 | Talking Heads	**Biosurveillance** 13:10–13:30 | Showcase Stage	

14:15–16:00	**Session 7: Auditorium**	
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
16:00–16:45	**Poster networking break**	
16:10–16:30	**Product demo** Showcase Stage **Data analysis demo** Data Café	
16:45–17:50	**Session 8: Auditorium**	
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 **Brynja Sigurpálsdóttir** | deCODE genetics, Iceland **(panellist)**	HUMAN & CLINICAL RESEARCH
17:45–17:50	**Closing remarks**	
17:50–19:00	**Evening networking event**	