

Workshop on Long-Read Sequencing

September 17 – 20, 2019

Event Schedule

All sessions will be held at the Jackson Laboratory for Genomic Medicine, Farmington, Conn.

Tuesday, September 17th

Session 0: Welcome

- 8:30 am Registration Opens
- 9:00 am Rachel Goldfeder, Ph.D., Computational Scientist, *The Jackson Laboratory*
- 9:05 am Chia-Lin Wei, Ph.D., Director of Genome Technology, *The Jackson Laboratory*

Session 1: Technology Overview

- 9:15 am **PacBio Technology Update**
Jonas Korlach, Ph.D., Chief Scientific Officer, *Pacific Biosciences*
- 9:40 am James Brayer, Associate Director for Market Development, *Oxford Nanopore*
- 10:05 am **Genome Imaging for High Throughput Structural Variation Detection in Cancer and Genetic Disease**
Sven Bocklandt, Ph.D., Director of Scientific Affairs, *Bionano Genomics*
- 10:30 am **Highly Scalable Linked Read Library Technology Enables Low Input and Single Tube Library Prep for Haplotype Phasing and De Novo Sequencing**
Tom Chen, Ph.D., Co-Founder & CSO, *Universal Sequencing*
- 10:40 am **Long Molecule Phasing With a Single-Tube Short Read Library Prep**
Joseph Mellor, Ph.D., *CEO, seqWell*
- 10:40 am Coffee Break

Session 2: Genome Variation

- 11:30 am **What's in a Single-Molecule Sequencing Genome?**

Mark Chaisson, Ph.D., Assistant Professor, *University of Southern California*

11:55 am **Mechanisms of Structural Variation**

Christine Beck, Ph.D., Assistant Professor, *The Jackson Laboratory*

12:20 pm **100 Genomes in 100 Days: The Structural Variant Landscape in Tomato Genomes**

Michael Schatz, Ph.D., Bloomberg Distinguished Associate Professor, *Johns Hopkins University*

12:45 pm Lunch

Session 3: Reference Genome

2:00 pm **Developing Benchmarks for Challenging Variants With Long Reads**

Justin Zook, Ph.D., Human Genomics Team Leader, *National Institute of Standards and Technology*

2:25 pm **Fish Genome Sequencing With the Help of Tulips**

Christiaan Henkel, Ph.D., Research Scientist, *Norwegian University of Life Sciences*

2:50 pm **Telomere to Telomere Assemblies of Human Chromosomes**

Karen Miga, Ph.D., Assistant Research Scientist, *UC Santa Cruz Genomics Institute*

3:15 pm Coffee Break

Session 4A: RNA Biology

4:00 pm **RNA Biology**

Jacques Banchereau, Ph.D., Director and Professor of Immunological Services, *The Jackson Laboratory*

4:25 pm **Full-length Alternative Transcript Isoform Analysis Using Nanopore Sequencing**

Angela Brooks, Ph.D., Assistant Professor of Biomolecular Engineering, *University of California, Santa Cruz*

4:50 pm **Towards High Quality Transcriptome Annotations**

Christopher Vollmers, Ph.D., Assistant Professor, *University of California, Santa Cruz*

Session 4B: Computational Biology

4:00 pm **Pilot Sequences and Long Read Technologies**

Olgica Milenkov, Ph.D., Professor, *University of Illinois, Urbana-Champaign*

4:25 pm **Size Matters: Accurate Detection and Phasing of Structural Variations**

Fritz Sedlazeck, Ph.D., Assistant Professor, Human Genome Sequencing Center,
Baylor College of Medicine

- 4:50 pm **Computational Biology**
Yijun Ruan, Ph.D., Professor & Director, JAX Genomic Services, *The Jackson Laboratory*
- 5:30 pm Welcome Reception

Wednesday, September 18

Session 5: Cancer

- 9:00 am **Telomere Analysis With Long Read Sequencing**
Matthew Meyerson, M.D., Ph.D., Professor of Pathology, *Dana-Farber Cancer Institute*
- 9:25 am Chia-Lin Wei, Ph.D., Director, Genome Technologies, *The Jackson Laboratory*
- 9:50 am **3D Genome Organization in Cancer Cells**
Feng Yue, Ph.D., Director, Center for Cancer Genomics & Associate Professor of Biochemistry and Molecular Genetics, *Northwestern University*
- 10:15 am Coffee Break & Vendor Expo

Session 6: Long Reads in the Clinic

- 11:30 am Robert Sebra, Ph.D., Associate Professor, Genetics and Genomics; Director of Technology Development & GCF, *Icahn School of Medicine at Mount Sinai*
- 11:55 am Cecilia Yeung, M.D., Associate Member, *Fred Hutchinson Cancer Research Center*
- 12:20 pm **Single Molecule Sequencing for Human Genome Variation: From Repeat Expansions to Whole Chromosome Rearrangements**
Matthew Hestand, Ph.D., Assistant Professor, Division of Human Genetics, *Cincinnati Children's Hospital Medical Center*
- 12:45 pm Lunch & Poster Session + Women in Science Networking

Session 7: Genome Assembly

- 2:25 pm **Aquila: Diploid Genome Assembly and Variant Detection Based on Linked Reads**
Arend Sidow, Ph.D., Professor, *Stanford University*
- 2:50 pm **Telomere-to-Telomere Assembly of a Complete Human X Chromosome**
Adam Phillippy, Ph.D., Investigator, *National Human Genome Research Institute*

Session 8: Selected Abstracts

- 3:15 pm **Utility of 10x Genomics Linked-Read Sequencing in Characterizing Short Tandem Repeat Expansion Mutations**
Indhu-Shree Rajan-Babu
- 3:25 pm **Nanopore Ultra-Long Read Sequencing Provides Insights Into Structural Variation in Cancer Genome**
Liang Gong
- 3:35 pm **Single-Molecule Long-Read Sequencing Reveals Intact RNAs in Sperm**
Yu Sun
- 3:45 pm Coffee Break

Session 9A: Microbiome and Infectious Disease

- 4:15 pm **Ultra-Deep Long-Read Metagenomics**
Samuel Nicholls, Ph.D., Research Fellow in Bioinformatics, *University of Birmingham*
- 4:40 pm **Resolving the Complexity of Human Skin Metagenomes Using Single-Molecule Sequencing**
Julia Oh, Ph.D., Assistant Professor, *The Jackson Laboratory*
- 5:05 pm **Microbiome and Infectious Disease**
Ivan Liachko, Ph.D., Founder & CEO, *Phase Genomics*

Session 9B: Epigenetics

- 4:15 pm **Using Nanopore Sequencing to Interrogate the Genome, Epigenome and Transcriptome**
Winston Timp, Ph.D., Assistant Professor, *Johns Hopkins University*
- 4:40 pm **Illuminating Bacterial Epigenomes to Characterize Pathogens and Microbiome**
Gang Fang, Ph.D., Associate Professor, *Icahn School of Medicine at Mount Sinai*
- 5:05 pm **Nanopore Direct RNA Sequencing Enables Comprehensive Transcriptome Profiling and Modification Detection**
Rachel Goldfeder, Ph.D., Computational Scientist, *The Jackson Laboratory*

Session 10: Keynote

- 5:30 pm Christopher Mason, Ph.D., Associate Professor, *Weill Cornell Medicine*
- 6:15 pm Dinner

Thursday, September 19

Session 11: Technical Skills: Long Read Technology Bioinformatics Analysis (Dry Lab Tutorial)

- 9:00 am Introduction & Basic Unix Commands and Cloud Computing
- 9:15 am **Analyzing Nanopore sequencing data (base calling, alignment, de novo assembly, SV detection, quality control, data visualization)**
Michael Micorescu, Ph.D., *Oxford Nanopore Technologies*
- 11:00 am **Nanopolish**
Joanna Pineda, Master of Science Candidate, *Ontario Institute for Cancer Research, University of Toronto*
- 12:00 pm **FAIR Data Principles**
Anne Deslattes Mays, Ph.D. Principal Computational Scientist, *The Jackson Laboratory*
- 12:20 pm Lunch
- 1:00 pm **Bionano Aces: Genome Visualization and Analysis**
Benjamin Clifford, Ph.D., Senior Field Application Scientist, *Bionano Genomics*
- 2:00 pm **Analyzing SMRT Sequencing Data** (generating circular consensus reads, alignment, SV detection, IsoSeq (RNA-Seq) mapping and iso-form detection, quality control, data visualization)
Roberto Lleras, Manager, M.S., Manager, Bioinformatics FAS, *Pacific Biosciences*
- 3:45 pm Coffee Break
- 4:15 pm **SV Detection**
Fritz Sedlazeck, Ph.D., Assistant Professor, *Baylor College of Medicine*

Friday, September 20th

Session 12: Technical Skills: Long Read Technology Library Preparation (Wet Lab Tutorial)

- 9:00 am **Introduction**
Jeremy Charette, B.S., Genomic Technologist, *The Jackson Laboratory*
- 9:30 am **Extracting High Molecular Weight DNA**
Jennifer Idol, M.S., Genomic Technologist, *The Jackson Laboratory*
- 12:00 pm Lunch & presentation (Chris Boles, Ph.D., Sage Sciences)
- 1:00 pm **Long Read Library Preparations & PacBio Express Iso-Seq Library Preparation**
Chris Kuhlberg, M.S., Genomic Technologist, *The Jackson Laboratory*
- 3:00 pm Coffee Break
- 3:15 pm **Sequencing Platforms Overview & Oxford Nanopore Rapid DNA Preparation and Sequencing**
Liang Gong, Ph.D., Postdoctoral Associate, *The Jackson Laboratory*

5:15 pm

Dinner