

The Jackson Laboratory's 2019 Workshop on Long-Read Sequencing

September 17 - Day 1:

Session 0: Welcome

- 8:30 Registration Opens
- 9:00 **Rachel Goldfeder**, PhD, Computational Scientist, The Jackson Laboratory
- 9:15 **Chia-Lin Wei**, PhD, Director of Genome Technology, The Jackson Laboratory

Session 1: Technology Overview

- 9:30 **Jonas Korf**, PhD, Chief Scientific Officer, Pacific Biosciences
- 10:05 TBD, Oxford Nanopore
- 10:40 **Michael Schnall-Levin**, PhD, VP Product, R&D and Strategy, 10x Genomics
- 11:15 **Sven Bocklandt**, PhD, Sr. Application Specialist, Bionano Genomics, Inc.
- 11:40 Lunch

Session 2: Genome Assembly and other methods to Resolve Complicated Regions of the Human Genome

- 12:45 **Karen Miga**, PhD, Assistant Research Scientist, UC Santa Cruz Genomics Institute
- 1:10 **Michael Schatz**, PhD, Associate Professor, Johns Hopkins University
- 1:35 **Fritz Sedlazeck**, PhD, Assistant Professor, Human Genome Sequencing Center, Baylor College of Medicine
- 2:00 **Hans Jansen**, PhD, CTO, Future Genomics Technologies
- 2:25 **Arend Sidow**, PhD, Professor, Stanford University
- 2:50 Coffee Break

Session 3: Gene Expression and Epigenetics

- 3:20 **Winston Timp**, PhD, Assistant Professor Johns Hopkins University
- 3:45 **Christopher Vollmers**, PhD, Assistant Professor, Biomolecular Engineering, UC Santa Cruz
- 4:10 **Angela Brooks**, PhD, Assistant Professor of Biomolecular Engineering, UC Santa Cruz

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Session 4: Long Read Technologies Help Characterize, Predict, and Find the Best Treatment for Human Disease

- 4:35 **Bobby Sebra**, PhD, Associate Professor, Director of Technology Development, Icahn Institute, VP of Technology Development at Sema4
- 5:00 **Jacques Banichereau**, PhD, Professor, The Jackson Laboratory
- 5:25 **Feng Yue**, PhD, Assistant Professor, Penn State University
- 6:00 Welcome Reception

September 18 - Day 2:

Session 5: Long Read Technologies Enable the Identification of Structural Variants

- 9:00 **Chia-Lin Wei**, PhD, Director of Genome Technology, The Jackson Laboratory
- 9:25 **Adam Phillippy**, PhD, Investigator, National Human Genome Research Institute
- 9:50 **Christine Beck**, PhD, Assistant Professor, The Jackson Laboratory
- 10:15 **Mark Chaisson**, PhD, Assistant Professor, University of Southern California
- 10:40 Coffee Break

Session 6: Reproducibility in Long-Read Sequencing

- 11:00 **Justin Zook**, PhD, National Institute of Standards and Technology
- 11:25 **Olgica Milenkovic**, PhD, Professor, University of Illinois, Urbana-Champaign

Session 7: Trainees use Long-Read Sequencing

- 11:50 TBD – Trainee
- 12:00 TBD – Trainee
- 12:10 TBD – Trainee

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Session 8: Exhibition and Poster Session

12:20 Lunch, Expo, Poster Session

Session 9: Studying Metagenomics & Microbiomes with Long-Read Sequencing

1:30 **Julia Oh**, PhD, Assistant Professor, The Jackson Laboratory

1:55 **Gang Fang**, PhD, Associate Professor, Genomics Department, Icahn School of Medicine at Mount Sinai

2:20 **Ashlee Earl**, PhD, Research Scientist, The Broad Institute

2:45 **Nick Loman**, PhD, Professor, University of Birmingham

3:10 Coffee Break

Session 10: Exciting Applications in Long-Read Sequencing & The Future of Long-Read Sequencing in the Clinic

3:30 **Matthew Hestand**, PhD, Assistant Professor, Division of Human Genetics, Cincinnati Children's Hospital Medical Center

3:55 **Yijun Ruan**, PhD, Professor, The Jackson Laboratory

4:20 **Cecilia Yeung**, MD, Assistant Professor, Medical Director- Molecular Oncology Laboratory, University of Washington and Fred Hutchinson Cancer Research Center

4:45 **Matthew Meyerson**, MD PhD, Director of Cancer Genomics, Dana-Farber Cancer Institute, Broad Institute, and Harvard Medical School

5:10 **Christopher Mason**, Associate Professor, PhD, Johns Hopkins University

5:35 Dinner

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September 19 - Day 3:

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

- 9:00 Introduction & Basic Unix Commands and Cloud Computing
- 9:30 Analyzing Nanopore sequencing data (base calling, alignment, de novo assembly, SV detection, quality control, data visualization)
- 11:30 Lunch
- 12:15 Analyzing SMRT sequencing data (generating circular consensus reads, alignment, SV detection, IsoSeq (RNA-Seq) mapping and iso-form detection, quality control, data visualization)
- 2:15 Analyzing synthetic linked reads sequencing data (bcl to FASTQ, alignment, de novo assembly, SV detection, quality control, data visualization)
- 4:15 Analyzing optical mapping data
- 5:15 Integrating long- and short-read data for increased accuracy

September 20 - Day 4:

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

- 9:00 Introduction
- 9:10 Extracting High Molecular Weight DNA
- Synthetic linked read Library Preparation*
- 10:15 Synthetic linked read library prep - GEM Generation
- 10:45 Synthetic linked read library prep - GEM cleanup
- 12:00 Lunch
- Single Molecule Real-Time sequencing Library Preparation*
- 1:00 Single Molecule Real-Time Sequencing - End Repair
- 2:00 Single Molecule Real-Time Sequencing – Adaptor Ligation
- 2:30 Coffee Break / Incubation Period

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3:15 Single Molecule Real-Time Sequencing – Cleanup

Oxford Nanopore Library Preparation and Sequencing

3:45 Nanopore – Rapid Library Preparation

4:30 Nanopore – Loading on a GridION

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