

SCIENTIFIC PRESENTATIONS

Thursday, February 16

Understanding Sequencing Bias Across Multiple Sequencing Technologies

Michael Ross, Broad Institute of MIT and Harvard
Concurrent Session: Genomic Technology
7:30 p.m. – 7:50 p.m.
Island Ballroom

Friday, February 17

Characterization of DNA Methyltransferase Specificities Using Single Molecule, Real-Time DNA Sequencing

Richard Roberts, New England Biolabs
Plenary Session: Genomic Studies and New Technologies
11:20 a.m. – 11:40 a.m.
Island Ballroom

Evaluating Targeted Resequencing as a Diagnostic Tool: A Prospective Clinical Trial

John McPherson, Ontario Institute for Cancer Research & Univ. of Toronto
Concurrent Session: Cancer and Transcriptomes
8:10 p.m. – 8:30 p.m.
Island Ballroom

Metassembler: Improving de novo Genome Assembly

Michael Schatz, Cold Spring Harbor Laboratory
Concurrent Session: Computational Biology
8:10 p.m. – 8:30 p.m.
Salon G – J

Metabolic RNA Labeling Coupled with Epigenetic Mapping Reveals the Dynamics of Transcriptome Control in Genetic Pathways of Algal Biodiesel Production

Chia-Lin Wei, Joint Genome Institute
Concurrent Session: Microbial Genomics
8:30 p.m. – 8:50 p.m.
Salon G – J

Near-Finished Prokaryotic Genome Assemblies from a Low-cost Combination of Short and Long Reads

David Jaffe, Broad Institute of MIT and Harvard
Concurrent Session: Computational Biology
8:30 p.m. – 8:50 p.m.
Salon G – J

Integrating Kinetic Variation Events Identified From SMRT® Sequencing Data with Other High-Dimension Molecular Profiling Data Uncovers Novel Regulatory Mechanisms

Eric Schadt, Pacific Biosciences, Inc.
Concurrent Session: Genome Biology
9:10 p.m. – 9:30 p.m.
Salon E & F

SCIENTIFIC POSTERS

Combining Sequences from Different Sequencing Platforms (Hiseq, Miseq, PacBio®) to Improve de novo Genome Assembly

E. Antoniou et al., Cold Spring Harbor Laboratory

Validation of SNP Detected by High Throughput Sequencing Using the Pacific Biosciences® RS or the Illumina MiSeq Instruments

E. Antoniou et al., Cold Spring Harbor Laboratory

SMRT® Sequencing of Whole Mitochondrial Genomes and Its Utility in Association Studies of Metabolic Disease

Penelope E. Bonnen et al., Department of Molecular and Human Genetics, Baylor College of Medicine

Evaluating the Potential of New Sequencing Technologies for Genotyping and Variation Discovery in Human Data

Mauricio Carneiro et al., Broad Institute

Applying Single Molecule Sequencing to de novo Genome Assembly

Feng Chen et al., Department of Energy, Joint Genome Institute

Sequencing with the PacBio® – Its First Year at the Sanger Institute

Paul Coupland et al., The Wellcome Trust Sanger Institute

Under the Hood of the 1000 Genomes Project

Mark A. DePristo et al., Broad Institute of MIT and Harvard

Mind the Gap: Upgrading Reference Genomes with the Pacific Biosciences® RS Long-Read Sequencing Technology

Adam English et al., Human Genome Sequencing Center, Baylor College of Medicine

Genomic Approaches to Understanding Mycobacterium Tuberculosis

Michael G. FitzGerald et al., Broad Institute of MIT and Harvard

Sequencing the Unsequenceable: Expanded CGG Repeats in the Human *FMR1* Gene

Paul J. Hagerman et al., Department of Biochemistry and Molecular Medicine, and MIND Institute, University of California, Davis

Genome Finishing with PacBio® Sequencing Technology

Cliff S. Han et al., The DOE Joint Genome Institute, Los Alamos National Laboratory

High Throughput, Long-Read DNA Sequencing Using PacBio® RS System

Yi Han et al., Department of Molecular & Human Genetics, Baylor College of Medicine

Application of Combined SMRT® and Long-Read Pyrosequencing to Produce Reference Genome Sequences of Bacteria Associated with Respiratory Disease Outbreaks in Beef Cattle

Gregory P. Harhay et al., USDA, ARS, U.S. Meat Animal Research Center

A Closer Look At the Arabidopsis Genome Using PacBio® Single Molecule Sequencing

Mingya Huang et al., Monsanto

PacBio® RS Instrument Delivers Haplotype Data that Shed Light on Risk Alleles for Familial Trios with Testicular Cancer

Kevin B. Jacobs et al., Division of Cancer Epidemiology and Genetics, National Cancer Institute

Integration of PacBio® RS into Massive Parallel Sequencing and Data Analysis Pipelining in Genome Center

Ryan W. Kim et al., Genome Center and Bioinformatics Program, University of California, Davis

Enabling Next-Gen Sequencing and Analysis at the USDA-ARS U.S. Meat Animal Research Center with MiniLIMS

Aaron Kitzmiller et al., The BioTeam, Inc

Combinatorial Data Sets: Pragmatic Applications Derived from Multiple Sequencing Technologies

Vincent Magrini et al., The Genome Institute at Washington University School of Medicine

Genome Sequence and Hybrid Assembly of the Aye-Aye (*Daubentonia Madagascariensis*), a Nocturnal Lemur from Madagascar

Christopher E. Mason et al., Department of Human Genetics, University of Chicago

The Establishment of Large-Scale Transcriptomic Resources for Humans and Other Primates

Christopher E. Mason et al., The Institute for Computational Biomedicine, Weill Cornell Medical College

The Pacific Biosciences® RS Platform Development at the Broad Institute

Jim Meldrim et al., The Broad Institute of MIT and Harvard

Toward a Recipe for Reference Plant Genome Sequences

Todd P. Michael et al., Monsanto Company, The Genome Analysis Center

A Qualitative and Quantitative Evaluation of Medium Throughput Sequencing Technologies

Laura Mullen et al., Ontario Institute for Cancer Research

Hybrid Error Correction and De Novo Assembly of Single-Molecule Sequencing Reads

Adam M. Phillippy et al., National Biodefense Analysis and Countermeasures Center

Deep Sequencing Allows Better Characterization of Hepatitis C Virus Quasispecies

Reinhold Pollner et al., Gen-Probe Incorporated

Real-Time Analysis of Translation

Joseph D. Puglisi, Department of Structural Biology, Stanford University

Whole-Genome Analysis of Escherichia coli O104:H4 Outbreaks in Europe, 2011

Carsten Russ et al., Broad Institute of MIT and Harvard

Full Length Transcript Discovery in the Human Genome Using Pacific Biosciences® Single-Molecule, Long Read Sequencing

Felix Schlesinger et al., Cold Spring Harbor Laboratory

Genomics Core Support Model at the National Cancer Institute

Michael W. Smith et al., SAIC-Frederick, National Cancer Institute at Frederick

PACIFIC BIOSCIENCES® SCIENTIFIC POSTERS

De Novo Hybrid Assembly of Bacterial Genomes

Ali Bashir et al., Pacific Biosciences, Inc.

Viral Informatics Using Single Molecule, Real-Time Sequencing

Michael Brown et al., Pacific Biosciences, Inc.

Data Model, Automatic Analysis, Workflow Management and an Open Source Approach for Sequencing Analytics

Jason Chin et al., Pacific Biosciences, Inc.

Direct Sequencing and Identification of Damaged DNA Bases

Tyson Clark et al., Pacific Biosciences, Inc.

Utilizing Single Molecule Accuracy

John Eid et al., Pacific Biosciences, Inc.

A Comparison of De Novo Assembly Tools Utilizing Long Read Sequencing Data

Lawrence Hon et al., Pacific Biosciences, Inc.

Pacific Biosciences® SMRT® Technology Enables Sequencing of “hard-to-target” Regions using Long Inserts Captured by SureSelect® Target Capture Method

Kathryn Keho et al., Pacific Biosciences, Inc.

Harnessing Kinetic Information in Single Molecule, Real-Time Sequencing

Jonas Korlach et al., Pacific Biosciences, Inc.

Full Length Human cDNA Sequencing on the PacBio® RS

Lawrence Lee et al., Pacific Biosciences, Inc.

Performance of SMRT® Sequencing in the Detection of Minor Variants and Viral Haplotypes

Ellen Paxinos et al., Pacific Biosciences, Inc.

Sequencing and De Novo Assembly of the 17q21.31 Disease-associated Region using Long Reads Generated by Pacific Biosciences® SMRT® Sequencing Technology

Swati Ranade et al., Pacific Biosciences, Inc.

Emerging SMRT® Sequencing Technologies Facilitating Extended Readlength

Robert Sebra et al., Pacific Biosciences, Inc.

Optimizing Barcoding Solutions for Single Molecule, Real-Time Sequencing Using the PacBio® RS for High-Fidelity Targeted Capture

Kevin Travers et al., Pacific Biosciences, Inc.

Counting the Tricky PolyA Tail: New Applications for Single Molecule, Real-Time (SMRT®) DNA Sequencing

Jason Underwood et al., Pacific Biosciences, Inc.

PACIFIC BIOSCIENCES® WORKSHOP

Friday, February 17, 12:15 p.m. - 2:15 p.m.
Palms Ballroom

SPEAKERS INCLUDE:

Adam Phillippy
Battelle National Biodefense Institute

Erich Jarvis
Duke University Medical Center

Mark DePristo
Broad Institute of MIT and Harvard

Paul Hagerman
University of California, Davis

Matt Waldor
Harvard Medical School and Brigham and Women's Hospital